R: A Language and Environment for Statistical Computing

Reference Index

The R Core Team

Version 4.3.2 Patched (2023-11-21)
I

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Part I
Chapter 1

The base package

---

**base-package**  
*The R Base Package*

---

**Description**

Base R functions

**Details**

This package contains the basic functions which let R function as a language: arithmetic, input/output, basic programming support, etc. Its contents are available through inheritance from any environment.

For a complete list of functions, use `library(help = "base")`.

---

**.bincode**  
*Bin a Numeric Vector*

---

**Description**

Bin a numeric vector and return integer codes for the binning.

**Usage**

```r
.bincode(x, breaks, right = TRUE, include.lowest = FALSE)
```

**Arguments**

- `x`: a numeric vector which is to be converted to integer codes by binning.
- `breaks`: a numeric vector of two or more cut points, sorted in increasing order.
- `right`: logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
- `include.lowest`: logical, indicating if an 'x[i]' equal to the lowest (or highest, for `right = FALSE`) 'breaks' value should be included in the first (or last) bin.
Details

This is a ‘barebones’ version of `cut.default(labels = FALSE)` intended for use in other functions which have checked the arguments passed. (Note the different order of the arguments they have in common.)

Unlike `cut`, the breaks do not need to be unique. An input can only fall into a zero-length interval if it is closed at both ends, so only if `include.lowest = TRUE` and it is the first (or last for `right = FALSE`) interval.

Value

An integer vector of the same length as `x` indicating which bin each element falls into (the leftmost bin being bin 1). NaN and NA elements of `x` are mapped to NA codes, as are values outside range of breaks.

See Also

cut, tabulate

Examples

```r
## An example with non-unique breaks:
x <- c(0, 0.01, 0.5, 0.99, 1)
b <- c(0, 0, 1, 1)
.bincode(x, b, TRUE)
.bincode(x, b, FALSE)
.bincode(x, b, TRUE, TRUE)
.bincode(x, b, FALSE, TRUE)
```

.Device

Lists of Open/Active Graphics Devices

Description

A pairlist of the names of open graphics devices is stored in `.Devices`. The name of the active device (see `dev.cur`) is stored in `.Device`. Both are symbols and so appear in the base namespace.

Value

`.Device` is a length-one character vector.

`.Devices` is a pairlist of length-one character vectors. The first entry is always “null device”, and there are as many entries as the maximal number of graphics devices which have been simultaneously active. If a device has been removed, its entry will be “” until the device number is reused.

Devices may add attributes to the character vector: for example devices which write to a file may record its path in attribute “filepath”.

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Devices may add attributes to the character vector: for example devices which write to a file may record its path in attribute “filepath”.
Description

`.Machine` is a variable holding information on the numerical characteristics of the machine \( R \) is running on, such as the largest double or integer and the machine’s precision.

Usage

`.Machine`

Details

The algorithm is based on Cody’s (1988) subroutine MACHAR. As all current implementations of \( R \) use 32-bit integers and use IEC 60559 floating-point (double precision) arithmetic, the “integer” and “double” related values are the same for almost all \( R \) builds.

Note that on most platforms smaller positive values than `.Machine$double.xmin` can occur. On a typical \( R \) platform the smallest positive double is about 5e-324.

Value

A list with components

- **double.ep** the smallest positive floating-point number \( x \) such that \( 1 + x \neq 1 \). It equals `double.base ^ ulp.digits` if either `double.base` is 2 or `double.rounding` is 0; otherwise, it is `(double.base ^ double.ulp.digits) / 2`. Normally `2.220446e-16`.

- **double.neg.ep** a small positive floating-point number \( x \) such that \( 1 - x \neq 1 \). It equals `double.base ^ double.neg.ulp.digits` if `double.base` is 2 or `double.rounding` is 0; otherwise, it is `(double.base ^ double.neg.ulp.digits) / 2`. Normally `1.110223e-16`. As `double.neg.ulp.digits` is bounded below by `-(double.digits + 3)`, `double.neg.ep` may not be the smallest number that can alter 1 by subtraction.

- **double.xmin** the smallest non-zero normalized floating-point number, a power of the radix, i.e., `double.base ^ double.min.exp`. Normally `2.225074e-308`.

- **double.xmax** the largest normalized floating-point number. Typically, it is equal to `(1 - double.neg.ep) * double.base ^ double.max.exp`, but on some machines it is only the second or third largest such number, being too small by 1 or 2 units in the last digit of the significand. Normally `1.797693e+308`. Note that larger unnormalized numbers can occur.

- **double.base** the radix for the floating-point representation: normally 2.

- **double.digits** the number of base digits in the floating-point significand: normally 53.

- **double.rounding** the rounding action, one of
  0 if floating-point addition chops;
  1 if floating-point addition rounds, but not in the IEEE style;
  2 if floating-point addition rounds in the IEEE style;
3 if floating-point addition chops, and there is partial underflow;
4 if floating-point addition rounds, but not in the IEEE style, and there is partial underflow;
5 if floating-point addition rounds in the IEEE style, and there is partial underflow.
Normally 5.

**double.guard** the number of guard digits for multiplication with truncating arithmetic. It is 1 if floating-point arithmetic truncates and more than double digits base
double.base digits participate in the post-normalization shift of the floating-point significand in multiplication, and 0 otherwise.
Normally 0.

**double.ulp.digits** the largest negative integer i such that 1 + double.base ^ i != 1, except that it is bounded below by -(double.digits + 3). Normally -52.

**double.neg.ulp.digits** the largest negative integer i such that 1 - double.base ^ i != 1, except that it is bounded below by -(double.digits + 3). Normally -53.

**double.exponent** the number of bits (decimal places if double.base is 10) reserved for the representation of the exponent (including the bias or sign) of a floating-point number. Normally 11.

**double.min.exp** the largest in magnitude negative integer i such that double.base ^ i is positive and normalized. Normally -1022.

**double.max.exp** the smallest positive power of double.base that overflows. Normally 1024.

**integer.max** the largest integer which can be represented. Always \(2^{31} - 1 = 2147483647\).

**sizeof.long** the number of bytes in a C long type: 4 or 8 (most 64-bit systems, but not Windows).

**sizeof.longlong** the number of bytes in a C long long type. Will be zero if there is no such type, otherwise usually 8.

**sizeof.longdouble** the number of bytes in a C long double type. Will be zero if there is no such type (or its use was disabled when R was built), otherwise possibly 12 (most 32-bit builds), 16 (most 64-bit builds) or 8 (CPUs such as ARM where for most compilers long double is identical to double).

**sizeof.pointer** the number of bytes in the C SEXP type. Will be 4 on 32-bit builds and 8 on 64-bit builds of R.

**sizeof.time_t** the number of bytes in the C time_t type: a 64-bit time_t (value 8) is much preferred these days. Note that this is the type used by code in R itself, not necessarily the system type if R was configured with '--with-internal-tzcode' as also used on Windows.

**longdouble.eps, longdouble.neg.eps, longdouble.digits, ...** introduced in R 4.0.0. When capabilities("long.double") is true, there are 10 such "longdouble.<kind>" values, specifying the long double property corresponding to its "double.*" counterpart. See also 'Note'.

**Note**
In the (typical) case where capabilities("long.double") is true, R uses the long double C type in quite a few places internally for accumulators in e.g. sum, reading non-integer numeric constants
into (binary) double precision numbers, or arithmetic such as \( x \%\% y \); also, long double can be read by \texttt{readBin}.

For this reason, in that case, \texttt{.Machine} contains ten further components, longdouble.eps, *.neg.eps, *.digits, *.rounding, *.guard, *.ulp.digits, *.neg.ulp.digits, *.exponent, *.min.exp, and *.max.exp, computed entirely analogously to their double.* counterparts, see there.

\texttt{sizeof.longdouble} only tells you the amount of storage allocated for a long double. Often what is stored is the 80-bit extended double type of IEC 60559, padded to the double alignment used on the platform — this seems to be the case for the common \texttt{R} platforms using ix86 and x86_64 chips. There are other implementations of long double, usually in software for example on Sparc Solaris and AIX.

Note that it is legal for a platform to have a long double \texttt{C} type which is identical to the double type — this happens on ARM cpus. In that case \texttt{capabilities("long.double")} will be false but on versions of \texttt{R} prior to 4.0.4, \texttt{.Machine} may contain "longdouble.<kind>" elements.

**Source**

Uses a C translation of Fortran code in the reference, modified by the R Core Team to defeat over-optimization in modern compilers.

**References**


**See Also**

\texttt{.Platform} for details of the platform.

**Examples**

```r
.Machine
## or for a neat printout
noquote(unlist(format(.Machine)))
```

---

**Description**

\texttt{.Platform} is a list with some details of the platform under which \texttt{R} was built. This provides means to write OS-portable \texttt{R} code.

**Usage**

\texttt{.Platform}
Value

A list with at least the following components:

- **OS.type**: character string, giving the Operating System (family) of the computer. One of "unix" or "windows".
- **file.sep**: character string, giving the file separator used on your platform: "/" on both Unix-alikes and Windows (but not on the former port to Classic Mac OS).
- **dynlib.ext**: character string, giving the file name extension of dynamically loadable libraries, e.g., ".dll" on Windows and ".so" or ".sl" on Unix-alikes. (Note for macOS users: these are shared objects as loaded by `dyn.load` and not dylibs: see `dyn.load`.)
- **GUI**: character string, giving the type of GUI in use, or "unknown" if no GUI can be assumed. Possible values are for Unix-alikes the values given via the `-g` command-line flag ("X11", "Tk"), "AQUA" (running under R.app on macOS), "RGui" and "RTerm" (Windows) and perhaps others under alternative front-ends or embedded R.
- **endianness**: character string, "big" or "little", giving the ‘endianness’ of the processor in use. This is relevant when it is necessary to know the order to read/write bytes of e.g. an integer or double from/to a connection: see `readBin`.
- **pkgType**: character string, the preferred setting for `options("pkgType")`. Values "source", "mac.binary" and "win.binary" are currently in use. This should **not** be used to identify the OS.
- **path.sep**: character string, giving the path separator, used on your platform, e.g., ";" on Unix-alikes and ";" on Windows. Used to separate paths in environment variables such as `PATH` and `TEXINPUTS`.
- **r_arch**: character string, possibly "". The name of an architecture-specific directory used in this build of R.

AQUA

`.Platform$GUI` is set to "AQUA" under the macOS GUI, R.app. This has a number of consequences:

- ‘/usr/local/bin’ is **appended** to the `PATH` environment variable.
- the default graphics device is set to `quartz`.
- selects native (rather than Tk) widgets for the `graphics = TRUE` options of `menu` and `select.list`.
- HTML help is displayed in the internal browser.
- the spreadsheet-like data editor/viewer uses a Quartz version rather than the X11 one.

See Also

`R.version` and `Sys.info` give more details about the OS. In particular, `R.version$platform` is the canonical name of the platform under which R was compiled. `osVersion` may give more details about the platform R is running on.

`.Machine` for details of the arithmetic used, and `system` for invoking platform-specific system commands.

`capabilities` and `extSoftVersion` (and links there) for availability of capabilities partly external to R but used from R functions.
Abbreviate Strings

Description

Abbreviate strings to at least minlength characters, such that they remain unique (if they were), unless strict = TRUE.

Usage

abbreviate(names.arg, minlength = 4, use.classes = TRUE, dot = FALSE, strict = FALSE, method = c("left.kept", "both.sides"), named = TRUE)

Arguments

names.arg a character vector of names to be abbreviated, or an object to be coerced to a character vector by as.character.

minlength the minimum length of the abbreviations.

use.classes logical: should lowercase characters be removed first?

dot logical: should a dot ("." ) be appended?

strict logical: should minlength be observed strictly? Note that setting strict = TRUE may return non-unique strings.

method a character string specifying the method used with default "left.kept", see 'Details' below. Partial matches allowed.

named logical: should names (with original vector) be returned.

Details

The default algorithm (method = "left.kept") used is similar to that of S. For a single string it works as follows. First spaces at the ends of the string are stripped. Then (if necessary) any other spaces are stripped. Next, lower case vowels are removed followed by lower case consonants. Finally if the abbreviation is still longer than minlength upper case letters and symbols are stripped.

Characters are always stripped from the end of the strings first. If an element of names.arg contains more than one word (words are separated by spaces) then at least one letter from each word will be retained.

Missing (NA) values are unaltered.

If use.classes is FALSE then the only distinction is to be between letters and space.
Value

A character vector containing abbreviations for the character strings in its first argument. Duplicates in the original names.arg will be given identical abbreviations. If any non-duplicated elements have the same minlength abbreviations then, if method = "both.sides" the basic internal abbreviate() algorithm is applied to the characterwise reversed strings; if there are still duplicated abbreviations and if strict = FALSE as by default, minlength is incremented by one and new abbreviations are found for those elements only. This process is repeated until all unique elements of names.arg have unique abbreviations.

If names is true, the character version of names.arg is attached to the returned value as a names attribute: no other attributes are retained.

If a input element contains non-ASCII characters, the corresponding value will be in UTF-8 and marked as such (see Encoding).

Warning

If use.classes is true (the default), this is really only suitable for English, and prior to R 3.3.0 did not work correctly with non-ASCII characters in multibyte locales. It will warn if used with non-ASCII characters (and required to reduce the length). It is unlikely to work well with inputs not in the Unicode Basic Multilingual Plane nor on (rare) platforms where wide characters are not encoded in Unicode.

As from R 3.3.0 the concept of ‘vowel’ is extended from English vowels by including characters which are accented versions of lower-case English vowels (including ‘o with stroke’). Of course, there are languages (even Western European languages such as Welsh) with other vowels.

See Also

substr.

Examples

x <- c("abcd", "efgh", "abce")
abbreviate(x, 2)
abbreviate(x, 2, strict = TRUE) # >> 1st and 3rd are == "ab"

(st.abb <- abbreviate(state.name, 2))
stopifnot(identical(unname(st.abb),
               abbreviate(state.name, 2, named=FALSE)))
table(nchar(st.abb)) # out of 50, 3 need 4 letters :
as <- abbreviate(state.name, 3, strict = TRUE)
as[which(as == "Mss")]

## and without distinguishing vowels:
st.abb2 <- abbreviate(state.name, 2, FALSE)
cbind(st.abb, st.abb2)[st.abb2 != st.abb, ]

## method = "both.sides" helps: no 4-letters, and only 4 3-letters:
st.ab2 <- abbreviate(state.name, 2, method = "both")
table(nchar(st.ab2))
## Compare the two methods:
cbind(st.abb, st.ab2)
agrep | Approximate String Matching (Fuzzy Matching)

Description

Searches for approximate matches to pattern (the first argument) within each element of the string x (the second argument) using the generalized Levenshtein edit distance (the minimal possibly weighted number of insertions, deletions and substitutions needed to transform one string into another).

Usage

agrep(pattern, x, max.distance = 0.1, costs = NULL,
       ignore.case = FALSE, value = FALSE, fixed = TRUE,
       useBytes = FALSE)

agrepl(pattern, x, max.distance = 0.1, costs = NULL,
       ignore.case = FALSE, fixed = TRUE, useBytes = FALSE)

Arguments

pattern | a non-empty character string to be matched. For fixed = FALSE this should contain an extended regular expression. Coerced by as.character to a string if possible.

x | character vector where matches are sought. Coerced by as.character to a character vector if possible.

max.distance | Maximum distance allowed for a match. Expressed either as integer, or as a fraction of the pattern length times the maximal transformation cost (will be replaced by the smallest integer not less than the corresponding fraction), or a list with possible components
cost: maximum number/fraction of match cost (generalized Levenshtein distance)
all: maximal number/fraction of all transformations (insertions, deletions and substitutions)
insertions: maximum number/fraction of insertions
deletions: maximum number/fraction of deletions
substitutions: maximum number/fraction of substitutions

If cost is not given, all defaults to 10%, and the other transformation number bounds default to all. The component names can be abbreviated.

costs | a numeric vector or list with names partially matching ‘insertions’, ‘deletions’ and ‘substitutions’ giving the respective costs for computing the generalized Levenshtein distance, or NULL (default) indicating using unit cost for all three possible transformations. Coerced to integer via as.integer if possible.

ignore.case | if FALSE, the pattern matching is case sensitive and if TRUE, case is ignored during matching.

value | if FALSE, a vector containing the (integer) indices of the matches determined is returned and if TRUE, a vector containing the matching elements themselves is returned.
fixed: logical. If TRUE (default), the pattern is matched literally (as is). Otherwise, it is matched as a regular expression.

useBytes: logical. In a multibyte locale, should the comparison be character-by-character (the default) or byte-by-byte.

Details

The Levenshtein edit distance is used as measure of approximateness: it is the (possibly cost-weighted) total number of insertions, deletions and substitutions required to transform one string into another.

This uses the `tre` code by Ville Laurikari (https://github.com/laurikari/tre), which supports MBCS character matching.

The main effect of `useBytes` is to avoid errors/warnings about invalid inputs and spurious matches in multibyte locales. It inhibits the conversion of inputs with marked encodings, and is forced if any input is found which is marked as "bytes" (see Encoding).

Value

`agrep` returns a vector giving the indices of the elements that yielded a match, or, if `value` is TRUE, the matched elements (after coercion, preserving names but no other attributes).

`agrepl` returns a logical vector.

Note

Since someone who read the description carelessly even filed a bug report on it, do note that this matches substrings of each element of `x` (just as `grep` does) and not whole elements. See also `adist` in package `utils`, which optionally returns the offsets of the matched substrings.

Author(s)

Original version in R < 2.10.0 by David Meyer. Current version by Brian Ripley and Kurt Hornik.

See Also

`grep`, `adist`. A different interface to approximate string matching is provided by `aregexec()`.

Examples

agrep("lasy", "1 lazy 2")
agrep("lasy", c("1 lazy 2", "1 lasy 2"), max.distance = list(sub = 0))
agrep("lasy", c("1 lazy", "1", "1 LAZY"), max.distance = 2)
agrep("lasy", c("1 lazy", "1", "1 LAZY"), max.distance = 2, value = TRUE)
agrep("lasy", c("1 lazy", "1", "1 LAZY"), max.distance = 2, ignore.case = TRUE)
Description

Given a set of logical vectors, are all of the values true?

Usage

\[ \text{all}(\ldots, \text{na.rm} = \text{FALSE}) \]

Arguments

\[ \ldots \]
zero or more logical vectors. Other objects of zero length are ignored, and the rest are coerced to logical ignoring any class.

\[ \text{na.rm} \]
logical. If true NA values are removed before the result is computed.

Details

This is a generic function: methods can be defined for it directly or via the \texttt{Summary} group generic. For this to work properly, the arguments \ldots should be unnamed, and dispatch is on the first argument.

Coercion of types other than integer (raw, double, complex, character, list) gives a warning as this is often unintentional.

This is a \texttt{primitive} function.

Value

The value is a logical vector of length one.

Let \( x \) denote the concatenation of all the logical vectors in \( \ldots \) (after coercion), after removing NAs if requested by \( \text{na.rm} = \text{TRUE} \).

The value returned is \texttt{TRUE} if all of the values in \( x \) are \texttt{TRUE} (including if there are no values), and \texttt{FALSE} if at least one of the values in \( x \) is \texttt{FALSE}. Otherwise the value is \texttt{NA} (which can only occur if \( \text{na.rm} = \text{FALSE} \) and \( \ldots \) contains no \texttt{FALSE} values and at least one \texttt{NA} value).

S4 methods

This is part of the S4 \texttt{Summary} group generic. Methods for it must use the signature \( x, \ldots, \text{na.rm} \).

Note

That \[ \text{all}(\text{logical}(\emptyset)) \] is true is a useful convention: it ensures that

\[ \text{all}(\text{all}(x), \text{all}(y)) = \text{all}(x, y) \]

even if \( x \) has length zero.

References

all.equal

See Also

equivalent, the 'complement' of all, and stopifnot(*) which is an all(*) 'insurance'.

Examples

range(x <- sort(round(stats::rnorm(10) - 1.2, 1)))
if(all(x < 0)) cat("all x values are negative\n")

all(logical(0)) # true, as all zero of the elements are true.

Description

all.equal(x, y) is a utility to compare R objects x and y testing 'near equality'. If they are
different, comparison is still made to some extent, and a report of the differences is returned. Do not
use all.equal directly in if expressions—either use isTRUE(all.equal(....)) or identical
if appropriate.

Usage

all.equal(target, current, ...)

## S3 method for class 'numeric'
all.equal(target, current, 
  tolerance = sqrt(.Machine$double.eps), scale = NULL, 
  countEQ = FALSE, 
  formatFUN = function(err, what) format(err), 
  ..., check.attributes = TRUE, giveErr = FALSE)

## S3 method for class 'list'
all.equal(target, current, ..., 
  check.attributes = TRUE, use.names = TRUE)

## S3 method for class 'environment'
all.equal(target, current, all.names = TRUE, 
  evaluate = TRUE, ...)

## S3 method for class 'function'
all.equal(target, current, check.environment=TRUE, ...)

## S3 method for class 'POSIXt'
all.equal(target, current, ..., tolerance = 1e-3, scale, 
  check.tzone = TRUE)

attr.all.equal(target, current, ..., 
  check.attributes = TRUE, check.names = TRUE)
all.equal

Arguments

target  R object.
current other R object, to be compared with target.

... further arguments for different methods, notably the following two, for numerical comparison:
tolerance numeric ≥ 0. Differences smaller than tolerance are not reported. The default value is close to 1.5e-8.
scale NULL or numeric > 0, typically of length 1 or length(target). See ‘Details’.
countEQ logical indicating if the target == current cases should be counted when computing the mean (absolute or relative) differences. The default, FALSE may seem misleading in cases where target and current only differ in a few places; see the extensive example.

formatFUN a function of two arguments, err, the relative, absolute or scaled error, and what, a character string indicating the kind of error; may be used, e.g., to format relative and absolute errors differently.

check.attributes logical indicating if the attributes of target and current (other than the names) should be compared.
giveErr logical indicating if the result should contain the numerical error as an "err" attribute.
use.names logical indicating if list comparison should report differing components by name (if matching) instead of integer index. Note that this comes after ... and so must be specified by its full name.
all.names logical passed to ls indicating if “hidden” objects should also be considered in the environments.
evaluate for the environment method: logical indicating if “promises should be forced”, i.e., typically formal function arguments be evaluated for comparison. If false, only the names of the objects in the two environments are checked for equality.

check.environment logical requiring that the environment()s of functions should be compared, too. You may need to set check.environment=FALSE in unexpected cases, such as when comparing two nls() fits.

check.tzone logical indicating if the “tzone” attributes of target and current should be compared.

check.names logical indicating if the names(.) of target and current should be compared.

Details

all.equal is a generic function, dispatching methods on the target argument. To see the available methods, use methods("all.equal"), but note that the default method also does some dispatching, e.g. using the raw method for logical targets.

Remember that arguments which follow ... must be specified by (unabbreviated) name. It is inadvisable to pass unnamed arguments in ... as these will match different arguments in different methods.

Numerical comparisons for scale = NULL (the default) are typically on a relative difference scale unless the target values are close to zero or infinite. Specifically, the scale is computed as the mean
absolute value of target. If this scale is finite and exceeds tolerance, differences are expressed relative to it; otherwise, absolute differences are used. Note that this scale and all further steps are computed only for those vector elements where target is not NA and differs from current. If countEQ is true, the equal and NA cases are counted in determining the “sample” size.

If scale is numeric (and positive), absolute comparisons are made after scaling (dividing) by scale. Note that if all of scale is close to 1 (specifically, within 1e-7), the difference is still reported as being on an absolute scale.

For complex target, the modulus (Mod) of the difference is used: all.equal.numeric is called so arguments tolerance and scale are available.

The list method compares components of target and current recursively, passing all other arguments, as long as both are “list-like”, i.e., fulfill either is.vector or is.list.

The environment method works via the list method, and is also used for reference classes (unless a specific all.equal method is defined).

The method for date-time objects uses all.equal.numeric to compare times (in "POSIXct" representation) with a default tolerance of 0.001 seconds, ignoring scale. A time zone mismatch between target and current is reported unless check.tzone = FALSE.

attr.all.equal is used for comparing attributes, returning NULL or a character vector.

Value

Either TRUE (NULL for attr.all.equal) or a vector of mode "character" describing the differences between target and current.

References


See Also

identical, isTRUE, ==, and all for exact equality testing.

Examples

all.equal(pi, 355/113)
# not precise enough (default tol) > relative error

quarts <- 1/4 + 1:10 # exact
d45 <- pi*quarts ; one <- rep(1, 10)
tan(d45) == one # mostly FALSE, as typically exact; embarrassingly,
tanpi(quarts) == one # (is always FALSE (Fedora 34; gcc 11.2.1))
stopifnot(all.equal(tan(d45), one)) # TRUE, but not if we are picky:
all.equal(tan(d45), one, tolerance = 0) # to see difference
all.equal(tan(d45), one, tolerance = 0, scale = 1)# "absolute diff..
all.equal(tan(d45), one, tolerance = 0, scale = 1+(-2:2)/1e9) # "absolute"
all.equal(tan(d45), one, tolerance = 0, scale = 1+(-2:2)/1e6) # "scaled"

## advanced: equality of environments
ae <- all.equal(as.environment("package:stats"),
asNamespace("stats"))
stopifnot(is.character(ae), length(ae) > 10,
## were incorrectly "considered equal" in R <= 3.1.1
all.equal(asNamespace("stats"), asNamespace("stats")))
## A situation where 'countEQ = TRUE' makes sense:
x1 <- x2 <- (1:100)/10; x2[2] <- 1.1*x1[2]
## 99 out of 100 pairs (x1[i], x2[i]) are equal:
plot(x1,x2, main = "all.equal.numeric() -- not counting equal parts")
all.equal(x1,x2) ## "Mean relative difference: 0.1"
mtext(paste("all.equal(x1,x2) ", all.equal(x1,x2)), line = -2)
##' extract the 'Mean relative difference' as number:
all.eqNum <- function(...) as.numeric(sub(".*:", '', all.equal(...)))
set.seed(17)
## When x2 is jittered, typically all pairs (x1[i],x2[i]) do differ:
summary(r <- replicate(100, all.eqNum(x1, x2*(1+rnorm(x1)*1e-7))))
mtext(paste("mean(all.equal(x1, x2*(1 + eps_k))) {100 x} Mean rel.diff.=",
  signif(mean(r), 3)), line = -4, adj=0)
## With argument countEQ=TRUE, get "the same" (w/o need for jittering):
mtext(paste("all.equal(x1,x2, countEQ=TRUE) :",
  signif(all.eqNum(x1,x2, countEQ=TRUE), 3)), line= -6, col=2)

## Using giveErr=TRUE:
x1. <- x1 * (1+ 1e-9*rnorm(x1))
str(all.equal(x1, x1., giveErr=TRUE))
## logi TRUE
## - attr(*, "err")= num 8.66e-10
## - attr(*, "what")= chr "relative"

## Used with stopifnot(), still *showing* diff:
all.equalShow <- function (...) {
  r <- all.equal(..., giveErr=TRUE)
  cat(attr(r,"what"), "err:", attr(r,"err"), "\n")
c(r) # can drop attributes, as not used anymore
}
# checks, showing error in any case:
stopifnot(all.equalShow(x1, x1.)) # -> relative err: 8.66002e-10
tryCatch(error=identity, stopifnot(all.equalShow(x1, 2*x1))) -> eAe
cat(eAMsg <- conditionMessage(eAe), "\n")
stopifnot(inherits(eAe, "error"), # stopifnot() giving smart msg:
  grep("are not equal", eAMsg, fixed=TRUE))

## comparison of date-time objects
now <- Sys.time()
stopifnot( all.equal(now, now + 1e-4) # TRUE (default tolerance = 0.001 seconds) )
all.equal(now, now + 0.2)
all.equal(now, as.POSIXlt(now, "UTC"))
stopifnot( all.equal(now, as.POSIXlt(now, "UTC"), check.tzone = FALSE) # TRUE )

all.names

## Find All Names in an Expression

**Description**

Return a character vector containing all the names which occur in an expression or call.
Usage

all.names(expr, functions = TRUE, max.names = -1L, unique = FALSE)

all.vars(expr, functions = FALSE, max.names = -1L, unique = TRUE)

Arguments

expr an expression or call from which the names are to be extracted.
functions a logical value indicating whether function names should be included in the result.
max.names the maximum number of names to be returned. -1 indicates no limit (other than vector size limits).
unique a logical value which indicates whether duplicate names should be removed from the value.

Details

These functions differ only in the default values for their arguments.

Value

A character vector with the extracted names.

See Also

substitute to replace symbols with values in an expression.

Examples

all.names(expression(sin(x+y)))
all.names(quote(sin(x+y))) # or a call
all.vars(expression(sin(x+y)))
aperm

Details

This is a generic function: methods can be defined for it directly or via the Summary group generic. For this to work properly, the arguments ... should be unnamed, and dispatch is on the first argument.

Coercion of types other than integer (raw, double, complex, character, list) gives a warning as this is often unintentional.

This is a primitive function.

Value

The value is a logical vector of length one.

Let x denote the concatenation of all the logical vectors in ... (after coercion), after removing NAs if requested by na.rm = TRUE.

The value returned is TRUE if at least one of the values in x is TRUE, and FALSE if all of the values in x are FALSE (including if there are no values). Otherwise the value is NA (which can only occur if na.rm = FALSE and ... contains no TRUE values and at least one NA value).

S4 methods

This is part of the S4 Summary group generic. Methods for it must use the signature x, ..., na.rm.

References


See Also

all, the 'complement' of any.

Examples

range(x <- sort(round(stats::rnorm(10) - 1.2, 1)))
if(any(x < 0)) cat("x contains negative values\n")

aperm

Array Transposition

Description

Transpose an array by permuting its dimensions and optionally resizing it.

Usage

aperm(a, perm, ...)
## Default S3 method:
aperm(a, perm = NULL, resize = TRUE, ...)
## S3 method for class 'table'
aperm(a, perm = NULL, resize = TRUE, keep.class = TRUE, ...)
Arguments

\(a\) the array to be transposed.

\(perm\) the subscript permutation vector, usually a permutation of the integers \(1:n\), where \(n\) is the number of dimensions of \(a\). When \(a\) has named dimnames, it can be a character vector of length \(n\) giving a permutation of those names. The default (used whenever \(perm\) has zero length) is to reverse the order of the dimensions.

\(resize\) a flag indicating whether the vector should be resized as well as having its elements reordered (default TRUE).

\(keep.class\) logical indicating if the result should be of the same class as \(a\).

\(...\) potential further arguments of methods.

Value

A transposed version of array \(a\), with subscripts permuted as indicated by the array \(perm\). If \(resize\) is TRUE, the array is reshaped as well as having its elements permuted, the dimnames are also permuted; if \(resize = FALSE\) then the returned object has the same dimensions as \(a\), and the dimnames are dropped. In each case other attributes are copied from \(a\).

The function \(t\) provides a faster and more convenient way of transposing matrices.

Author(s)

Jonathan Rougier, \(<\text{J.C.Rougier@durham.ac.uk}>\) did the faster C implementation.

References


See Also

\(t\), to transpose matrices.

Examples

\[
\text{# interchange the first two subscripts on a 3-way array } x
\]
\[
x \leftarrow \text{array}(1:24, 2:4)
\]
\[
x_t \leftarrow \text{aperm}(x, c(2,1,3))
\]
\[
\text{stopifnot}(t(x_t[,,2]) == x[,,2],}
\]
\[
t(x_t[,,3]) == x[,,3],
\]
\[
t(x_t[,,4]) == x[,,4])
\]
\[
\text{UCB} \leftarrow \text{aperm(UCBAdmissions, c(2,1,3))}
\]
\[
\text{UCB[1,,]}
\]
\[
\text{summary(UCB) \# UCB is still a contingency table}
\]
**append**  

**Vector Merging**

**Description**

Add elements to a vector.

**Usage**

```r
append(x, values, after = length(x))
```

**Arguments**

- `x`: the vector the values are to be appended to.
- `values`: to be included in the modified vector.
- `after`: a subscript, after which the values are to be appended.

**Value**

A vector containing the values in `x` with the elements of `values` appended after the specified element of `x`.

**References**


**Examples**

```r
append(1:5, 0:1, after = 3)
```

**apply**  

**Apply Functions Over Array Margins**

**Description**

Returns a vector or array or list of values obtained by applying a function to margins of an array or matrix.

**Usage**

```r
apply(X, MARGIN, FUN, ..., simplify = TRUE)
```
apply

Arguments

- **X**: an array, including a matrix.
- **MARGIN**: a vector giving the subscripts which the function will be applied over. E.g., for a matrix 1 indicates rows, 2 indicates columns, c(1, 2) indicates rows and columns. Where X has named dimnames, it can be a character vector selecting dimension names.
- **FUN**: the function to be applied: see ‘Details’. In the case of functions like +, %*%, etc., the function name must be backquoted or quoted.
- **...**: optional arguments to FUN.
- **simplify**: a logical indicating whether results should be simplified if possible.

Details

If X is not an array but an object of a class with a non-null `dim` value (such as a data frame), apply attempts to coerce it to an array via `as.matrix` if it is two-dimensional (e.g., a data frame) or via `as.array`.

FUN is found by a call to `match.fun` and typically is either a function or a symbol (e.g., a backquoted name) or a character string specifying a function to be searched for from the environment of the call to apply.

Arguments in ... cannot have the same name as any of the other arguments, and care may be needed to avoid partial matching to MARGIN or FUN. In general-purpose code it is good practice to name the first three arguments if ... is passed through: this both avoids partial matching to MARGIN or FUN and ensures that a sensible error message is given if arguments named X, MARGIN or FUN are passed through ....

Value

If each call to FUN returns a vector of length n, and simplify is TRUE, then apply returns an array of dimension c(n, dim(X)[MARGIN]) if n > 1. If n equals 1, apply returns a vector if MARGIN has length 1 and an array of dimension dim(X)[MARGIN] otherwise. If n is 0, the result has length 0 but not necessarily the ‘correct’ dimension.

If the calls to FUN return vectors of different lengths, or if simplify is FALSE, apply returns a list of length prod(dim(X)[MARGIN]) with dim set to MARGIN if this has length greater than one.

In all cases the result is coerced by `as.vector` to one of the basic vector types before the dimensions are set, so that (for example) factor results will be coerced to a character array.

References


See Also

`lapply` and there, `simplify2array`; `tapply`, and convenience functions `sweep` and `aggregate`.

Examples

```r
## Compute row and column sums for a matrix:
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
dimnames(x)[[1]] <- letters[1:8]
aply(x, 2, mean, trim = .2)
```
col.sums <- apply(x, 2, sum)
row.sums <- apply(x, 1, sum)
rbind(cbind(x, Rtot = row.sums), Ctot = c(col.sums, sum(col.sums)))

stopifnot( apply(x, 2, is.vector))

## Sort the columns of a matrix
apply(x, 2, sort)

## keeping named dimnames
names(dimnames(x)) <- c("row", "col")
x3 <- array(x, dim = c(dim(x), 3),
   dimnames = c(dimnames(x), list(C = paste0("cop." , 1:3))))
identical(x, apply( x, 2, identity))
identical(x3, apply(x3, 2:3, identity))

## function with extra args:
cave <- function(x, c1, c2) c(mean(x[c1]), mean(x[c2]))
apply(x, 1, cave, c1 = "x1", c2 = c("x1", "x2"))

ma <- matrix(c(1:4, 1, 6:8), nrow = 2)
ma
apply(ma, 1, table) #--> a list of length 2
apply(ma, 1, stats::quantile) # 5 x n matrix with rownames
stopifnot(dim(ma) == dim(apply(ma, 1:2, sum)))

## Example with different lengths for each call
z <- array(1:24, dim = 2:4)
zseq <- apply(z, 1:2, function(x) seq_len(max(x)))
zseq # 2 x 3 matrix
typeof(zseq) # list
dim(zseq) # 2 3
zseq[1,]
apply(z, 3, function(x) seq_len(max(x))) # a list without a dim attribute

---

**args**

*Argument List of a Function*

**Description**

Displays the argument names and corresponding default values of a (non-primitive or primitive) function.

**Usage**

`args(name)`

**Arguments**

`name` a function (a primitive or a closure, i.e., “non-primitive”). If `name` is a character string then the function with that name is found and used.
Details

This function is mainly used interactively to print the argument list of a function. For programming, consider using `formals` instead.

Value

For a closure, a closure with identical formal argument list but an empty (NULL) body.

For a primitive (function), a closure with the documented usage and NULL body. Note that some primitives do not make use of named arguments and match by position rather than name.

NULL in case of a non-function.

References


See Also

`formals`, `help`; `str` also prints the argument list of a function.

Examples

```r
## "regular" (non-primitive) functions "print their arguments"
## (by returning another function with NULL body which you also see):
args(ls)
args(graphics::plot.default)
utils::str(ls) # (just "prints": does not show a NULL)

## You can also pass a string naming a function.
args("scan")
## ...but :: package specification doesn't work in this case.
tryCatch(args("graphics::plot.default"), error = print)

## As explained above, args() gives a function with empty body:
list(is.f = is.function(args(scan)), body = body(args(scan)))

## Primitive functions mostly behave like non-primitive functions.
args(c)
args("+")
## primitive functions without well-defined argument list return NULL:
args("if")
```

Arithmetic

### Arithmetic Operators

Description

These unary and binary operators perform arithmetic on numeric or complex vectors (or objects which can be coerced to them).
**Usage**

+ x  
- x  
x + y  
x - y  
x * y  
x / y  
x ^ y  
x %% y  
x %/% y

**Arguments**

x, y numeric or complex vectors or objects which can be coerced to such, or other objects for which methods have been written.

**Details**

The unary and binary arithmetic operators are generic functions: methods can be written for them individually or via the `Ops` group generic function. (See `Ops` for how dispatch is computed.)

If applied to arrays the result will be an array if this is sensible (for example it will not if the recycling rule has been invoked).

Logical vectors will be coerced to integer or numeric vectors, FALSE having value zero and TRUE having value one.

1 ^ y and y ^ 0 are 1, always. x ^ y should also give the proper limit result when either (numeric) argument is infinite (one of `Inf` or `-Inf`).

Objects such as arrays or time-series can be operated on this way provided they are conformable.

For double arguments, % can be subject to catastrophic loss of accuracy if x is much larger than y, and a warning is given if this is detected.

%% and x %/% y can be used for non-integer y, e.g. 1 %/% 0.2, but the results are subject to representation error and so may be platform-dependent. Because the IEC 60559 representation of 0.2 is a binary fraction slightly larger than 0.2, the answer to 1 %/% 0.2 should be 4 but most platforms give 5.

Users are sometimes surprised by the value returned, for example why (-8) ^ (1/3) is NaN. For double inputs, R makes use of IEC 60559 arithmetic on all platforms, together with the C system function `pow` for the ^ operator. The relevant standards define the result in many corner cases. In particular, the result in the example above is mandated by the C99 standard. On many Unix-alike systems the command `man pow` gives details of the values in a large number of corner cases.

Arithmetic on type double in R is supposed to be done in ‘round to nearest, ties to even’ mode, but this does depend on the compiler and FPU being set up correctly.

**Value**

Unary + and unary - return a numeric or complex vector. All attributes (including class) are preserved if there is no coercion: logical x is coerced to integer and names, dims and dimnames are preserved.

The binary operators return vectors containing the result of the element by element operations. If involving a zero-length vector the result has length zero. Otherwise, the elements of shorter vectors are recycled as necessary (with a warning when they are recycled only fractionally). The operators are + for addition, - for subtraction, * for multiplication, / for division and ^ for exponentiation.
%% indicates \( x \mod y \) ("x modulo y"), i.e., computes the 'remainder' \( r < x \mod y \), and \%/\% indicates integer division, where R uses "floored" integer division, i.e., \( q < x \mod y = \text{floor}(x/y) \), as promoted by Donald Knuth, see the Wikipedia page on 'Modulo operation', and hence \( \text{sign}(r) = \text{sign}(y) \). It is guaranteed that
\[
x = (x \mod y) + y \times (x \mod y)
\]
(up to rounding error)
unless \( y == 0 \) where the result of \( \% \) is \text{NA}\_\text{integer} or \text{NaN} (depending on the \text{typeof} of the arguments) or for some non-finite arguments, e.g., when the RHS of the identity above amounts to \text{Inf} - \text{Inf}.

If either argument is complex the result will be complex, otherwise if one or both arguments are numeric, the result will be numeric. If both arguments are of type integer, the type of the result of / and ^ is numeric and for the other operators it is integer (with overflow, which occurs at \( \pm(2^{31} - 1) \), returned as \text{NA}\_\text{integer} with a warning).

The rules for determining the attributes of the result are rather complicated. Most attributes are taken from the longer argument. Names will be copied from the first if it is the same length as the answer, otherwise from the second if that is. If the arguments are the same length, attributes will be copied from both, with those of the first argument taking precedence when the same attribute is present in both arguments. For time series, these operations are allowed only if the series are compatible, when the class and \text{tsp} attribute of whichever is a time series (the same, if both are) are used. For arrays (and an array result) the dimensions and dimnames are taken from first argument if it is an array, otherwise the second.

**S4 methods**

These operators are members of the S4 \texttt{Arith} group generic, and so methods can be written for them individually as well as for the group generic (or the \texttt{Ops} group generic), with arguments \( c(e_1, e_2) \) (with \( e_2 \) missing for a unary operator).

**Implementation limits**

R is dependent on OS services (and they on FPUs) for floating-point arithmetic. On all current R platforms IEC 60559 (also known as IEEE 754) arithmetic is used, but some things in those standards are optional. In particular, the support for denormal aka subnormal numbers (those outside the range given by \texttt{.Machine}) may differ between platforms and even between calculations on a single platform.

Another potential issue is signed zeroes: on IEC 60559 platforms there are two zeroes with internal representations differing by sign. Where possible R treats them as the same, but for example direct output from C code often does not do so and may output ‘-0.0’ (and on Windows whether it does so or not depends on the version of Windows). One place in R where the difference might be seen is in division by zero: \( 1/x \) is \text{Inf} or \text{-Inf} depending on the sign of zero \( x \). Another place is \text{identical}(0, -0, \text{num.eq} = \text{FALSE}).

**Note**

All logical operations involving a zero-length vector have a zero-length result.

The binary operators are sometimes called as functions as e.g. `\&` (\( x, y \)): see the description of how argument-matching is done in \texttt{Ops}.

\( ** \) is translated in the parser to `\^` , but this was undocumented for many years. It appears as an index entry in Becker et al (1988), pointing to the help for \texttt{Deprecated} but is not actually mentioned on that page. Even though it had been deprecated in S for 20 years, it was still accepted in R in 2008.
array

References


Also available at https://docs.oracle.com/cd/E19957-01/806-3568/ncg_goldberg.html.


See Also

sqrt for miscellaneous and Special for special mathematical functions.

Syntax for operator precedence.

** for matrix multiplication.

Examples

```R
x <- -1:12
x + 1
2 * x + 3
x %% 3 # is periodic 2 0 1 2 0 1 ...  
x %% -3 # (ditto) -1 0 -2 -1 0 -2 ...  
x %/% 5
x %% Inf # now is defined by limit (gave NaN in earlier versions of R)
```

array

Multi-way Arrays

Description

Creates or tests for arrays.

Usage

array(data = NA, dim = length(data), dimnames = NULL)  
as.array(x, ...)  
is.array(x)

Arguments

data a vector (including a list or expression vector) giving data to fill the array. Non-atomic classed objects are coerced by as.vector.

dim the dim attribute for the array to be created, that is an integer vector of length one or more giving the maximal indices in each dimension.
array

dimnames
either NULL or the names for the dimensions. This must be a list (or it will be ignored) with one component for each dimension, either NULL or a character vector of the length given by dim for that dimension. The list can be named, and the list names will be used as names for the dimensions. If the list is shorter than the number of dimensions, it is extended by NULLs to the length required.

x
an R object.

... additional arguments to be passed to or from methods.

Details

An array in R can have one, two or more dimensions. It is simply a vector which is stored with additional attributes giving the dimensions (attribute "dim") and optionally names for those dimensions (attribute "dimnames").

A two-dimensional array is the same thing as a matrix.

One-dimensional arrays often look like vectors, but may be handled differently by some functions: str does distinguish them in recent versions of R.

The "dim" attribute is an integer vector of length one or more containing non-negative values: the product of the values must match the length of the array.

The "dimnames" attribute is optional: if present it is a list with one component for each dimension, either NULL or a character vector of the length given by the element of the "dim" attribute for that dimension.

is.array is a primitive function.

For a list array, the print methods prints entries of length not one in the form ‘integer,7’ indicating the type and length.

Value

array returns an array with the extents specified in dim and naming information in dimnames. The values in data are taken to be those in the array with the leftmost subscript moving fastest. If there are too few elements in data to fill the array, then the elements in data are recycled. If data has length zero, NA of an appropriate type is used for atomic vectors (0 for raw vectors) and NULL for lists.

Unlike matrix, array does not currently remove any attributes left by as.vector from a classed list data, so can return a list array with a class attribute.

as.array is a generic function for coercing to arrays. The default method does so by attaching a dim attribute to it. It also attaches dimnames if x has names. The sole purpose of this is to make it possible to access the dim[<names>] attribute at a later time.

is.array returns TRUE or FALSE depending on whether its argument is an array (i.e., has a dim attribute of positive length) or not. It is generic: you can write methods to handle specific classes of objects, see InternalMethods.

Note

is.array is a primitive function.

References

array2DF

See Also
aperm, matrix, dim, dimnames.

Examples

dim(as.array(letters))
array(1:3, c(2,4)) # recycle 1:3 "2 2/3 times"
# [1,] [2,] [3,] [4,]
# [1,] 1 3 2 1
# [2,] 2 1 3 2

array2DF

Convert array to data frame

Description
array2DF converts an array, including list arrays commonly returned by tapply, into data frames for use in further analysis or plotting functions.

Usage
array2DF(x, responseName = "Value",
sep = "", base = list(LETTERS),
simplify = TRUE, allowLong = TRUE)

Arguments
x an array object.
responseName character string, used for creating column name(s) in the result, if required.
sep character string, used as separator when creating new names, if required.
base character vector, giving an initial set of names to create dimnames of x, if missing.
simplify logical, whether to attempt simplification of the result.
allowLong logical, specifying whether a long format data frame should be returned if x is a list array and all elements of x are unnamed atomic vectors. Ignored unless simplify = TRUE.

Details
The main use of array2DF is to convert an array, as typically returned by tapply, into a data frame. When simplify = FALSE, this is similar to as.data.frame.table, except that it works for list arrays as well as atomic arrays. Specifically, the resulting data frame has one row for each element of the array, with one column for each dimension of the array giving the corresponding dimnames. The contents of the array are placed in a column whose name is given by the responseName argument. The mode of this column is the same as that of x, usually an atomic vector or a list. If x does not have dimnames, they are automatically created using base and sep.

In the default case, when simplify = TRUE, some common cases are handled specially.
If all components of \( x \) are data frames with identical column names (with possibly different numbers of rows), they are \texttt{rbind}-ed to form the response. The additional columns giving \texttt{dimnames} are repeated according to the number of rows, and \texttt{responseName} is ignored in this case.

If all components of \( x \) are \textit{unnamed} atomic vectors and \texttt{allowLong = TRUE}, each component is treated as a single-column data frame with column name given by \texttt{responseName}, and processed as above.

In all other cases, an attempt to simplify is made by \texttt{simplify2array}. If this results in multiple unnamed columns, names are constructed using \texttt{responseName} and \texttt{sep}.

**Value**

A data frame with at least \( \text{length}(\text{dim}(x)) + 1 \) columns. The first \( \text{length}(\text{dim}(x)) \) columns each represent one dimension of \( x \) and gives the corresponding values of \texttt{dimnames}, which are implicitly created if necessary. The remaining columns contain the contents of \( x \), after attempted simplification if requested.

**See Also**

\texttt{tapply, as.data.frame.table, split, aggregate}.

**Examples**

```r
s1 <- with(ToothGrowth, 
  tapply(len, list(dose, supp), mean, simplify = TRUE))

s2 <- with(ToothGrowth, 
  tapply(len, list(dose, supp), mean, simplify = FALSE))

str(s1) # atomic array
str(s2) # list array

str(array2DF(s1, simplify = FALSE)) # Value column is vector
str(array2DF(s2, simplify = FALSE)) # Value column is list
str(array2DF(s2, simplify = TRUE)) # simplified to vector

### The remaining examples use the default 'simplify = TRUE'

## List array with list components: columns are lists (no simplification)
with(ToothGrowth, 
  tapply(len, list(dose, supp), 
  function(x) t.test(x)[c("p.value", "alternative")]) |>
  array2DF() |>
  str()

## List array with data frame components: columns are atomic (simplified)
with(ToothGrowth, 
  tapply(len, list(dose, supp), 
  function(x) with(t.test(x), data.frame(p.value, alternative))) |>
  array2DF() |>
  str()

## named vectors
with(ToothGrowth, 
  tapply(len, list(dose, supp),
```
functions to check if an object is a data frame, or coerce it if possible.

Usage

as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S3 method for class 'character'
as.data.frame(x, ...,
  stringsAsFactors = FALSE)

## S3 method for class 'list'
as.data.frame(x, row.names = NULL, optional = FALSE, ...,
  cut.names = FALSE, col.names = names(x), fix.empty.names = TRUE,
  check.names = !optional,
as.data.frame

## S3 method for class 'matrix'

as.data.frame(x, row.names = NULL, optional = FALSE,
make.names = TRUE, ...,
stringsAsFactors = FALSE)

as.data.frame.vector(x, row.names = NULL, optional = FALSE, ...
  nm = deparse1(substitute(x)))

is.data.frame(x)

Arguments

x
   any R object.
row.names
   NULL or a character vector giving the row names for the data frame. Missing
   values are not allowed.

optional
   logical. If TRUE, setting row names and converting column names (to syntac-
   tic names: see make.names) is optional. Note that all of R’s base package
   as.data.frame() methods use optional only for column names treatment, ba-
   sically with the meaning of data.frame(*, check.names = !optional). See
   also the make.names argument of the matrix method.

... additional arguments to be passed to or from methods.

stringsAsFactors
   logical: should the character vector be converted to a factor?
cut.names
   logical or integer: indicating if column names with more than 256 (or cut.names
   if that is numeric) characters should be shortened (and the last 6 characters re-
   placed by "...”).
col.names
   (optional) character vector of column names.
fix.empty.names
   logical indicating if empty column names, i.e., "" should be fixed up (in
   data.frame) or not.
check.names
   logical; passed to the data.frame() call.
make.names
   a logical, i.e., one of FALSE, NA, TRUE, indicating what should happen if the
   row names (of the matrix x) are invalid. If they are invalid, the default, TRUE,
   calls make.names(*, unique=TRUE); make.names=NA will use “automatic” row
   names and a FALSE value will signal an error for invalid row names.

nm
   a character string to be used as column name.

Details

as.data.frame is a generic function with many methods, and users and packages can supply fur-
ther methods. For classes that act as vectors, often a copy of as.data.frame.vector will work as
the method.

Since R 4.3.0, the default method will call as.data.frame.vector() for atomic (as by
is.atomic) non-NULL x.

Direct calls to as.data.frame.<class>() are still possible (base package!), for
12 atomic base classes, but will deprecated (already visibly by setting environment
variable _R_CHECK_AS_DATA_FRAME_EXPLICIT_METHOD_ to non-empty) where calling
as.data.frame.vector() instead is recommended.
If a list is supplied, each element is converted to a column in the data frame. Similarly, each column of a matrix is converted separately. This can be overridden if the object has a class which has a method for `as.data.frame`: two examples are matrices of class "model.matrix" (which are included as a single column) and list objects of class "POSIXlt" which are coerced to class "POSIXct".

Arrays can be converted to data frames. One-dimensional arrays are treated like vectors and two-dimensional arrays like matrices. Arrays with more than two dimensions are converted to matrices by ‘flattening’ all dimensions after the first and creating suitable column labels.

Character variables are converted to factor columns unless protected by `I`.

If a data frame is supplied, all classes preceding "data.frame" are stripped, and the row names are changed if that argument is supplied.

If `row.names = NULL`, row names are constructed from the names or dimnames of `x`, otherwise are the integer sequence starting at one. Few of the methods check for duplicated row names. Names are removed from vector columns unless `I`.

Value

`as.data.frame` returns a data frame, normally with all row names "" if optional = TRUE.

`is.data.frame` returns TRUE if its argument is a data frame (that is, has "data.frame" amongst its classes) and FALSE otherwise.

References


See Also

data.frame, `as.data.frame.table` for the table method (which has additional arguments if called directly).

---

**as.Date**

*Date Conversion Functions to and from Character*

**Description**

Functions to convert between character representations and objects of class "Date" representing calendar dates.

**Usage**

```r
as.Date(x, ...)  # S3 method for class 'character'
as.Date(x, format, tryformats = c("%Y-%m-%d", "%Y/%m/%d"),
        optional = FALSE, ...)  # S3 method for class 'numeric'
as.Date(x, origin, ...)  # S3 method for class 'POSIXct'
as.Date(x, tz = "UTC", ...)  # S3 method for class 'POSIXct'
```
## S3 method for class 'Date'
format(x, ...)

## S3 method for class 'Date'
as.character(x, ...)

### Arguments

- **x**: an object to be converted.
- **format**: character string. If not specified, it will try `tryFormats` one by one on the first non-NA element, and give an error if none works. Otherwise, the processing is via `strptime()` whose help page describes available conversion specifications.
- **tryFormats**: character vector of format strings to try if `format` is not specified.
- **optional**: logical indicating to return NA (instead of signalling an error) if the format guessing does not succeed.
- **origin**: a `Date` object, or something which can be coerced by `as.Date(origin, ...)` to such an object or `missing`. In that case, "1970-01-01" is used.
- **tz**: a time zone name.
- **...**: further arguments to be passed from or to other methods, including `format` for `as.character` and `as.Date` methods.

### Details

The usual vector re-cycling rules are applied to `x` and `format` so the answer will be of length that of the longer of the vectors.

Locale-specific conversions to and from character strings are used where appropriate and available. This affects the names of the days and months.

The `as.Date` methods accept character strings, factors, logical NA and objects of classes "POSIXlt" and "POSIXct". (The last is converted to days by ignoring the time after midnight in the representation of the time in specified time zone, default UTC.) Also objects of class "date" (from package `date`) and "dates" (from package `chron`). Character strings are processed as far as necessary for the format specified: any trailing characters are ignored.

`as.Date` will accept numeric data (the number of days since an epoch), since R 4.3.0 also when `origin` is not supplied.

The `format` and `as.character` methods ignore any fractional part of the date.

### Value

The `format` and `as.character` methods return a character vector representing the date. NA dates are returned as `NA_character_`.

The `as.Date` methods return an object of class "Date".

### Conversion from other Systems

Most systems record dates internally as the number of days since some origin, but this is fraught with problems, including

- Is the origin day 0 or day 1? As the ‘Examples’ show, Excel manages to use both choices for its two date systems.
• If the origin is far enough back, the designers may show their ignorance of calendar systems. For example, Excel’s designer thought 1900 was a leap year (claiming to copy the error from earlier DOS spreadsheets), and Matlab’s designer chose the non-existent date of ‘January 0, 0000’ (there is no such day), not specifying the calendar. (There is such a year in the ‘Gregorian’ calendar as used in ISO 8601:2004, but that does say that it is only to be used for years before 1582 with the agreement of the parties in information exchange.)

The only safe procedure is to check the other systems values for known dates: reports on the Internet (including R-help) are more often wrong than right.

Note

The default formats follow the rules of the ISO 8601 international standard which expresses a day as “2001-02-03”.

If the date string does not specify the date completely, the returned answer may be system-specific. The most common behaviour is to assume that a missing year, month or day is the current one. If it specifies a date incorrectly, reliable implementations will give an error and the date is reported as NA. Unfortunately some common implementations (such as ‘glibc’) are unreliable and guess at the intended meaning.

Years before 1CE (aka 1AD) will probably not be handled correctly.

References


See Also

Date for details of the date class; locales to query or set a locale.

Your system’s help pages on strftime and strptime to see how to specify their formats. Windows users will find no help page for strptime: code based on ‘glibc’ is used (with corrections), so all the format specifiers described here are supported, but with no alternative number representation nor era available in any locale.

Examples

```r
## locale-specific version of the date
format(Sys.Date(), "%a %b %d")

## read in date info in format 'dmmmyyyy'
## This will give NA(s) in some locales; setting the C locale
## as in the commented lines will overcome this on most systems.
## lct <- Sys.getlocale("LC_TIME"); Sys.setlocale("LC_TIME", "C")
x <- c("1jan1960", "2jan1960", "31mar1960", "30jul1960")
z <- as.Date(x, "%d%b%Y")
## Sys.setlocale("LC_TIME", lct)
# z

## read in date/time info in format 'm/d/y'
dates <- c("02/27/92", "02/27/92", "01/14/92", "02/28/92", "02/01/92")
as.Date(dates, "%m/%d/%y")

## date given as number of days since 1900-01-01 (a date in 1989)
```
as.Date(32768, origin = "1900-01-01")
## Excel is said to use 1900-01-01 as day 1 (Windows default) or
## 1904-01-01 as day 0 (Mac default), but this is complicated by Excel
## incorrectly treating 1900 as a leap year.
## So for dates (post-1901) from Windows Excel
as.Date(35981, origin = "1899-12-30") # 1998-07-05
## and Mac Excel
as.Date(34519, origin = "1904-01-01") # 1998-07-05
## (these values come from http://support.microsoft.com/kb/214330)
## Experiment shows that Matlab's origin is 719529 days before ours,
## (it takes the non-existent 0000-01-01 as day 1)
## so Matlab day 734373 can be imported as
as.Date(734373) - 719529 # 2010-08-23
## (value from

## Time zone effect
z <- ISOdate(2010, 04, 13, c(0,12)) # midnight and midday UTC
as.Date(z) # in UTC
## these time zone names are common
as.Date(z, tz = "NZ")
as.Date(z, tz = "HST") # Hawaii

---

### as.environment

**Coerce to an Environment Object**

**Description**

A generic function coercing an R object to an environment. A number or a character string is converted to the corresponding environment on the search path.

**Usage**

as.environment(x)

**Arguments**

x

an R object to convert. If it is already an environment, just return it. If it is a positive number, return the environment corresponding to that position on the search list. If it is -1, the environment it is called from. If it is a character string, match the string to the names on the search list.

If it is a list, the equivalent of `list2env(x, parent = emptyenv())` is returned. If `is.object(x)` is true and it has a class for which an as.environment method is found, that is used.

**Details**

This is a primitive generic function: you can write methods to handle specific classes of objects, see `InternalMethods`.

**Value**

The corresponding environment object.
as.function

Author(s)
John Chambers

See Also
environment for creation and manipulation, search; list2env.

Examples

as.environment(1) ## the global environment
identical(globalenv(), as.environment(1)) ## is TRUE
try( ## <<- stats need not be attached
    as.environment("package:stats"))
ee <- as.environment(list(a = "A", b = pi, ch = letters[1:8]))
ls(ee) # names of objects in ee
utils::ls.str(ee)

as.function

Convert Object to Function

Description
as.function is a generic function which is used to convert objects to functions.
as.function.default works on a list x, which should contain the concatenation of a formal argument list and an expression or an object of mode "call" which will become the function body. The function will be defined in a specified environment, by default that of the caller.

Usage

as.function(x, ...)

## Default S3 method:
as.function(x, envir = parent.frame(), ...)

Arguments

x object to convert, a list for the default method.
...
additional arguments, depending on object
envir environment in which the function should be defined

Value
The desired function.

Author(s)
Peter Dalgaard

See Also
function; alist which is handy for the construction of argument lists, etc.
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as.POSIX*

Examples
as.function(alist(a = , b = 2, a+b))
as.function(alist(a = , b = 2, a+b))(3)

as.POSIX*

Date-time Conversion Functions

Description
Functions to manipulate objects of classes "POSIXlt" and "POSIXct" representing calendar dates
and times.
Usage
as.POSIXct(x, tz = "", ...)
as.POSIXlt(x, tz = "", ...)
## S3 method for class 'character'
as.POSIXlt(x, tz = "", format,
tryFormats = c("%Y-%m-%d %H:%M:%OS",
"%Y/%m/%d %H:%M:%OS",
"%Y-%m-%d %H:%M",
"%Y/%m/%d %H:%M",
"%Y-%m-%d",
"%Y/%m/%d"),
optional = FALSE, ...)
## Default S3 method:
as.POSIXlt(x, tz = "",
optional = FALSE, ...)
## S3 method for class 'numeric'
as.POSIXlt(x, tz = "", origin, ...)
## S3 method for
as.POSIXct(x, tz
## S3 method for
as.POSIXlt(x, tz
## S3 method for
as.POSIXct(x, tz

class 'Date'
= "UTC", ...)
class 'Date'
= "UTC", ...)
class 'numeric'
= "", origin, ...)

## S3 method for class 'POSIXlt'
as.double(x, ...)
Arguments
x

R object to be converted.

tz

a character string. The time zone specification to be used for the conversion,
if one is required. System-specific (see time zones), but "" is the current time
zone, and "GMT" is UTC (Universal Time, Coordinated). Invalid values are most
commonly treated as UTC, on some platforms with a warning.

...

further arguments to be passed to or from other methods.


format character string giving a date-time format as used by `strptime`.

tryFormats character vector of format strings to try if format is not specified.

optional logical indicating to return NA (instead of signalling an error) if the format guessing does not succeed.

origin a date-time object, or something which can be coerced by `as.POSIXct(tz = "GMT")` to such an object. Optional since R 4.3.0, where the equivalent of "1970-01-01" is used.

Details

The `as.POSIX*` functions convert an object to one of the two classes used to represent date/times (calendar dates plus time to the nearest second). They can convert objects of the other class and of class "Date" to these classes. Dates without times are treated as being at midnight UTC.

They can also convert character strings of the formats "2001-02-03" and "2001/02/03" optionally followed by white space and a time in the format "14:52" or "14:52:03". (Formats such as "01/02/03" are ambiguous but can be converted via a format specification by `strptime`.) Fractions of seconds are allowed. Alternatively, format can be specified for character vectors or factors: if it is not specified and no standard format works for all non-NA inputs an error is thrown.

If `format` is specified, remember that some of the format specifications are locale-specific, and you may need to set the LC_TIME category appropriately via `Sys.setlocale`. This most often affects the use of %a, %A (weekday names), %b, %B (month names) and %p (AM/PM).

Logical NAs can be converted to either of the classes, but no other logical vectors can be.

If you are given a numeric time as the number of seconds since an epoch, see the examples.

Character input is first converted to class "POSIXlt" by `strptime`: numeric input is first converted to "POSIXct". Any conversion that needs to go between the two date-time classes requires a time zone: conversion from "POSIXlt" to "POSIXct" will validate times in the selected time zone. One issue is what happens at transitions to and from DST, for example in the UK:

```r
as.POSIXct(strptime("2011-03-27 01:30:00", "%Y-%m-%d %H:%M:%S"))
as.POSIXct(strptime("2010-10-31 01:30:00", "%Y-%m-%d %H:%M:%S"))
```

are respectively invalid (the clocks went forward at 1:00 GMT to 2:00 BST) and ambiguous (the clocks went back at 2:00 BST to 1:00 GMT). What happens in such cases is OS-specific: one should expect the first to be NA, but the second could be interpreted as either BST or GMT (and common OSes give both possible values). Note too (see `strftime`) that OS facilities may not format invalid times correctly.

Value

`as.POSIXct` and `as.POSIXlt` return an object of the appropriate class. If `tz` was specified, `as.POSIXlt` will give an appropriate "tzone" attribute. Date-times known to be invalid will be returned as NA.

Note

Some of the concepts used have to be extended backwards in time (the usage is said to be 'proleptic'). For example, the origin of time for the "POSIXct" class, ‘1970-01-01 00:00:00 UTC’, is before UTC was defined. More importantly, conversion is done assuming the Gregorian calendar which was introduced in 1582 and not used near-universally until the 20th century. One of the re-interpretations assumed by ISO 8601:2004 is that there was a year zero, even though current year numbering (and zero) is a much later concept (525 CE for year numbers from 1 CE).
Conversions between "POSIXlt" and "POSIXct" of future times are speculative except in UTC. The main uncertainty is in the use of and transitions to/from DST (most systems will assume the continuation of current rules but these can be changed at short notice).

If you want to extract specific aspects of a time (such as the day of the week) just convert it to class "POSIXlt" and extract the relevant component(s) of the list, or if you want a character representation (such as a named day of the week) use the format method.

If a time zone is needed and that specified is invalid on your system, what happens is system-specific but attempts to set it will probably be ignored.

Conversion from character needs to find a suitable format unless one is supplied (by trying common formats in turn): this can be slow for long inputs.

See Also

DateTimeClasses for details of the classes; 
strptime for conversion to and from character representations.
Sys.timezone for details of the (system-specific) naming of time zones.
locales for locale-specific aspects.

Examples

```r
(z <- Sys.time()) # the current datetime, as class "POSIXct"
unclass(z) # a large integer
floor(unclass(z)/86400) # the number of days since 1970-01-01 (UTC)
(now <- as.POSIXlt(Sys.time())) # the current datetime, as class "POSIXlt"
str(unclass(now)) # the internal list ; use now$hour, etc :
now$year + 1900 # see ?DateTimeClasses
months(now); weekdays(now) # see ?months; using LC_TIME locale
```

## suppose we have a time in seconds since 1960-01-01 00:00:00 GMT
## (the origin used by SAS)
```r
z <- 1472562988
# ways to convert this
as.POSIXct(z, origin = "1960-01-01") # local
as.POSIXct(z, origin = "1960-01-01", tz = "GMT") # in UTC
```

## SPSS dates (R-help 2006-02-16)
```r
z <- c(10485849600, 10477641600, 10561104000, 10562745600)
as.Date(as.POSIXct(z, origin = "1582-10-14", tz = "GMT"))
```

## Stata date-times: milliseconds since 1960-01-01 00:00:00 GMT
## format %tc excludes leap-seconds, assumed here
## For format %tc including leap seconds, see foreign::read.dta()
```r
z <- 1579598122120
op <- options(digits.secs = 3)
# avoid rounding down: milliseconds are not exactly representable
as.POSIXct((z+0.1)/1000, origin = "1960-01-01")
options(op)
```

## Matlab 'serial day number' (days and fractional days)
```r
z <- 7.343736909722223e5 # 2010-08-23 16:35:00
as.POSIXlt((z - 719529)*86400, origin = "1970-01-01", tz = "GMT")
as.POSIXlt(Sys.time(), "GMT") # the current time in UTC
```
These may not be correct names on your system

```r
as.POSIXlt(Sys.time(), "America/New_York") # in New York
as.POSIXlt(Sys.time(), "EST-EDT") # alternative.
as.POSIXlt(Sys.time(), "EST") # somewhere in Eastern Canada
as.POSIXlt(Sys.time(), "HST") # in Hawaii
as.POSIXlt(Sys.time(), "Australia/Darwin")
```

```r
tab <- file.path(R.home("share"), "zoneinfo", "zone1970.tab")
if(file.exists(tab)) { # typically on Windows, *not* on Linux
cols <- c("code", "coordinates", "TZ", "comments")
tmp <- read.delim(tab,
    header = FALSE, comment.char = ",", col.names = cols)
if(interactive()) View(tmp)
head(tmp, 10)
}
```

---

**AsIs**

**Inhibit Interpretation/Conversion of Objects**

### Description

Change the class of an object to indicate that it should be treated 'as is'.

### Usage

```r
I(x)
```

### Arguments

- `x` an object

### Details

Function `I` has two main uses.

- In function `data.frame`. Protecting an object by enclosing it in `I()` in a call to `data.frame` inhibits the conversion of character vectors to factors and the dropping of names, and ensures that matrices are inserted as single columns. I can also be used to protect objects which are to be added to a data frame, or converted to a data frame via `as.data.frame`.

  It achieves this by prepending the class "AsIs" to the object's classes. Class "AsIs" has a few of its own methods, including for [], `as.data.frame`, `print` and `format`.

- In function `formula`. There it is used to inhibit the interpretation of operators such as "+", "-", "+" and "+" as formula operators, so they are used as arithmetical operators. This is interpreted as a symbol by `terms.formula`.

### Value

A copy of the object with class "AsIs" prepended to the class(es).

### References

See Also
data.frame, formula

---

**asplit**

**Split Array/Matrix By Its Margins**

**Description**

Split an array or matrix by its margins.

**Usage**

```r
asplit(x, MARGIN)
```

**Arguments**

- `x`: an array, including a matrix.
- `MARGIN`: a vector giving the margins to split by. E.g., for a matrix 1 indicates rows, 2 indicates columns, `c(1, 2)` indicates rows and columns. Where `x` has named dimnames, it can be a character vector selecting dimension names.

**Details**

Since R 4.1.0, one can also obtain the splits (less efficiently) using `apply(x, MARGIN, identity, simplify = FALSE)`. The values of the splits can also be obtained (less efficiently) by `split(x, slice.index(x, MARGIN))`.

**Value**

A “list array” with dimension `dv` and each element an array of dimension `de` and dimnames preserved as available, where `dv` and `de` are, respectively, the dimensions of `x` included and not included in `MARGIN`.

**Examples**

```r
## A 3-dimensional array of dimension 2 x 3 x 4:
d <- 2 : 4
x <- array(seq_len(prod(d)), d)
x
## Splitting by margin 2 gives a 1-d list array of length 3
## consisting of 2 x 4 arrays:
asplit(x, 2)
## Splitting by margins 1 and 2 gives a 2 x 3 list array
## consisting of 1-d arrays of length 4:
asplit(x, c(1, 2))
## Compare to
split(x, slice.index(x, c(1, 2)))

## A 2 x 3 matrix:
(x <- matrix(1 : 6, 2, 3))
## To split x by its rows, one can use
asplit(x, 1)
```
assign

## or less efficiently
split(x, slice.index(x, 1))  
split(x, row(x))

assign

Assign a Value to a Name

Description

Assign a value to a name in an environment.

Usage

assign(x, value, pos = -1, envir = as.environment(pos),  
       inherits = FALSE, immediate = TRUE)

Arguments

x
  a variable name, given as a character string. No coercion is done, and the first  
element of a character vector of length greater than one will be used, with a  
warning.

value
  a value to be assigned to x.

pos
  where to do the assignment. By default, assigns into the current environment.  
  See ‘Details’ for other possibilities.

envir
  the environment to use. See ‘Details’.

inherits
  should the enclosing frames of the environment be inspected?

immediate
  an ignored compatibility feature.

Details

There are no restrictions on the name given as x: it can be a non-syntactic name (see make.names).  
The pos argument can specify the environment in which to assign the object in any of several  
ways: as -1 (the default), as a positive integer (the position in the search list); as the character  
string name of an element in the search list; or as an environment (including using sys.frame to  
access the currently active function calls). The envir argument is an alternative way to specify an  
environment, but is primarily for back compatibility.

assign does not dispatch assignment methods, so it cannot be used to set elements of vectors,  
names, attributes, etc.

Note that assignment to an attached list or data frame changes the attached copy and not the original  
object: see attach and with.

Value

This function is invoked for its side effect, which is assigning value to the variable x. If no envir  
is specified, then the assignment takes place in the currently active environment.

If inherits is TRUE, enclosing environments of the supplied environment are searched until the  
variable x is encountered. The value is then assigned in the environment in which the variable is  
encountered (provided that the binding is not locked: see lockBinding: if it is, an error is signaled).
If the symbol is not encountered then assignment takes place in the user’s workspace (the global environment).

If inherits is FALSE, assignment takes place in the initial frame of envir, unless an existing binding is locked or there is no existing binding and the environment is locked (when an error is signaled).

References


See Also

<-, get, the inverse of assign(), exists, environment.

Examples

```r
for(i in 1:6) { #-- Create objects  'r.1', 'r.2', ... 'r.6' --
   nam <- paste("r", i, sep = ".")
   assign(nam, 1:i)
}
ls(pattern = "^r..$")

###-- Global assignment within a function:
myf <- function(x) {
   innerf <- function(x) assign("Global.res", x^2, envir = .GlobalEnv)
   innerf(x+1)
}
myf(3)
Global.res # 16

a <- 1:4
assign("a[1]", 2)
a[1] == 2 # FALSE
get("a[1]") == 2 # TRUE
```

assignOps

Assignment Operators

Description

Assign a value to a name.

Usage

```r
x <- value
x <<- value
value -> x
value ->> x
x = value
```
Arguments

x       a variable name (possibly quoted).
value   a value to be assigned to x.

Details

There are three different assignment operators: two of them have leftwards and rightwards forms. The operators <- and = assign into the environment in which they are evaluated. The operator <- can be used anywhere, whereas the operator = is only allowed at the top level (e.g., in the complete expression typed at the command prompt) or as one of the subexpressions in a braced list of expressions.

The operators <<- and --> are normally only used in functions, and cause a search to be made through parent environments for an existing definition of the variable being assigned. If such a variable is found (and its binding is not locked) then its value is redefined, otherwise assignment takes place in the global environment. Note that their semantics differ from that in the S language, but are useful in conjunction with the scoping rules of R. See ‘The R Language Definition’ manual for further details and examples.

In all the assignment operator expressions, x can be a name or an expression defining a part of an object to be replaced (e.g., z[[i]]). A syntactic name does not need to be quoted, though it can be (preferably by backticks).

The leftwards forms of assignment <- = <<- group right to left, the other from left to right.

Value

value. Thus one can use a <- b <- c <- 6.

References


See Also

assign (and its inverse get), for “subassignment” such as x[i] <- v, see [<-. further, environment.

attach       Attach Set of R Objects to Search Path

Description

The database is attached to the R search path. This means that the database is searched by R when evaluating a variable, so objects in the database can be accessed by simply giving their names.

Usage

attach(what, pos = 2L, name = deparse1(substitute(what), backtick=FALSE),
       warn.conflicts = TRUE)
Arguments

what  ‘database’. This can be a data.frame or a list or a R data file created with save or NULL or an environment. See also ‘Details’.

pos  integer specifying position in search() where to attach.

name  name to use for the attached database. Names starting with package: are reserved for library.

warn.conflicts  logical. If TRUE, message()s are printed about conflicts from attaching the database, unless that database contains an object .conflicts.OK. A conflict is a function masking a function, or a non-function masking a non-function.

NB: Even though the name is warn.conflicts for historical reasons, the messages about conflicts are not warning()s but message()s.

Details

When evaluating a variable or function name R searches for that name in the databases listed by search. The first name of the appropriate type is used.

By attaching a data frame (or list) to the search path it is possible to refer to the variables in the data frame by their names alone, rather than as components of the data frame (e.g., in the example below, height rather than women$height).

By default the database is attached in position 2 in the search path, immediately after the user’s workspace and before all previously attached packages and previously attached databases. This can be altered to attach later in the search path with the pos option, but you cannot attach at pos = 1.

The database is not actually attached. Rather, a new environment is created on the search path and the elements of a list (including columns of a data frame) or objects in a save file or an environment are copied into the new environment. If you use <<- or assign to assign to an attached database, you only alter the attached copy, not the original object. (Normal assignment will place a modified version in the user’s workspace: see the examples.) For this reason attach can lead to confusion.

One useful ‘trick’ is to use what = NULL (or equivalently a length-zero list) to create a new environment on the search path into which objects can be assigned by assign or load or sys.source.

Names starting "package:" are reserved for library and should not be used by end users. Attached files are by default given the name file:what. The name argument given for the attached environment will be used by search and can be used as the argument to as.environment.

Value

The environment is returned invisibly with a "name" attribute.

Good practice

attach has the side effect of altering the search path and this can easily lead to the wrong object of a particular name being found. People do often forget to detach databases.

In interactive use, with is usually preferable to the use of attach/detach, unless what is a save()-produced file in which case attach() is a (safety) wrapper for load().

In programming, functions should not change the search path unless that is their purpose. Often with can be used within a function. If not, good practice is to

• Always use a distinctive name argument, and

• To immediately follow the attach call by an on.exit call to detach using the distinctive name.
This ensures that the search path is left unchanged even if the function is interrupted or if code after the attach call changes the search path.

References


See Also

`library`, `detach`, `search`, `objects`, `environment`, `with`.

Examples

```r
require(utils)

summary(women$height) # refers to variable 'height' in the data frame
attach(women)
summary(height) # The same variable now available by name
height <- height+2.54 # Don't do this. It creates a new variable
                     # in the user's workspace
find("height")
summary(height) # The new variable in the workspace
rm(height)
summary(height) # The original variable.
height <<- height*25.4 # Change the copy in the attached environment
find("height")
summary(height) # The changed copy
detach("women")
summary(women$height) # unchanged

## Not run: ##
## create an environment on the search path and populate it
sys.source("myfuns.R", envir = attach(NULL, name = "myfuns"))

## End(Not run)
```

attr

**Object Attributes**

Get or set specific attributes of an object.

Usage

```r
attr(x, which, exact = FALSE)
attr(x, which) <- value
```

Arguments

- **x**: an object whose attributes are to be accessed.
- **which**: a non-empty character string specifying which attribute is to be accessed.
- **exact**: logical: should which be matched exactly?
- **value**: an object, the new value of the attribute, or NULL to remove the attribute.
Details

These functions provide access to a single attribute of an object. The replacement form causes the named attribute to take the value specified (or create a new attribute with the value given).

The extraction function first looks for an exact match to which amongst the attributes of \( x \), then (unless \( \text{exact} = \text{TRUE} \)) a unique partial match. (Setting \texttt{options(warnPartialMatchAttr = TRUE)} causes partial matches to give warnings.)

The replacement function only uses exact matches.

Note that some attributes (namely \texttt{class}, \texttt{comment}, \texttt{dim}, \texttt{dimnames}, \texttt{names}, \texttt{row.names} and \texttt{tsp}) are treated specially and have restrictions on the values which can be set. (Note that this is not true of \texttt{levels} which should be set for factors via the \texttt{levels} replacement function.)

The extractor function allows (and does not match) empty and missing values of which the replacement function does not.

\texttt{NULL} objects cannot have attributes and attempting to assign one by \texttt{attr} gives an error.

Both are \texttt{primitive} functions.

Value

For the extractor, the value of the attribute matched, or \texttt{NULL} if no exact match is found and no or more than one partial match is found.

References


See Also

\texttt{attributes}

Examples

```r
# create a 2 by 5 matrix
x <- 1:10
attr(x,"dim") <- c(2, 5)
```

attributes \hspace{1cm} Object Attribute Lists

Description

These functions access an object’s attributes. The first form below returns the object’s attribute list. The replacement forms uses the list on the right-hand side of the assignment as the object’s attributes (if appropriate).

Usage

```r
attributes(x)
attributes(x) <- value
mostattributes(x) <- value
```
Attributes

Arguments

\(x\) \hspace{1cm} \text{any R object}

\(\text{value}\) \hspace{1cm} \text{an appropriate named list of attributes, or NULL.}

Details

Unlike \text{attr} it is not an error to set attributes on a NULL object: it will first be coerced to an empty list.

Note that some attributes (namely \text{class}, \text{comment}, \text{dim}, \text{dimnames}, \text{names}, \text{row.names} and \text{tsp}) are treated specially and have restrictions on the values which can be set. (Note that this is not true of \text{levels} which should be set for factors via the \text{levels} replacement function.)

Attributes are not stored internally as a list and should be thought of as a set and not a vector, i.e., the order of the elements of \text{attributes()} does not matter. This is also reflected by \text{identical()}’s behaviour with the default argument \text{attrib.as.set = TRUE}. Attributes must have unique names (and \text{NA} is taken as "NA", not a missing value).

Assigning attributes first removes all attributes, then sets any \text{dim} attribute and then the remaining attributes in the order given: this ensures that setting a \text{dim} attribute always precedes the \text{dimnames} attribute.

The \text{mostattributes} assignment takes special care for the \text{dim}, \text{names} and \text{dimnames} attributes, and assigns them only when known to be valid whereas an \text{attributes} assignment would give an error if any are not. It is principally intended for arrays, and should be used with care on classed objects. For example, it does not check that \text{row.names} are assigned correctly for data frames.

The names of a pairlist are not stored as attributes, but are reported as if they were (and can be set by the replacement form of \text{attributes}).

\text{NULL} objects cannot have attributes and attempts to assign them will promote the object to an empty list.

Both assignment and replacement forms of \text{attributes} are \text{primitive} functions.

References


See Also

\text{attr}, \text{structure}.

Examples

\begin{verbatim}
x <- cbind(a = 1:3, pi = pi) # simple matrix with dimnames
attributes(x)

# strip an object's attributes:
attributes(x) <- "NA"
x # now just a vector of length 6

mostattributes(x) <- list(mycomment = "really special", dim = 3:2,
                        dimnames = list(LETTERS[1:3], letters[1:5]), names = paste(1:6))
x # dim(), but not (dim)names
\end{verbatim}
### autoload

**On-demand Loading of Packages**

#### Description

autoload creates a promise-to-evaluate autoloader and stores it with name `name` in `.AutoloadEnv` environment. When R attempts to evaluate `name`, autoloader is run, the package is loaded and `name` is re-evaluated in the new package's environment. The result is that R behaves as if package was loaded but it does not occupy memory.

`.Autoloaded` contains the names of the packages for which autoloading has been promised.

#### Usage

```r
autoload(name, package, reset = FALSE, ...)
autoloader(name, package, ...)
```

> `.AutoloadEnv`
> `.Autoloaded`

#### Arguments

- `name` string giving the name of an object.
- `package` string giving the name of a package containing the object.
- `reset` logical: for internal use by autoloader.
- `...` other arguments to `library`.

#### Value

This function is invoked for its side-effect. It has no return value.

#### See Also

- `delayedAssign`
- `library`

#### Examples

```r
require(stats)
autoload("interpSpline", "splines")
search()
ls("Autoloads")
.Autoloaded

x <- sort(stats::rnorm(12))
y <- x^2
is <- interpSpline(x, y)
search() # now has splines
detach("package:splines")
search()
is2 <- interpSpline(x, y+x)
search() # and again
detach("package:splines")
```
backsolve

Solve an Upper or Lower Triangular System

Description

Solves a triangular system of linear equations.

Usage

backsolve(r, x, k = ncol(r), upper.tri = TRUE, transpose = FALSE)
forwardsolve(l, x, k = ncol(l), upper.tri = FALSE, transpose = FALSE)

Arguments

r, l
  an upper (or lower) triangular matrix giving the coefficients for the system to be
  solved. Values below (above) the diagonal are ignored.

x
  a matrix whose columns give the right-hand sides for the equations.

k
  The number of columns of r and rows of x to use.

upper.tri
  logical; if TRUE (default), the upper triangular part of r is used. Otherwise, the
  lower one.

transpose
  logical; if TRUE, solve r′∗y = x for y, i.e., t(r) %*% y == x.

Details

Solves a system of linear equations where the coefficient matrix is upper (or ‘right’, ‘R’) or lower
(‘left’, ‘L’) triangular.

x <- backsolve(R, b) solves Rx = b, and
x <- forwardsolve(L, b) solves Lx = b, respectively.

The r/l must have at least k rows and columns, and x must have at least k rows.

This is a wrapper for the level-3 BLAS routine dtrsm.

Value

The solution of the triangular system. The result will be a vector if x is a vector and a matrix if x is
a matrix.

References

Brooks/Cole.


See Also

chol, qr, solve.
Examples

```r
## upper triangular matrix 'r':
r <- rbind(c(1,2,3),
c(0,1,1),
c(0,0,2))
( y <- backsolve(r, x <- c(8,4,2)) ) # -1 3 1
r %*% y # == x = (8,4,2)
backsolve(r, x, transpose = TRUE) # 8 -12 -5
```

Description

Utilities to ‘balance’ objects of class "POSIXlt".

`unCfillPOSIXlt(x)` is a fast primitive version of `balancePOSIXlt(x, fill.only=TRUE, classed=FALSE)` or equivalently, `unclass(balancePOSIXlt(x, fill.only=TRUE))` from where it is named.

Usage

```r
balancePOSIXlt(x, fill.only = FALSE, classed = TRUE)
unCfillPOSIXlt(x)
```

Arguments

- `x` an R object inheriting from "POSIXlt", see POSIXlt.
- `fill.only` a logical specifying if `balancePOSIXlt(x, ..)` should only “fill up” by recycling, but not re-check validity nor recompute, e.g., `x$wday` and `x$yday`.
- `classed` a logical specifying if the result should be classed, true by default. Using `balancePOSIXlt(x, classed = FALSE)` is equivalent to but faster than `unclass(balancePOSIXlt(x))`.

“Ragged” and Out-of-range vs “Balanced” POSIXlt

Note that "POSIXlt" objects `x` may have their (9 to 11) list components of different lengths, by simply recycling them to full length. Prior to R 4.3.0, this has worked in printing, formatting, and conversion to "POSIXct", but often not for `length()`, conversion to "Date" or indexing, i.e., subsetting, `[`, or subassigning, `[]<-`.

Relatdly, components `sec`, `min`, `hour`, `mday` and `mon` could have been out of their designated range (say, 0–23 for hours) and still work correctly, e.g. in conversions and printing. This is supported as well, since R 4.3.0, at least when the values are not extreme.

Function `balancePOSIXlt(x)` will now return a version of the "POSIXlt" object `x` which by default is balanced in both ways: All the internal list components are of full length, and their values are inside their ranges as specified in `as.POSIXlt`'s ‘Details on POSIXlt’. Setting `fill.only = TRUE` will only recycle the list components to full length, but not check them at all. This is particularly faster when all components of `x` are already of full length.

Experimentally, `balancePOSIXlt()` and other functions returning POSIXlt objects now set a logical attribute "balanced" with NA meaning “filled-in”, i.e., not “ragged” and TRUE means (fully) balanced.
See Also

For more details about many aspects of valid POSIXlt objects, notably their internal list components, see 'DateTimeClasses', e.g., as.POSIXlt, notably the section 'Details on POSIXlt'.

Examples

## FIXME: this should also work for regular (non-UTC) time zones.
TZ <- "UTC"
# Could be
# d1 <- as.POSIXlt("2000-01-02 3:45", tz = TZ)
# on systems (almost all) which have tm_zone.
oldTZ <- Sys.getenv('TZ', unset = "unset")
Sys.setenv(TZ = "UTC")
d1 <- as.POSIXlt("2000-01-02 3:45")
d1$min <- d1$min + (0:16)*20L
(f1 <- format(d1))
str(unclass(d1))  # only $min is of length > 1
df <- balancePOSIXlt(d1, fill.only = TRUE)  # a "POSIXlt" object
str(unclass(df))  # all of length 17; 'min' unchanged
db <- balancePOSIXlt(d1, classed = FALSE)  # a list
stopifnot(identical(
    unCfillPOSIXlt(d1),
    balancePOSIXlt(d1, fill.only = TRUE, classed = FALSE)))
str(db) # of length 17 and in range

if(oldTZ == "unset") Sys.unsetenv('TZ') else Sys.setenv(TZ = oldTZ)

Manipulate File Paths

Description

basename removes all of the path up to and including the last path separator (if any).
dirname returns the part of the path up to but excluding the last path separator, or "." if there is no path separator.

Usage

basename(path)
dirname(path)

Arguments

path character vector, containing path names.

Details

tilde expansion of the path will be performed.

Trailing path separators are removed before dissecting the path, and for dirname any trailing file separators are removed from the result.
Value

A character vector of the same length as path. A zero-length input will give a zero-length output with no error.

Paths not containing any separators are taken to be in the current directory, so dirname returns ".".

If an element of path is NA, so is the result.

"" is not a valid pathname, but is returned unchanged.

Behaviour on Windows

On Windows this will accept either \ or / as the path separator, but dirname will return a path using / (except if on a network share, when the leading \ will be preserved). Expect these only to be able to handle complete paths, and not for example just a network share or a drive.

UTF-8-encoded path names not valid in the current locale can be used.

Note

These are not wrappers for the POSIX system functions of the same names: in particular they do not have the special handling of the path "/" and of returning "." for empty strings.

See Also

file.path, path.expand.

Examples

basename(file.path("","p1","p2","p3", c("file1", "file2")))
dirname (file.path("","p1","p2","p3", "filename"))

Bessel Functions

Bessel Functions of integer and fractional order, of first and second kind, $J_\nu$ and $Y_\nu$, and Modified Bessel functions (of first and third kind), $I_\nu$ and $K_\nu$.

Usage

besselI(x, nu, expon.scaled = FALSE)
besselK(x, nu, expon.scaled = FALSE)
besselJ(x, nu)
besselY(x, nu)

Arguments

x numeric, \( \geq 0 \).

nu numeric; The order (maybe fractional and negative) of the corresponding Bessel function.

expon.scaled logical; if TRUE, the results are exponentially scaled in order to avoid overflow ($I_\nu$) or underflow ($K_\nu$), respectively.
Details

If `expon.scaled = TRUE`, \( e^{-x}I_\nu(x) \) or \( e^xK_\nu(x) \) are returned.

For \( \nu < 0 \), formulae 9.1.2 and 9.6.2 from Abramowitz & Stegun are applied (which is probably suboptimal), except for `besselK` which is symmetric in \( \nu \).

The current algorithms will give warnings about accuracy loss for large arguments. In some cases, these warnings are exaggerated, and the precision is perfect. For large \( \nu \), say in the order of millions, the current algorithms are rarely useful.

Value

Numeric vector with the (scaled, if `expon.scaled = TRUE`) values of the corresponding Bessel function.

The length of the result is the maximum of the lengths of the parameters. All parameters are recycled to that length.

Author(s)

Original Fortran code: W. J. Cody, Argonne National Laboratory
Translation to C and adaptation to R: Martin Maechler <maechler@stat.math.ethz.ch>.

Source

The C code is a translation of Fortran routines from https://netlib.org/specfun/ribesl, ‘../rjbesl’, etc. The four source code files for `bessel[IJKY]` each contain a paragraph “Acknowledgement” and “References”, a short summary of which is

- `besselJ` as `besselI`
- `besselK` based on (code) by J. B. Campbell (1980). … Modifications…
- `besselY` draws heavily on Temme’s Algol program for \( Y_\nu(x) \) and on Campbell’s programs for \( Y_\nu(x) \) heavily modified.

References


In order of “Source” citation above:


See Also

Other special mathematical functions, such as \texttt{gamma}, \( \Gamma(x) \), and \texttt{beta}, \( B(x) \).

Examples

\begin{verbatim}
require(graphics)

nus <- c(0:5, 10, 20)
x <- seq(0, 4, length.out = 501)
plot(x, x, ylim = c(0, 6), ylab = "", type = "n",
     main = "Bessel Functions \( I_n(x) \)"
for(nu in nus) lines(x, besselI(x, nu = nu), col = nu + 2)
legend(0, 6, legend = paste("nu=", nus), col = nus + 2, lwd = 1)

x <- seq(0, 40, length.out = 801); yl <- c(-.5, 1)
plot(x, x, ylim = yl, ylab = "", type = "n",
     main = "Bessel Functions \( J_n(x) \)"
abline(h=0, v=0, lty=3)
for(nu in nus) lines(x, besselJ(x, nu = nu), col = nu + 2)
legend("topright", legend = paste("nu=", nus), col = nus + 2, lwd = 1, bty="n")

## Negative nu's ----------------------------------------
xx <- 2:7
nu <- seq(-10, 9, length.out = 2001)
## --- I() --- --- --- ---
matplot(nu, t(outer(xx, nu, besselI)), type = "l", ylim = c(-50, 200),
       main = expression(paste("Bessel \( I_n(x) \) for fixed \( x \), as \( f(nu) \)),
       xlab = expression(nu))
abline(v = 0, col = "light gray", lty = 3)
legend("topright", legend = paste("x=", xx), col = seq(xx), lty = 1)

## --- J() --- --- --- ---
bJ <- t(outer(xx, nu, besselJ))
matplot(nu, bJ, type = "l", ylim = c(-500, 200),
       xlab = quote(nu), ylab = quote(\( J_n(x) \)),
       main = expression(paste("Bessel \( J_n(x) \) for fixed \( x \))))
abline(v = 0, col = "light gray", lty = 3)
legend("topright", legend = paste("x=", xx), col = seq(xx), lty = 1)

## ZOOM into right part:
matplot(nu[nu > -2], bJ[nu > -2,], type = "l",
       xlab = quote(nu), ylab = quote(\( J_n(x) \)),
       main = expression(paste("Bessel \( J_n(x) \) for fixed \( x \))))
abline(h=0, v = 0, col = "gray60", lty = 3)
legend("topright", legend = paste("x=", xx), col = seq(xx), lty = 1)

##--------------- x --> 0 -----------------------------
x0 <- 2^seq(-16, 5, length.out=256)
plot(range(x0), c(1e-40, 1), log = "xy", xlab = "x", ylab = "",
     type = "n",
     main = "Bessel Functions \( J_n(x) \) near 0\n\log-log scale") ; axis(2, at=1)
for(nu in sort(c(nus, nus+0.5)))
    lines(x0, besselJ(x0, nu = nu), col = nu + 2, lty= 1 + (nu%%1 > 0))
legend("right", legend = paste("nu=", paste(nus, nus+0.5, sep=" ")),
\end{verbatim}
```
col = nus + 2, lwd = 1, bty="n")
x0 <- 2*seq(-10, 8, length.out=256)
plot(range(x0), 10^c(-100, 80), log = "xy", xlab = "x", ylab = "", type = "n",
     main = "Bessel Functions K_nu(x) near 0\nlog - log scale") ; axis(2, at=1)
for(nu in sort(c(nus, nus+0.5)))
  lines(x0, besselK(x0, nu = nu), col = nu + 2, lty= 1+ (nu%%1 > 0))
legend("topright", legend = paste("nu=", paste(nus, nus + 0.5, sep = ", ", sep = " ")),
       col = nus + 2, lwd = 1, bty="n")
x <- x[x > 0]
plot(x, x, ylim = c(1e-18, 1e11), log = "y", ylab = "", type = "n",
     main = "Bessel Functions K_nu(x)"); axis(2, at=1)
for(nu in nus) lines(x, besselK(x, nu = nu), col = nu + 2)
legend(0, 1e-5, legend=paste("nu=", nus), col = nus + 2, lwd = 1)

yl <- c(-1.6, .6)
plot(x, x, ylim = yl, ylab = "", type = "n",
     main = "Bessel Functions Y_nu(x)");
for(nu in nus){
  xx <- x[x > .6*nu]
  lines(xx, besselY(xx, nu=nu), col = nu+2)
}
legend(25, -.5, legend = paste("nu=", nus), col = nus+2, lwd = 1)
## negative nu in bessel_Y -- was bogus for a long time
curve(besselY(x, -0.1), 0, 10, ylim = c(-3,1), ylab = "")
for(nu in c(seq(-0.2, -2, by = -0.1)))
  curve(besselY(x, nu), add = TRUE)
title(expression(besselY(x, nu) * " * " *
    (nu == list(-0.1, -0.2, ..., -2))))
```

---

**bindenv**

**Binding and Environment Locking, Active Bindings**

**Description**

These functions represent an interface for adjustments to environments and bindings within environments. They allow for locking environments as well as individual bindings, and for linking a variable to a function.

**Usage**

- `lockEnvironment(env, bindings = FALSE)`
- `environmentIsLocked(env)`
- `lockBinding(sym, env)`
- `unlockBinding(sym, env)`
- `bindingIsLocked(sym, env)`
- `makeActiveBinding(sym, fun, env)`
- `bindingIsActive(sym, env)`
- `activeBindingFunction(sym, env)`
Arguments

- **env**: an environment.
- **bindings**: logical specifying whether bindings should be locked.
- **sym**: a name object or character string.
- **fun**: a function taking zero or one arguments.

Details

The function `lockEnvironment` locks its environment argument. Locking the environment prevents adding or removing variable bindings from the environment. Changing the value of a variable is still possible unless the binding has been locked. The namespace environments of packages with namespaces are locked when loaded.

`lockBinding` locks individual bindings in the specified environment. The value of a locked binding cannot be changed. Locked bindings may be removed from an environment unless the environment is locked.

`makeActiveBinding` installs `fun` in environment `env` so that getting the value of `sym` calls `fun` with no arguments, and assigning to `sym` calls `fun` with one argument, the value to be assigned. This allows the implementation of things like C variables linked to R variables and variables linked to databases, and is used to implement `setRefClass`. It may also be useful for making thread-safe versions of some system globals. Currently active bindings are not preserved during package installation, but they can be created in `.onLoad`.

Value

The `bindingIsLocked` and `environmentIsLocked` return a length-one logical vector. The remaining functions return `NULL`, invisibly.

Author(s)

Luke Tierney

Examples

```r
# locking environments
e <- new.env()
assign("x", 1, envir = e)
get("x", envir = e)
lockEnvironment(e)
get("x", envir = e)
assign("x", 2, envir = e)
try(assign("y", 2, envir = e)) # error

# locking bindings
e <- new.env()
assign("x", 1, envir = e)
get("x", envir = e)
lockBinding("x", e)
try(assign("x", 2, envir = e)) # error
unlockBinding("x", e)
assign("x", 2, envir = e)
get("x", envir = e)

# active bindings
```
f <- local( {
  x <- 1
  function(v) {
    if (missing(v))
      cat("get\n")
    else {
      cat("set\n")
      x <<- v
    }
    x
  }
})
makeActiveBinding("fred", f, .GlobalEnv)
bindingIsActive("fred", .GlobalEnv)
fred
fred <- 2
fred

---

**bitwise**

*Bitwise Logical Operations*

**Description**

Logical operations on integer vectors with elements viewed as sets of bits.

**Usage**

- `bitwNot(a)`
- `bitwAnd(a, b)`
- `bitwOr(a, b)`
- `bitwXor(a, b)`
- `bitwShiftL(a, n)`
- `bitwShiftR(a, n)`

**Arguments**

- `a, b` integer vectors; numeric vectors are coerced to integer vectors.
- `n` non-negative integer vector of values up to 31.

**Details**

- Each element of an integer vector has 32 bits.
- Pairwise operations can result in integer `NA`.
- Shifting is done assuming the values represent unsigned integers.

**Value**

An integer vector of length the longer of the arguments, or zero length if one is zero-length.

The output element is `NA` if an input is `NA` (after coercion) or an invalid shift.
See Also

The logical operators, !, &., |, xor. Notably these do work bitwise for raw arguments.

The classes "octmode" and "hexmode" whose implementation of the standard logical operators is based on these functions.

Package bitops has similar functions for numeric vectors which differ in the way they treat integers $2^{31}$ or larger.

Examples

\[
\begin{align*}
\text{bitwNot}(0:12) & \# -1 -2 \ldots -13 \\
\text{bitwAnd}(15L, 7L) & \# 7 \\
\text{bitwOr} (15L, 7L) & \# 15 \\
\text{bitwXor}(15L, 7L) & \# 8 \\
\text{bitwXor}(-1L, 1L) & \# -2 \\
\end{align*}
\]

## The "same" for 'raw' instead of integer :

\[
\begin{align*}
nr12 & \leftarrow \text{as.raw}(0:12) \ ; \ \text{rbind}(n12, !n12) \\
c(n15 &n 15L, 7L) & \leftarrow \text{as.raw}(7)) \ # 0f 07 \\
r15 & r7 & \# 07 \\
r15 | r7 & \# 0f \\
xor(r15, r7)& \# 08 \\
\end{align*}
\]

\[
\text{bitwShiftR}(-1, 1:31) \ # \text{shifts of } 2^{32}-1 = 4294967295
\]

---

### Description

Get or set the body of a function which is basically all of the function definition but its formal arguments (formals), see the ‘Details’.

### Usage

\[
\begin{align*}
\text{body}(\text{fun} = \text{sys.function}(	ext{sys.parent}())) \\
\text{body}(\text{fun}, \text{envir} = \text{environment}(\text{fun})) & \leftarrow \text{value}
\end{align*}
\]

### Arguments

- **fun**: a function object, or see ‘Details’.
- **envir**: environment in which the function should be defined.
- **value**: an object, usually a language object: see section ‘Value’.

### Details

For the first form, fun can be a character string naming the function to be manipulated, which is searched for from the parent frame. If it is not specified, the function calling body is used.

The bodies of all but the simplest are braced expressions, that is calls to \( \cdot \): see the ‘Examples’ section for how to create such a call.
**Value**

body returns the body of the function specified. This is normally a *language object*, most often a call to `{`, but it can also be a *symbol* such as `pi` or a constant (e.g., `3` or "R") to be the return value of the function.

The replacement form sets the body of a function to the object on the right hand side, and (potentially) resets the *environment* of the function, and drops *attributes*. If `value` is of class "*expression" the first element is used as the body: any additional elements are ignored, with a warning.

**See Also**

The three parts of a (non-primitive) function are its *formals*, *body*, and *environment*.

Further, see *alist, args, function*.

**Examples**

```r
body(body)
f <- function(x) x^5
body(f) <- quote(5^x)
## or equivalently body(f) <- expression(5^x)
f(3) # = 125
body(f)

## creating a multi-expression body
e <- expression(y <- x^2, return(y)) # or a list
body(f) <- as.call(c(as.name(""), e))
f
f(8)

## Using substitute() may be simpler than 'as.call(c(as.name(""),..)))':
stopifnot(identical(body(f), substitute({ y <- x^2; return(y) })))
```

---

**bquote**

*Partial substitution in expressions*

**Description**

An analogue of the LISP backquote macro. `bquote` quotes its argument except that terms wrapped in `.()` are evaluated in the specified *where* environment. If `splice = TRUE` then terms wrapped in `..()` are evaluated and spliced into a call.

**Usage**

`bquote(expr, where = parent.frame(), splice = FALSE)`

**Arguments**

- `expr` A *language object*.
- `where` An environment.
- `splice` Logical; if TRUE splicing is enabled.
Value

A language object.

See Also

quote, substitute

Examples

require(graphics)

a <- 2

bquote(a == a)
quote(a == a)

bquote(a == .(a))
substitute(a == A, list(A = a))

plot(1:10, a*(1:10), main = bquote(a == .(a)))

## to set a function default arg
default <- 1
bquote( function(x, y = .(default)) x+y )

exprs <- expression(x <- 1, y <- 2, x + y)

bquote(function() {..(exprs)}, splice = TRUE)

----------------------------------------

browser                     Environment Browser
----------------------------------------

Description

Interrupt the execution of an expression and allow the inspection of the environment where browser was called from.

Usage

browser(text = "", condition = NULL, expr = TRUE, skipCalls = 0L)

Arguments

text     a text string that can be retrieved once the browser is invoked.
condition a condition that can be retrieved once the browser is invoked.
expr      a "condition". By default, and whenever not false after being coerced to logical, the debugger will be invoked, otherwise control is returned directly.
skipCalls how many previous calls to skip when reporting the calling context.
Details

A call to browser can be included in the body of a function. When reached, this causes a pause in the execution of the current expression and allows access to the R interpreter.

The purpose of the text and condition arguments are to allow helper programs (e.g., external debuggers) to insert specific values here, so that the specific call to browser (perhaps its location in a source file) can be identified and special processing can be achieved. The values can be retrieved by calling browserText and browserCondition.

The purpose of the expr argument is to allow for the illusion of conditional debugging. It is an illusion, because execution is always paused at the call to browser, but control is only passed to the evaluator described below if expr is not FALSE after coercion to logical. In most cases it is going to be more efficient to use an if statement in the calling program, but in some cases using this argument will be simpler.

The skipCalls argument should be used when the browser() call is nested within another debugging function: it will look further up the call stack to report its location.

At the browser prompt the user can enter commands or R expressions, followed by a newline. The commands are

c  exit the browser and continue execution at the next statement.
cont  synonym for c.
fm  finish execution of the current loop or function
help  print this list of commands
n  evaluate the next statement, stepping over function calls. For byte compiled functions interrupted by browser calls, n is equivalent to c.
s  evaluate the next statement, stepping into function calls. Again, byte compiled functions make s equivalent to c.
where  print a stack trace of all active function calls.
r  invoke a "resume" restart if one is available; interpreted as an R expression otherwise. Typically "resume" restarts are established for continuing from user interrupts.
Q  exit the browser and the current evaluation and return to the top-level prompt.

Leading and trailing whitespace is ignored, except for an empty line. Handling of empty lines depends on the "browserNLdisabled" option; if it is TRUE, empty lines are ignored. If not, an empty line is the same as n (or s, if it was used most recently).

Anything else entered at the browser prompt is interpreted as an R expression to be evaluated in the calling environment: in particular typing an object name will cause the object to be printed, and ls() lists the objects in the calling frame. (If you want to look at an object with a name such as n, print it explicitly, or use autoprint via (n).

The number of lines printed for the deparsed call can be limited by setting options(deparse.max.lines).

The browser prompt is of the form Browse[n]>: here var{n} indicates the ‘browser level’. The browser can be called when browsing (and often is when debug is in use), and each recursive call increases the number. (The actual number is the number of ‘contexts’ on the context stack: this is usually 2 for the outer level of browsing and 1 when examining dumps in debugger.)

This is a primitive function but does argument matching in the standard way.
References


See Also
d debug, and traceback for the stack on error. browserText for how to retrieve the text and condition.

browserText

Functions to Retrieve Values Supplied by Calls to the Browser

Description

A call to browser can provide context by supplying either a text argument or a condition argument. These functions can be used to retrieve either of these arguments.

Usage

```
browserText(n = 1)
browserCondition(n = 1)
browserSetDebug(n = 1)
```

Arguments

```
n  The number of contexts to skip over, it must be non-negative.
```

Details

Each call to browser can supply either a text string or a condition. The functions browserText and browserCondition provide ways to retrieve those values. Since there can be multiple browser contexts active at any time we also support retrieving values from the different contexts. The innermost (most recently initiated) browser context is numbered 1: other contexts are numbered sequentially. browserSetDebug provides a mechanism for initiating the browser in one of the calling functions. See sys.frame for a more complete discussion of the calling stack. To use browserSetDebug you select some calling function, determine how far back it is in the call stack and call browserSetDebug with n set to that value. Then, by typing c at the browser prompt you will cause evaluation to continue, and provided there are no intervening calls to browser or other interrupts, control will halt again once evaluation has returned to the closure specified. This is similar to the up functionality in gdb or the “step out” functionality in other debuggers.

Value

browserText returns the text, while browserCondition returns the condition from the specified browser context.

browserSetDebug returns NULL, invisibly.
Note

It may be of interest to allow for querying further up the set of browser contexts and this functionality may be added at a later date.

Author(s)

R. Gentleman

See Also

browser

---

**builtins**  
*Returns the Names of All Built-in Objects*

**Description**

Return the names of all the built-in objects. These are fetched directly from the symbol table of the R interpreter.

**Usage**

`builtins(internal = FALSE)`

**Arguments**

- `internal`  
a logical indicating whether only ‘internal’ functions (which can be called via `.Internal`) should be returned.

**Details**

`builtins()` returns an unsorted list of the objects in the symbol table, that is all the objects in the base environment. These are the built-in objects plus any that have been added subsequently when the base package was loaded. It is less confusing to use `ls(baseenv(), all.names = TRUE)`.

`builtins(TRUE)` returns an unsorted list of the names of internal functions, that is those which can be accessed as `.Internal(foo(args ...))` for `foo` in the list.

**Value**

A character vector.
by

Apply a Function to a Data Frame Split by Factors

Description

Function by is an object-oriented wrapper for `tapply` applied to data frames.

Usage

```
by(data, INDICES, FUN, ..., simplify = TRUE)
```

Arguments

- **data**: an R object, normally a data frame, possibly a matrix.
- **INDICES**: a factor or a list of factors, each of length `nrow(data)`. For the data frame method, INDICES can also be a formula as in the `f` argument of the `split` method for data frames.
- **FUN**: a function to be applied to (usually data-frame) subsets of data.
- **...**: further arguments to `FUN`.
- **simplify**: logical: see `tapply`.

Details

A data frame is split by row into data frames subsetted by the values of one or more factors, and function `FUN` is applied to each subset in turn.

For the default method, an object with dimensions (e.g., a matrix) is coerced to a data frame and the data frame method applied. Other objects are also coerced to a data frame, but `FUN` is applied separately to (subsets of) each column of the data frame.

Value

An object of class "by", giving the results for each subset. This is always a list if `simplify` is false, otherwise a list or array (see `tapply`).

See Also

- `tapply`, `simplify2array`, `array2DF` to convert result to a data frame. `ave` also applies a function block-wise.

Examples

```r
require(stats)
by(warpbreaks[, 1:2], warpbreaks[,"tension"], summary)
by(warpbreaks[, 1], warpbreaks[, -1], summary)
by(warpbreaks, warpbreaks[,"tension"],
  function(x) lm(breaks ~ wool, data = x))
## now suppose we want to extract the coefficients by group
tmp1 <- with(warpbreaks,
  by(warpbreaks, tension,
    function(x) lm(breaks ~ wool, data = x)))
```
sapply(tmp1, coef)

## another way
tmp2 <- by(warpbreaks, ~ tension,
          with, coef(lm(breaks ~ wool)))
array2DF(tmp2, simplify = TRUE)

---

**Combine Values into a Vector or List**

**Description**

This is a generic function which combines its arguments.

The default method combines its arguments to form a vector. All arguments are coerced to a common type which is the type of the returned value, and all attributes except names are removed.

**Usage**

```
## S3 Generic function
c(...)  
## Default S3 method:  
c(..., recursive = FALSE, use.names = TRUE)
```

**Arguments**

- `...` objects to be concatenated. All `NULL` entries are dropped before method dispatch unless at the very beginning of the argument list.
- `recursive` logical. If `recursive = TRUE`, the function recursively descends through lists (and pairlists) combining all their elements into a vector.
- `use.names` logical indicating if `names` should be preserved.

**Details**

The output type is determined from the highest type of the components in the hierarchy `NULL < raw < logical < integer < double < complex < character < list < expression`. Pairlists are treated as lists, whereas non-vector components (such as `names` / `symbols` and `calls`) are treated as one-element lists which cannot be unlisted even if `recursive = TRUE`.

There is a `c.factor` method which combines factors into a factor.

c is sometimes used for its side effect of removing attributes except names, for example to turn an `array` into a vector. `as.vector` is a more intuitive way to do this, but also drops names. Note that methods other than the default are not required to do this (and they will almost certainly preserve a class attribute).

This is a **primitive** function.

**Value**

`NULL` or an expression or a vector of an appropriate mode. (With no arguments the value is `NULL`.)
S4 methods

This function is S4 generic, but with argument list (x, ...).

References


See Also

`unlist` and `as.vector` to produce attribute-free vectors.

Examples

c(1,7:9)
c(1:5, 10.5, "next")

```r
## uses with a single argument to drop attributes
x <- 1:4
names(x) <- letters[1:4]
x
c(x)   # has names
as.vector(x) # no names
dim(x) <- c(2,2)
x
c(x)
as.vector(x)
```

```r
## append to a list:
ll <- list(A = 1, c = "C")
## do *not* use
c(ll, d = 1:3) # which is == c(ll, as.list(c(d = 1:3)))
## but rather
c(ll, d = list(1:3)) # c() combining two lists

c(list(A = c(B = 1)), recursive = TRUE)
c(options(), recursive = TRUE)
c(list(A = c(B = 1, C = 2), B = c(E = 7)), recursive = TRUE)
```

---

call Function Calls

Description

Create or test for objects of mode "call" (or "()", see Details).

Usage

call(name, ...)
is.call(x)
as.call(x)
Arguments

name       a non-empty character string naming the function to be called.

...       arguments to be part of the call.

x          an arbitrary R object.

Details

call returns an unevaluated function call, that is, an unevaluated expression which consists of the
named function applied to the given arguments (name must be a string which gives the name
of a function to be called). Note that although the call is unevaluated, the arguments ... are
evaluated.
call is a primitive, so the first argument is taken as name and the remaining arguments as
arguments for the constructed call: if the first argument is named the name must partially
match name.

is.call is used to determine whether x is a call (i.e., of mode "call" or ")

• is.call(x) is strictly equivalent to typeof(x) == "language".
• is.language() is also true for calls (but also for symbols and expressions where
is.call() is false).

as.call(x): Objects of mode "list" can be coerced to mode "call". The first element of the
list becomes the function part of the call, so should be a function or the name of one (as a
symbol; a character string will not do).
If you think of using as.call(<string>), consider using str2lang(*) which is an efficient
version of parse(text=*) Note that call() and as.call(), when applicable, are much
preferable to these parse() based approaches.

All three are primitive functions.

as.call is generic: you can write methods to handle specific classes of objects, see InternalMeth-
ods.

Warning

call should not be used to attempt to evade restrictions on the use of .Internal and other non-API
calls.

References

Brooks/Cole.

See Also

do.call for calling a function by name and argument list; Recall for recursive calling of functions;
further is.language, expression, function.

Producing calls etc from character: str2lang and parse.

Examples

is.call(call) #-> FALSE: Functions are NOT calls

## set up a function call to round with argument 10.5
c1 <- call("round", 10.5)
is.call(cl) # TRUE
cl
identical(quote(round(10.5)), # <- less functional, but the same
c1) # TRUE
## such a call can also be evaluated.
eval(cl) # [1] 10

class(cl) # "call"
typeof(cl)# "language"
is.call(cl) && is.language(cl) # always TRUE for "call"s

A <- 10.5
call("round", A) # round(10.5)
call("round", quote(A)) # round(A)
f <- "round"
call(f, quote(A)) # round(A)
## if we want to supply a function we need to use as.call or similar
f <- round
## Not run: call(f, quote(A)) # error: first arg must be character
(g <- as.call(list(f, quote(A))))
eval(g)
## alternatively but less transparently
g <- list(f, quote(A))
mode(g) <- "call"
g
eval(g)
## see also the examples in the help for do.call

---
callCC

*Call With Current Continuation*

**Description**

A downward-only version of Scheme’s call with current continuation.

**Usage**

`callCC(fun)`

**Arguments**

- `fun` function of one argument, the exit procedure.

**Details**

`callCC` provides a non-local exit mechanism that can be useful for early termination of a computation. `callCC` calls `fun` with one argument, an *exit function*. The exit function takes a single argument, the intended return value. If the body of `fun` calls the exit function then the call to `callCC` immediately returns, with the value supplied to the exit function as the value returned by `callCC`.

**Author(s)**

Luke Tierney
Examples

# The following all return the value 1
callCC(function(k) 1)
callCC(function(k) k(1))
callCC(function(k) (k(1); 2))
callCC(function(k) repeat k(1))

Description

Functions to pass \( \mathbb{R} \) objects to compiled C/C++ code that has been loaded into \( \mathbb{R} \).

Usage

\[
\text{.Call(\_NAME, \ldots, PACKAGE)} \\
\text{.External(\_NAME, \ldots, PACKAGE)}
\]

Arguments

\_NAME a character string giving the name of a C function, or an object of class "NativeSymbolInfo", "RegisteredNativeSymbol" or "NativeSymbol" referring to such a name.  
\ldots arguments to be passed to the compiled code. Up to 65 for \text{.Call}.  
PACKAGE if supplied, confine the search for a character string \_NAME to the DLL given by this argument (plus the conventional extension, ‘.so’, ‘.dll’, …). This argument follows \ldots and so its name cannot be abbreviated. This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols, and also speeds up the search (see ‘Note’).

Details

The functions are used to call compiled code which makes use of internal \( \mathbb{R} \) objects, passing the arguments to the code as a sequence of \( \mathbb{R} \) objects. They assume C calling conventions, so can usually also be used for C++ code.

For details about how to write code to use with these functions see the chapter on ‘System and foreign language interfaces’ in the ‘Writing R Extensions’ manual. They differ in the way the arguments are passed to the C code: \text{.External} allows for a variable or unlimited number of arguments. These functions are primitive, and \_NAME is always matched to the first argument supplied (which should not be named). For clarity, avoid using names in the arguments passed to \ldots that match or partially match \_NAME.

Value

An \( \mathbb{R} \) object constructed in the compiled code.
Header files for external code

Writing code for use with these functions will need to use internal \texttt{R} structures defined in \`Rinternals.h\' and/or the macros in \`Rdefines.h\'.

Note

If one of these functions is to be used frequently, do specify \texttt{PACKAGE} (to confine the search to a single DLL) or pass \texttt{.NAME} as one of the native symbol objects. Searching for symbols can take a long time, especially when many namespaces are loaded.

You may see \texttt{PACKAGE = "base"} for symbols linked into \texttt{R}. Do not use this in your own code: such symbols are not part of the API and may be changed without warning.

\texttt{PACKAGE = ""} used to be accepted (but was undocumented): it is now an error.

References


See Also

\texttt{dyn.load}, \texttt{.C}, \texttt{.Fortran}.

The \textquote{Writing \texttt{R} Extensions} manual.

---

capabilities  \textit{Report Capabilities of this Build of \texttt{R}}

Description

Report on the optional features which have been compiled into this build of \texttt{R}.

Usage

\begin{verbatim}
capabilities(what = NULL,
             Xchk = any(nas %in% c("X11", "jpeg", "png", "tiff")))
\end{verbatim}

Arguments

- \texttt{what} character vector or \texttt{NULL}, specifying required components. \texttt{NULL} implies that all are required.

- \texttt{Xchk} \texttt{logical} with a smart default, indicating if X11-related capabilities should be fully checked, notably on macOS. If set to false, may avoid a warning \textquote{No protocol specified} and e.g., the "X11" capability may be returned as \texttt{NA}.

Value

A named logical vector. Current components are

- \texttt{jpeg} is the \texttt{jpeg} function operational?

- \texttt{png} is the \texttt{png} function operational?

- \texttt{tiff} is the \texttt{tiff} function operational?
### capabilities

<table>
<thead>
<tr>
<th>Package</th>
<th>Operational?</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>tcltk</td>
<td></td>
<td>is the tcltk package operational? Note that to make use of Tk you will always need to check that “X11” is also available.</td>
</tr>
<tr>
<td>X11</td>
<td></td>
<td>are the X11 graphics device and the X11-based data editor available? This loads the X11 module if not already loaded, and checks that the default display can be contacted unless a X11 device has already been used.</td>
</tr>
<tr>
<td>aqua</td>
<td></td>
<td>is the quartz function operational? Only on some macOS builds, including CRAN binary distributions of R. Note that this is distinct from .Platform$GUI == &quot;AQUA&quot;, which is true only when using the Mac R.app GUI console.</td>
</tr>
<tr>
<td>http/ftp</td>
<td></td>
<td>does the default method for url and download.file support ‘http://’ and ‘ftp://’ URLs? Always TRUE as from R 3.3.0. However, in recent versions the default method is &quot;libcurl&quot; which depends on an external library and it is conceivable that library might not support ‘ftp://’ in future.</td>
</tr>
<tr>
<td>sockets</td>
<td></td>
<td>are make.socket and related functions available? Always TRUE as from R 3.3.0.</td>
</tr>
<tr>
<td>libxml</td>
<td></td>
<td>is there support for integrating libxml with the R event loop? TRUE as from R 3.3.0, FALSE as from R 4.2.0.</td>
</tr>
<tr>
<td>fifo</td>
<td></td>
<td>are FIFO connections supported?</td>
</tr>
<tr>
<td>cledit</td>
<td></td>
<td>is command-line editing available in the current R session? This is false in non-interactive sessions. It will be true for the command-line interface if readline support has been compiled in and ‘--no-readline’ was not used when R was invoked. (If ‘--interactive’ was used, command-line editing will not actually be available.)</td>
</tr>
<tr>
<td>iconv</td>
<td></td>
<td>is internationalization conversion via icov supported? Always true in current R.</td>
</tr>
<tr>
<td>NLS</td>
<td></td>
<td>is there Natural Language Support (for message translations)?</td>
</tr>
<tr>
<td>Rprof</td>
<td></td>
<td>is there support for Rprof() profiling? This is true if R was configured (before compilation) with default settings which include --enable-R-profiling.</td>
</tr>
<tr>
<td>profmem</td>
<td></td>
<td>is there support for memory profiling? See tracemem.</td>
</tr>
<tr>
<td>cairo</td>
<td></td>
<td>is there support for the svg, cairo_pdf and cairo_ps devices, and for type = &quot;cairo&quot; in the bmp, jpeg, png and tiff devices? Prior to R 4.1.0 this also indicated Cairo support in the X11 device, but it is now possible to build R with Cairo support for the bitmap devices without support for the X11 device (usually when that is not supported at all).</td>
</tr>
<tr>
<td>ICU</td>
<td></td>
<td>is ICU available for collation? See the help on Comparison and icuSetCollate: it is never used for a C locale.</td>
</tr>
<tr>
<td>long.double</td>
<td></td>
<td>does this build use a C long double type which is longer than double? Some platforms do not have such a type, and on others its use can be suppressed by the configure option ‘--disable-long-double’. Although not guaranteed, it is a reasonable assumption that if present long doubles will have at least as much range and accuracy as the ISO/IEC 60559 80-bit ‘extended precision’ format. Since R 4.0.0 .Machine gives information on the long-double type (if present).</td>
</tr>
<tr>
<td>libcurl</td>
<td></td>
<td>is libcurl available in this build? Used by function curlGetHeaders and optionally by download.file and url. As from R 3.3.0 always true for Unix-alikes, and as from R 4.2.0 true on Windows.</td>
</tr>
</tbody>
</table>
Note to macOS users

Capabilities "jpeg", "png" and "tiff" refer to the X11-based versions of these devices. If capabilities("aqua") is true, then these devices with type = "quartz" will be available, and out-of-the-box will be the default type. Thus for example the tiff device will be available if capabilities("aqua") || capabilities("tiff") if the defaults are unchanged.

See Also

.Platform, extSoftVersion, and grSoftVersion (and links there) for availability of capabilities external to R but used from R functions.

Examples

```r
capabilities()
if(!capabilities("ICU"))
  warning("ICU is not available")

## Does not call the internal X11-checking function:
capabilities(Xchk = FALSE)

## See also the examples for 'connections'.
```

---

cat

Concatenate and Print

Description

Outputs the objects, concatenating the representations. cat performs much less conversion than print.

Usage

```r
cat(... , file = "", sep = " ", fill = FALSE, labels = NULL,
     append = FALSE)
```

Arguments

...   R objects (see ‘Details’ for the types of objects allowed).

file   A connection, or a character string naming the file to print to. If "" (the default),
cat prints to the standard output connection, the console unless redirected by
sink. If it is "|cmd", the output is piped to the command given by ‘cmd’, by
opening a pipe connection.

sep   a character vector of strings to append after each element.

fill   a logical or (positive) numeric controlling how the output is broken into suc-
cessive lines. If FALSE (default), only newlines created explicitly by ‘\n’ are
printed. Otherwise, the output is broken into lines with print width equal to the
option width if fill is TRUE, or the value of fill if this is numeric. Linefeeds
are only inserted between elements, strings wider than fill are not wrapped.
Non-positive fill values are ignored, with a warning.

labels   character vector of labels for the lines printed. Ignored if fill is FALSE.
append logical. Only used if the argument file is the name of file (and not a connection or "|cmd"). If TRUE output will be appended to file; otherwise, it will overwrite the contents of file.

Details

cat is useful for producing output in user-defined functions. It converts its arguments to character vectors, concatenates them to a single character vector, appends the given \texttt{sep = string(s)} to each element and then outputs them.

No line feeds (aka “newline’s”) are output unless explicitly requested by ‘”\n” or if generated by filling (if argument fill is TRUE or numeric).

If file is a connection and open for writing it is written from its current position. If it is not open, it is opened for the duration of the call in “wt” mode and then closed again.

Currently only \texttt{atomic} vectors and \texttt{names} are handled, together with \texttt{NULL} and other zero-length objects (which produce no output). Character strings are output ‘as is’ (unlike \texttt{print.default} which escapes non-printable characters and backslash — use \texttt{encodeString} if you want to output encoded strings using \texttt{cat}). Other types of \texttt{R} object should be converted (e.g., by \texttt{as.character} or \texttt{format}) before being passed to \texttt{cat}. That includes factors, which are output as integer vectors.

\texttt{cat} converts numeric/complex elements in the same way as \texttt{print} (and not in the same way as \texttt{as.character} which is used by the S equivalent), so \texttt{options} “digits” and “scipen” are relevant. However, it uses the minimum field width necessary for each element, rather than the same field width for all elements.

Value

None (invisible \texttt{NULL}).

Note

If any element of \texttt{sep} contains a newline character, it is treated as a vector of terminators rather than separators, an element being output after every vector element \textit{and} a newline after the last. Entries are recycled as needed.

References


See Also

\texttt{print}, \texttt{format}, and \texttt{paste} which concatenates into a string.

Examples

\begin{verbatim}
iter <- stats::rpois(1, lambda = 10)
## print an informative message
cat("iteration = ", iter <- iter + 1, "\n")

## 'fill' and label lines:
cat(paste(letters, 100* 1:26), fill = TRUE, labels = paste0("","1:10", ""))
\end{verbatim}
cbind

Combine R Objects by Rows or Columns

Description

Take a sequence of vector, matrix or data-frame arguments and combine by columns or rows, respectively. These are generic functions with methods for other R classes.

Usage

cbind(..., deparse.level = 1)
rbind(..., deparse.level = 1)
## S3 method for class 'data.frame'
rbind(..., deparse.level = 1, make.row.names = TRUE,
       stringsAsFactors = FALSE, factor.exclude = TRUE)

Arguments

... (generalized) vectors or matrices. These can be given as named arguments. Other R objects may be coerced as appropriate, or S4 methods may be used: see sections ‘Details’ and ‘Value’. (For the "data.frame" method of cbind these can be further arguments to data.frame such as stringsAsFactors.)

deparse.level integer controlling the construction of labels in the case of non-matrix-like arguments (for the default method):
derparse.level = 0 constructs no labels;
the default deparse.level = 1 typically and deparse.level = 2 always construct labels from the argument names, see the ‘Value’ section below.

make.row.names (only for data frame method:) logical indicating if unique and valid row.names should be constructed from the arguments.

stringsAsFactors logical, passed to as.data.frame; only has an effect when the ... arguments contain a (non-data.frame) character.

factor.exclude if the data frames contain factors, the default TRUE ensures that NA levels of factors are kept, see PR#17562 and the ‘Data frame methods’. In R versions up to 3.6.x, factor.exclude = NA has been implicitly hardcoded (R <= 3.6.0) or the default (R = 3.6.x, x >= 1).

Details

The functions cbind and rbind are S3 generic, with methods for data frames. The data frame method will be used if at least one argument is a data frame and the rest are vectors or matrices. There can be other methods; in particular, there is one for time series objects. See the section on ‘Dispatch’ for how the method to be used is selected. If some of the arguments are of an S4 class, i.e., isS4(.) is true, S4 methods are sought also, and the hidden cbind / rbind functions from package methods maybe called, which in turn build on cbind2 or rbind2, respectively. In that case, deparse.level is obeyed, similarly to the default method.

In the default method, all the vectors/matrices must be atomic (see vector) or lists. Expressions are not allowed. Language objects (such as formulae and calls) and pairlists will be coerced to lists: other objects (such as names and external pointers) will be included as elements in a list result.
Any classes the inputs might have are discarded (in particular, factors are replaced by their internal codes).

If there are several matrix arguments, they must all have the same number of columns (or rows) and this will be the number of columns (or rows) of the result. If all the arguments are vectors, the number of columns (rows) in the result is equal to the length of the longest vector. Values in shorter arguments are recycled to achieve this length (with a warning if they are recycled only fractionally).

When the arguments consist of a mix of matrices and vectors the number of columns (rows) of the result is determined by the number of columns (rows) of the matrix arguments. Any vectors have their values recycled or subsetted to achieve this length.

For `cbind` (`rbind`), vectors of zero length (including `NULL`) are ignored unless the result would have zero rows (columns), for S compatibility. (Zero-extent matrices do not occur in S3 and are not ignored in R.)

Matrices are restricted to less than $2^{31}$ rows and columns even on 64-bit systems. So input vectors have the same length restriction: as from R 3.2.0 input matrices with more elements (but meeting the row and column restrictions) are allowed.

**Value**

For the default method, a matrix combining the ... arguments column-wise or row-wise. (Exception: if there are no inputs or all the inputs are `NULL`, the value is `NULL`.)

The type of a matrix result determined from the highest type of any of the inputs in the hierarchy raw < logical < integer < double < complex < character < list.

For `cbind` (`rbind`) the column (row) names are taken from the `colnames` (`rownames`) of the arguments if these are matrix-like. Otherwise from the names of the arguments or where those are not supplied and `deparse.level > 0`, by deparsing the expressions given, for `deparse.level = 1` only if that gives a sensible name (a 'symbol', see `is.symbol`).

For `cbind` row names are taken from the first argument with appropriate names: `rownames` for a matrix, or names for a vector of length the number of rows of the result.

For `rbind` column names are taken from the first argument with appropriate names: `colnames` for a matrix, or names for a vector of length the number of columns of the result.

**Data frame methods**

The `cbind` data frame method is just a wrapper for `data.frame(..., check.names = FALSE)`. This means that it will split matrix columns in data frame arguments, and convert character columns to factors unless `stringsAsFactors = FALSE` is specified.

The `rbind` data frame method first drops all zero-column and zero-row arguments. (If that leaves none, it returns the first argument with columns otherwise a zero-column zero-row data frame.)

It then takes the classes of the columns from the first data frame, and matches columns by name (rather than by position). Factors have their levels expanded as necessary (in the order of the levels of the level sets of the factors encountered) and the result is an ordered factor if and only if all the components were ordered factors. (The last point differs from S-PLUS.) Old-style categories (integer vectors with levels) are promoted to factors.

Note that for result column j, `factor(., exclude = X(j))` is applied, where

\[
X(j) := \begin{cases} 
\text{if(isTRUE(factor.exclude))} \\
\text{if(!NA.lev[j]) \# else NULL} 
\end{cases}
\]

where `NA.lev[j]` is true iff any contributing data frame has had a `factor` in column j with an explicit NA level.
Dispatch

The method dispatching is not done via UseMethod(), but by C-internal dispatching. Therefore there is no need for, e.g., rbind.default.

The dispatch algorithm is described in the source file (".../src/main/bind.c") as

1. For each argument we get the list of possible class memberships from the class attribute.
2. We inspect each class in turn to see if there is an applicable method.
3. If we find a method, we use it. Otherwise, if there was an S4 object among the arguments, we try S4 dispatch; otherwise, we use the default code.

If you want to combine other objects with data frames, it may be necessary to coerce them to data frames first. (Note that this algorithm can result in calling the data frame method if all the arguments are either data frames or vectors, and this will result in the coercion of character vectors to factors.)

References


See Also

c to combine vectors (and lists) as vectors, data.frame to combine vectors and matrices as a data frame.

Examples

```r
m <- cbind(1, 1:7) # the '1' (= shorter vector) is recycled
m <- cbind(m, 8:14[, c(1, 3, 2)]) # insert a column
m <- cbind(1:7, diag(3)) # vector is subset -> warning

ccbind(0, rbind(1, 1:3))
ccbind(I = 0, X = rbind(a = 1, b = 1:3)) # use some names
xx <- data.frame(I = rep(0, 2))
ccbind(xx, X = rbind(a = 1, b = 1:3)) # named differently

cbind(0, matrix(1, nrow = 0, ncol = 4)) #> Warning (making sense)
dim(ccbind(0, matrix(1, nrow = 2, ncol = 0))) #> 2 x 1

## deparse.level
dd <- 10
rbind(1:4, c = 2, "a++" = 10, dd, deparse.level = 0) # middle 2 rownames
rbind(1:4, c = 2, "a++" = 10, dd, deparse.level = 1) # 3 rownames (default)
rbind(1:4, c = 2, "a++" = 10, dd, deparse.level = 2) # 4 rownames

## cheap row names:
b0 <- gl(3, 4, labels=letters[1:3])
b0 <- setNames(b0, paste0("o", seq_along(b0)))
df <- data.frame(a = 1, B = b0, f = gl(4,3))
df. <- data.frame(a = 1, B = b0, f = gl(4,3))
new <- data.frame(a = 1, B = b0, f = "I")
(df1 <- rbind(df, new))
(df.1 <- rbind(df, new))
```
char.expand

Expand a String with Respect to a Target Table

Description

Seeks a unique match of its first argument among the elements of its second. If successful, it returns this element; otherwise, it performs an action specified by the third argument.

Usage

char.expand(input, target, nomatch = stop("no match"))

Arguments

input  a character string to be expanded.

input  a character vector with the values to be matched against.

nomatch  an R expression to be evaluated in case expansion was not possible.

Details

This function is particularly useful when abbreviations are allowed in function arguments, and need to be uniquely expanded with respect to a target table of possible values.

Value

A length-one character vector, one of the elements of target (unless nomatch is changed to be a non-error, when it can be a zero-length character string).

See Also

charmatch and pmatch for performing partial string matching.

Examples

locPars <- c("mean", "median", "mode")
char.expand("me", locPars, warning("Could not expand!"))
char.expand("mo", locPars)
character

Character Vectors

Description
Create or test for objects of type "character".

Usage

character(length = 0)
as.character(x, ...)
is.character(x)

Arguments

length A non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
x object to be coerced or tested.
... further arguments passed to or from other methods.

Details

as.character and is.character are generic: you can write methods to handle specific classes of objects, see InternalMethods. Further, for as.character the default method calls as.vector, so, only if(is.object(x)) is true, dispatch is first on methods for as.character and then for methods for as.vector.

as.character represents real and complex numbers to 15 significant digits (technically the compiler's setting of the ISO C constant DBL_DIG, which will be 15 on machines supporting IEC60559 arithmetic according to the C99 standard). This ensures that all the digits in the result will be reliable (and not the result of representation error), but does mean that conversion to character and back to numeric may change the number. If you want to convert numbers to character with the maximum possible precision, use format.

Value

character creates a character vector of the specified length. The elements of the vector are all equal to "".

as.character attempts to coerce its argument to character type; like as.vector it strips attributes including names. For lists and pairlists (including language objects such as calls) it deparses the elements individually, except that it extracts the first element of length-one character vectors.

is.character returns TRUE or FALSE depending on whether its argument is of character type or not.

Note

as.character breaks lines in language objects at 500 characters, and inserts newlines. Prior to 2.15.0 lines were truncated.
References


See Also

options: options scipen and OutDec affect the conversion of numbers.
paste, substr and strsplit for character concatenation and splitting, chartr for character translation and casefolding (e.g., upper to lower case) and sub, grep etc for string matching and substitutions. Note that help.search(keyword = "character") gives even more links.
deparse, which is normally preferable to as.character for language objects.
Quotes on how to specify character / string constants, including raw ones.

Examples

form <- y ~ a + b + c  
as.character(form)  ## length 3  
deparse(form)  ## like the input  
a0 <- 11/999  # has a repeating decimal representation  
(a1 <- as.character(a0))  
format(a0, digits = 16)  # shows one more digit  
a2 <- as.numeric(a1)  
a2 - a0  # normally around -1e-17  
as.character(a2)  # normally different from a1  
print(c(a0, a2), digits = 16)

---

**charmatch**  
*Partial String Matching*

Description

charmatch seeks matches for the elements of its first argument among those of its second.

Usage

charmatch(x, table, nomatch = NA_integer_)

Arguments

x  
the values to be matched: converted to a character vector by as.character.  
Long vectors are supported.

table  
the values to be matched against: converted to a character vector. Long vectors 
are not supported.

nomatch  
the (integer) value to be returned at non-matching positions.
Details

Exact matches are preferred to partial matches (those where the value to be matched has an exact match to the initial part of the target, but the target is longer).

If there is a single exact match or no exact match and a unique partial match then the index of the matching value is returned; if multiple exact or multiple partial matches are found then 0 is returned and if no match is found then nomatch is returned.

NA values are treated as the string constant "NA".

Value

An integer vector of the same length as x, giving the indices of the elements in table which matched, or nomatch.

Author(s)

This function is based on a C function written by Terry Therneau.

See Also

pmatch, match.

startsWith for another matching of initial parts of strings; grep or regexpr for more general (regexp) matching of strings.

Examples

charmatch("", ") # returns 1
charmatch("m", c("mean", "median", "mode").) # returns 0
charmatch("med", c("mean", "median", "mode").) # returns 2

chartr

Character Translation and Casefolding

Description

Translate characters in character vectors, in particular from upper to lower case or vice versa.

Usage

chartr(old, new, x)
tolower(x)
toupper(x)
casefold(x, upper = FALSE)

Arguments

x a character vector, or an object that can be coerced to character by as.character.
old a character string specifying the characters to be translated. If a character vector of length 2 or more is supplied, the first element is used with a warning.
new a character string specifying the translations. If a character vector of length 2 or more is supplied, the first element is used with a warning.
upper logical: translate to upper or lower case?.
Details

cahrtr translates each character in x that is specified in old to the corresponding character specified in new. Ranges are supported in the specifications, but character classes and repeated characters are not. If old contains more characters than new, an error is signaled; if it contains fewer characters, the extra characters at the end of new are ignored.

tolower and toupper convert upper-case characters in a character vector to lower-case, or vice versa. Non-alphabetic characters are left unchanged. More than one character can be mapped to a single upper-case character.

casefold is a wrapper for tolower and toupper provided for compatibility with S-PLUS.

Value

A character vector of the same length and with the same attributes as x (after possible coercion).

Elements of the result will be have the encoding declared as that of the current locale (see Encoding) if the corresponding input had a declared encoding and the current locale is either Latin-1 or UTF-8. The result will be in the current locale’s encoding unless the corresponding input was in UTF-8 or Latin-1, when it will be in UTF-8.

Note

These functions are platform-dependent, usually using OS services. The latter can be quite deficient, for example only covering ASCII characters in 8-bit locales. The definition of ‘alphabetic’ is platform-dependent and liable to change over time as most platforms are based on the frequently-updated Unicode tables.

See Also

sub and gsub for other substitutions in strings.

Examples

```r
x <- "MiXeD cAsE 123"
chartr("iXs", "why", x)
chartr("a-cX", "D-Fw", x)
tolower(x)
toupper(x)
## "Mixed Case" Capitalizing - toupper( every first letter of a word ) :

.simpleCap <- function(x) {
  s <- strsplit(x, " ")[[1]]
  paste(toupper(substring(s, 1, 1)), substring(s, 2),
         sep = " ", collapse = " ")
}
.simpleCap("the quick red fox jumps over the lazy brown dog")
## -> [1] "The Quick Red Fox Jumps Over The Lazy Brown Dog"

## and the better, more sophisticated version:
capwords <- function(s, strict = FALSE) {
  cap <- function(s) paste(toupper(substring(s, 1, 1))),
    s <- substring(s, 2); if(strict) tolower(s) else s),
    sep = " ", collapse = " ")
  sapply(strsplit(s, split = " "), cap, USE.NAMES = !is.null(names(s)))
}
```
Warn About Extraneous Arguments in the "..." of Its Caller

Description

Warn about extraneous arguments in the ... of its caller. A utility to be used e.g., in S3 methods which need a formal ... argument but do not make any use of it. This helps catching user errors in calling the function in question (which is the caller of chkDots()).

Usage

chkDots(..., which.call = -1, allowed = character(0))

Arguments

... “the dots”, as passed from the caller.
which.call passed to sys.call(). A caller may use -2 if the message should mention its caller.
allowed not yet implemented: character vector of named elements in ... which are “allowed” and hence not warned about.

Author(s)

Martin Maechler, first version outside base, June 2012.

See Also

warning, ....
Examples

```r
seq.default ## <- you will see 'chkDots(...)' 

seq(1,5, foo = "bar") # gives warning via chkDots()
```

```r
## warning with more than one ...-entry:
density.f <- function(x, ...) NextMethod("density")
x <- density(structure(rnorm(10), class="f"), bar=TRUE, baz=TRUE)
```

chol

The Cholesky Decomposition

Description

Compute the Cholesky factorization of a real symmetric positive-definite square matrix.

Usage

```r
chol(x, ...)
```

## Default S3 method:
```r
c chol(x, pivot = FALSE, LINPACK = FALSE, tol = -1, ...)
```

Arguments

- `x`: an object for which a method exists. The default method applies to numeric (or logical) symmetric, positive-definite matrices.
- `...`: arguments to be based to or from methods.
- `pivot`: Should pivoting be used?
- `LINPACK`: logical. Should LINPACK be used (now an error)?
- `tol`: A numeric tolerance for use with pivot = TRUE.

Details

chol is generic: the description here applies to the default method.

Note that only the upper triangular part of x is used, so that $R' R = x$ when x is symmetric.

If pivot = FALSE and x is not non-negative definite an error occurs. If x is positive semi-definite (i.e., some zero eigenvalues) an error will also occur as a numerical tolerance is used.

If pivot = TRUE, then the Cholesky decomposition of a positive semi-definite x can be computed.

The rank of x is returned as attr(Q, "rank"), subject to numerical errors. The pivot is returned as attr(Q, "pivot"). It is no longer the case that t(Q) %*% Q equals x. However, setting pivot <- attr(Q, "pivot") and oo <- order(pivot), it is true that t(Q[, oo]) %*% Q[, oo] equals x, or, alternatively, t(Q) %*% Q equals x[pivot, pivot]. See the examples.

The value of tol is passed to LAPACK, with negative values selecting the default tolerance of (usually) nrow(x) * .Machine$double.neg. eps * max(diag(x)). The algorithm terminates once the pivot is less than tol.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.
The upper triangular factor of the Cholesky decomposition, i.e., the matrix \( R \) such that \( R' R = x \) (see example).

If pivoting is used, then two additional attributes "pivot" and "rank" are also returned.

The code does not check for symmetry.

If pivot = TRUE and \( x \) is not non-negative definite then there will be a warning message but a meaningless result will occur. So only use pivot = TRUE when \( x \) is non-negative definite by construction.

This is an interface to the LAPACK routines DPOTRF and DPSTRF.

LAPACK is from https://netlib.org/lapack/ and its guide is listed in the references.


See Also

`chol2inv` for its inverse (without pivoting), `backsolve` for solving linear systems with upper triangular left sides.

`qr`, `svd` for related matrix factorizations.

Examples

```r
(m <- matrix(c(5,1,1,3),2,2))
(cm <- chol(m))
t(cm) %*% cm #-- = 'm'
crossprod(cm) #-- = 'm'

# now for something positive semi-definite
x <- matrix(c(1:5, (1:5)^2), 5, 2)
x <- cbind(x, x[, 1] + 3*x[, 2])
colnames(x) <- letters[20:22]
m <- crossprod(x)
qr(m)$rank # is 2, as it should be

# chol() may fail, depending on numerical rounding:
# chol() unlike qr() does not use a tolerance.
try(chol(m))

(Q <- chol(m, pivot = TRUE))
## we can use this by
pivot <- attr(Q, "pivot")
crossprod(Q[, order(pivot)]) # recover m

## now for a non-positive-definite matrix
```
chol2inv

( m <- matrix(c(5,-5,-5,3), 2, 2) )
try(chol(m)) # fails
(Q <- chol(m, pivot = TRUE)) # warning
crossprod(Q) # not equal to m

chol2inv

Inverse from Cholesky (or QR) Decomposition

Description

Invert a symmetric, positive definite square matrix from its Cholesky decomposition. Equivalently, compute \((X'X)^{-1}\) from the \((R\) part) of the QR decomposition of \(X\).

Usage

chol2inv(x, size = NCOL(x), LINPACK = FALSE)

Arguments

x

a matrix. The first size columns of the upper triangle contain the Cholesky decomposition of the matrix to be inverted.

size

the number of columns of \(x\) containing the Cholesky decomposition.

LINPACK

logical. Defunct and gives an error.

Value

The inverse of the matrix whose Cholesky decomposition was given.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Source

This is an interface to the LAPACK routine \(\text{DPOTRI}\). LAPACK is from https://netlib.org/lapack/ and its guide is listed in the references.

References


See Also

chol, solve.

Examples

cma <- chol(ma <- cbind(1, 1:3, c(1,3,7)))
ma %%% chol2inv(cma)
chooseOpsMethod  

Choose the Appropriate Method for Ops

Description

chooseOpsMethod is a function called by the Ops Group Generic when two suitable methods are found for a given call. It determines which method to use for the operation based on the objects being dispatched.

The function is first called with reverse = FALSE, where x corresponds to the first argument and y to the second argument of the group generic call. If chooseOpsMethod() returns FALSE for x, then chooseOpsMethod is called again, with x and y swapped, mx and my swapped, and reverse = TRUE.

Usage

chooseOpsMethod(x, y, mx, my, cl, reverse)

Arguments

x, y  
The objects being dispatched on by the group generic.

mx, my  
The methods found for objects x and y.

cl  
The call to the group generic.

reverse  
A logical value indicating whether x and y are reversed from the way they were supplied to the generic.

Value

This function must return either TRUE or FALSE. A value of TRUE indicates that method mx should be used.

See Also

Ops

Examples

# Create two objects with custom Ops methods
foo_obj <- structure(1, class = "foo")
bar_obj <- structure(1, class = "bar")

`+.foo` <- function(e1, e2) "foo"
Ops.bar <- function(e1, e2) "bar"

invisible(foo_obj + bar_obj) # Warning: Incompatible methods
chooseOpsMethod.bar <- function(x, y, mx, my, cl, reverse) TRUE

stopifnot(exprs = {
  identical(foo_obj + bar_obj, "bar")
  identical(bar_obj + foo_obj, "bar")
})

# cleanup
rm(foo_obj, bar_obj, `+.foo`, Ops.bar, chooseOpsMethod.bar)
**class**

Object Classes

**Description**

R possesses a simple generic function mechanism which can be used for an object-oriented style of programming. Method dispatch takes place based on the class of the first argument to the generic function.

**Usage**

```
class(x)
class(x) <- value
unclass(x)
inherits(x, what, which = FALSE)
nameOfClass(x)
isa(x, what)

oldClass(x)
oldClass(x) <- value
$class2(x)
```

**Arguments**

- `x`: a R object
- `what, value`: a character vector naming classes. `value` can also be `NULL`. `what` can also be a non-character R object with a `nameOfClass()` method.
- `which`: logical affecting return value: see 'Details'.

**Details**

Here, we describe the so called “S3” classes (and methods). For “S4” classes (and methods), see ‘Formal classes’ below.

Many R objects have a class attribute, a character vector giving the names of the classes from which the object inherits. (Functions `oldClass` and `oldClass<-` get and set the attribute, which can also be done directly.)

If the object does not have a class attribute, it has an implicit class, notably "matrix", "array", "function" or "numeric" or the result of `typeof(x)` (which is similar to `mode(x)`), but for type "language" and mode "call", where the following extra classes exist for the corresponding functions `calls`: if, while, for, =, <=, {.call.

Note that for objects `x` of an implicit (or an S4) class, when a (S3) generic function `foo(x)` is called, method dispatch may use more classes than are returned by `class(x)`, e.g., for a numeric matrix, the `foo.numeric()` method may apply. The exact full character vector of the classes which `UseMethod()` uses, is available as `.class2(x)` since R version 4.0.0. (This also applies to S4 objects when S3 dispatch is considered, see below.)

Beware that using `.class2()` for other reasons than didactical, diagnostic or for debugging may rather be a misuse than smart.

`NULL` objects (of implicit class "NULL") cannot have attributes (hence no class attribute) and attempting to assign a class is an error.
When a generic function `fun` is applied to an object with class attribute `c("first", "second")`, the system searches for a function called `fun.first` and, if it finds it, applies it to the object. If no such function is found, a function called `fun.second` is tried. If no class name produces a suitable function, the function `fun.default` is used (if it exists). If there is no class attribute, the implicit class is tried, then the default method.

The function `class` prints the vector of names of classes an object inherits from. Correspondingly, `class<-` sets the classes an object inherits from. Assigning an empty character vector or NULL removes the class attribute, as for `oldClass<-` or direct attribute setting. Whereas it is clearer to explicitly assign NULL to remove the class, using an empty vector is more natural in e.g., `class(x) <- setdiff(class(x), "ts")`.

`unclass` returns (a copy of) its argument with its class attribute removed. (It is not allowed for objects which cannot be copied, namely environments and external pointers.)

`inherits` indicates whether its first argument inherits from any of the classes specified in the `what` argument. If `which` is `TRUE` then an integer vector of the same length as `what` is returned. Each element indicates the position in the `class(x)` matched by the element of `what`; zero indicates no match. If `which` is `FALSE` then `TRUE` is returned by `inherits` if any of the names in `what` match with any class.

`nameOfClass` is an S3 generic. It is called by `inherits` to get the class name for `what`, allowing for `what` to be values other than a character vector. `nameOfClass` methods are expected to return a character vector of length 1.

`isa` tests whether `x` is an object of class(es) as given in `what` by using `is` if `x` is an S4 object, and otherwise giving `TRUE` iff all elements of `class(x)` are contained in `what`.

All but `inherits` and `isa` are primitive functions.

**Formal classes**

An additional mechanism of *formal classes*, nicknamed “S4”, is available in package `methods` which is attached by default. For objects which have a formal class, its name is returned by `class` as a character vector of length one and method dispatch can happen on several arguments, instead of only the first. However, S3 method selection attempts to treat objects from an S4 class as if they had the appropriate S3 class attribute, as does `inherits`. Therefore, S3 methods can be defined for S4 classes. See the 'Introduction' and 'Methods_for_S3' help pages for basic information on S4 methods and for the relation between these and S3 methods.

The replacement version of the function sets the class to the value provided. For classes that have a formal definition, directly replacing the class this way is strongly deprecated. The expression `as(object, value)` is the way to coerce an object to a particular class.

The analogue of `inherits` for formal classes is `is`. The two functions behave consistently with one exception: S4 classes can have conditional inheritance, with an explicit test. In this case, `is` will test the condition, but `inherits` ignores all conditional superclasses.

**Note**

Functions `oldClass` and `oldClass<-` behave in the same way as functions of those names in S-PLUS 5/6, but in R `UseMethod` dispatches on the class as returned by `class` (with some interpolated classes: see the link) rather than `oldClass`. However, group generics dispatch on the `oldClass` for efficiency, and internal generics only dispatch on objects for which `is.object` is true.

**See Also**

`UseMethod`, `NextMethod`, ‘group generic’, ‘internal generic’
Examples

```r
x <- 10
class(x) # "numeric"
oldClass(x) # NULL
inherits(x, "a") #FALSE
class(x) <- c("a", "b")
inherits(x,"a") # TRUE
inherits(x, "a", TRUE) # 1
inherits(x, c("a", "b", "c"), TRUE) # 1 2 0

class( quote(pi) ) # "name"
## regular calls
class( quote(sin(pi*x)) ) # "call"
## special calls
class( quote(x <- 1) ) # "<-"
class( quote((1 < 2)) ) # "("
class( quote( if(8<3) pi ) ) # "if"

.col2(pi) # "double" "numeric"
.col2(matrix(1:6, 2,3)) # "matrix" "array" "integer" "numeric"
```

---

**col**

Column Indexes

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Returns a matrix of integers indicating their column number in a matrix-like object, or a factor of column labels.</td>
</tr>
</tbody>
</table>

**Usage**

```r
col(x, as.factor = FALSE)
.col(dim)
```

**Arguments**

- `x`: a matrix-like object, that is one with a two-dimensional dim.
- `dim`: a matrix dimension, i.e., an integer valued numeric vector of length two (with non-negative entries).
- `as.factor`: a logical value indicating whether the value should be returned as a factor of column labels (created if necessary) rather than as numbers.

**Value**

An integer (or factor) matrix with the same dimensions as x and whose i-j-th element is equal to j (or the j-th column label).

**References**

See Also

row to get rows; slice.index for a general way to get slice indices in an array.

Examples

# extract an off-diagonal of a matrix
ma <- matrix(1:12, 3, 4)
ma[row(ma) == col(ma) + 1]

# create an identity 5-by-5 matrix more slowly than diag(n = 5):
x <- matrix(0, nrow = 5, ncol = 5)
x[row(x) == col(x)] <- 1

(i34 <- .col(3:4))
stopifnot(identical(i34, .col(c(3,4)))) # 'dim' maybe "double"

Colon

Colon Operator

Description

Generate regular sequences.

Usage

from:to
  a:b

Arguments

from       starting value of sequence.
to         (maximal) end value of the sequence.
a, b       factors of the same length.

Details

The binary operator : has two meanings: for factors a:b is equivalent to interaction(a, b) (but the levels are ordered and labelled differently).

For other arguments from:to is equivalent to seq(from, to), and generates a sequence from from to to in steps of 1 or -1. Value to will be included if it differs from from by an integer up to a numeric fuzz of about 1e-7. Non-numeric arguments are coerced internally (hence without dispatching methods) to numeric—complex values will have their imaginary parts discarded with a warning.

Value

For numeric arguments, a numeric vector. This will be of type integer if from is integer-valued and the result is representable in the R integer type, otherwise of type "double" (aka mode "numeric").

For factors, an unordered factor with levels labelled as 1a:1b and ordered lexicographically (that is, 1b varies fastest).
References

(for numeric arguments: S does not have : for factors.)

See Also

`seq` (a generalization of `from:to`).
As an alternative to using : for factors, `interaction`.
For : used in the formal representation of an interaction, see `formula`.

Examples

1:4
pi:6 # real
6:pi # integer

f1 <- gl(2, 3); f1
f2 <- gl(3, 2); f2
f1:f2 # a factor, the "cross" f1 x f2

colSums

Form Row and Column Sums and Means

Description

Form row and column sums and means for numeric arrays (or data frames).

Usage

```r
colSums (x, na.rm = FALSE, dims = 1)
rowSums (x, na.rm = FALSE, dims = 1)
colMeans(x, na.rm = FALSE, dims = 1)
rowMeans(x, na.rm = FALSE, dims = 1)
```

Arguments

- `x` an array of two or more dimensions, containing numeric, complex, integer or logical values, or a numeric data frame. For `.colSums()` etc, a numeric, integer or logical matrix (or vector of length m * n).
- `na.rm` logical. Should missing values (including NaN) be omitted from the calculations?
- `dims` integer: Which dimensions are regarded as ‘rows’ or ‘columns’ to sum over. For `row*`, the sum or mean is over dimensions `dims+1, ...`; for `col*` it is over dimensions `1:dims`.
- `m, n` the dimensions of the matrix `x` for `.colSums()` etc.
Details

These functions are equivalent to use of \texttt{apply} with \texttt{FUN = mean} or \texttt{FUN = sum} with appropriate margins, but are a lot faster. As they are written for speed, they blur over some of the subtleties of \texttt{NaN} and \texttt{NA}. If \texttt{na.rm = FALSE} and either \texttt{NaN} or \texttt{NA} appears in a sum, the result will be one of \texttt{NaN} or \texttt{NA}, but which might be platform-dependent.

Notice that omission of missing values is done on a per-column or per-row basis, so column means may not be over the same set of rows, and vice versa. To use only complete rows or columns, first select them with \texttt{na.omit} or \texttt{complete.cases} (possibly on the transpose of \texttt{x}).

The versions with an initial dot in the name (\texttt{.colSums()} etc) are ‘bare-bones’ versions for use in programming: they apply only to numeric (like) matrices and do not name the result.

Value

A numeric or complex array of suitable size, or a vector if the result is one-dimensional. For the first four functions the \texttt{dimnames} (or names for a vector result) are taken from the original array.

If there are no values in a range to be summed over (after removing missing values with \texttt{na.rm = TRUE}), that component of the output is set to 0 (*Sums*) or \texttt{NaN} (*Means*), consistent with \texttt{sum} and \texttt{mean}.

See Also

\texttt{apply}, \texttt{rowsum}

Examples

```r
## Compute row and column sums for a matrix:
set.seed(1)
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
rowSums(x); colSums(x)
dimnames(x)[[1]] <- letters[1:8]
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
x[] <- as.integer(x)
rowSums(x); colSums(x)
x[] <- x < 3
rowSums(x); colSums(x)
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
x[3, ] <- NA; x[4, 2] <- NA
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
rowSums(x, na.rm = TRUE); colSums(x, na.rm = TRUE)
rowMeans(x, na.rm = TRUE); colMeans(x, na.rm = TRUE)

## an array
dim(UCBAdmissions)
rowSums(UCBAdmissions); rowSums(UCBAdmissions, dims = 2)
colSums(UCBAdmissions); colSums(UCBAdmissions, dims = 2)

## complex case
x <- cbind(x1 = 3 + 2i, x2 = c(4:1, 2:5) - 5i)
x[3, ] <- NA; x[4, 2] <- NA
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
rowSums(x, na.rm = TRUE); colSums(x, na.rm = TRUE)
rowMeans(x, na.rm = TRUE); colMeans(x, na.rm = TRUE)
```
**commandArgs**

**Extract Command Line Arguments**

**Description**

Provides access to a copy of the command line arguments supplied when this R session was invoked.

**Usage**

commandArgs(trailingOnly = FALSE)

**Arguments**

trailingOnly logical. Should only arguments after ‘--args’ be returned?

**Details**

These arguments are captured before the standard R command line processing takes place. This means that they are the unmodified values. This is especially useful with the ‘--args’ command-line flag to R, as all of the command line after that flag is skipped.

**Value**

A character vector containing the name of the executable and the user-supplied command line arguments. The first element is the name of the executable by which R was invoked. The exact form of this element is platform dependent: it may be the fully qualified name, or simply the last component (or basename) of the application, or for an embedded R it can be anything the programmer supplied. If trailingOnly = TRUE, a character vector of those arguments (if any) supplied after ‘--args’.

**See Also**

R.home(), Startup and BATCH

**Examples**

```r
commandArgs()
## Spawn a copy of this application as it was invoked,
## subject to shell quoting issues
## system(paste(commandArgs(), collapse = " "))
```

**comment**

**Query or Set a "comment" Attribute**

**Description**

These functions set and query a comment attribute for any R objects. This is typically useful for data.frames or model fits.

Contrary to other attributes, the comment is not printed (by print or print.default).

Assigning NULL or a zero-length character vector removes the comment.
Usage

comment(x)
comment(x) <- value

Arguments

x   any R object
value a character vector, or NULL.

See Also

attributes and attr for other attributes.

Examples

x <- matrix(1:12, 3, 4)
comment(x) <- c("This is my very important data from experiment #0234",
"Jun 5, 1998")
x
comment(x)

Comparison

Relational Operators

Description

Binary operators which allow the comparison of values in atomic vectors.

Usage

x < y
x > y
x <= y
x >= y
x == y
x != y

Arguments

x, y atomic vectors, symbols, calls, or other objects for which methods have been written.

Details

The binary comparison operators are generic functions: methods can be written for them individually or via the Ops group generic function. (See Ops for how dispatch is computed.)

Comparison of strings in character vectors is lexicographic within the strings using the collating sequence of the locale in use: see locales. The collating sequence of locales such as ‘en_US’ is normally different from ‘C’ (which should use ASCII) and can be surprising. Beware of making any assumptions about the collation order: e.g. in Estonian Z comes between S and T, and collation is not necessarily character-by-character – in Danish aa sorts as a single letter, after z. In Welsh ng
Comparison

may or may not be a single sorting unit: if it is it follows $g$. Some platforms may not respect the locale and always sort in numerical order of the bytes in an 8-bit locale, or in Unicode code-point order for a UTF-8 locale (and may not sort in the same order for the same language in different character sets). Collation of non-letters (spaces, punctuation signs, hyphens, fractions and so on) is even more problematic.

Character strings can be compared with different marked encodings (see Encoding): they are translated to UTF-8 before comparison.

Raw vectors should not really be considered to have an order, but the numeric order of the byte representation is used.

At least one of $x$ and $y$ must be an atomic vector, but if the other is a list $R$ attempts to coerce it to the type of the atomic vector: this will succeed if the list is made up of elements of length one that can be coerced to the correct type.

If the two arguments are atomic vectors of different types, one is coerced to the type of the other, the (decreasing) order of precedence being character, complex, numeric, integer, logical and raw.

Missing values (NA) and NaN values are regarded as non-comparable even to themselves, so comparisons involving them will always result in NA. Missing values can also result when character strings are compared and one is not valid in the current collation locale.

Language objects such as symbols and calls are deparsed to character strings before comparison.

Value

A logical vector indicating the result of the element by element comparison. The elements of shorter vectors are recycled as necessary.

Objects such as arrays or time-series can be compared this way provided they are conformable.

S4 methods

These operators are members of the S4 Compare group generic, and so methods can be written for them individually as well as for the group generic (or the Ops group generic), with arguments $c(e1, e2)$.

Note

Do not use \texttt{==} and \texttt{!=} for tests, such as in if expressions, where you must get a single TRUE or FALSE. Unless you are absolutely sure that nothing unusual can happen, you should use the identical function instead.

For numerical and complex values, remember $\texttt{==}$ and $\texttt{!=}$ do not allow for the finite representation of fractions, nor for rounding error. Using \texttt{all.equal} with identical or \texttt{isTRUE} is almost always preferable; see the examples. (This also applies to the other comparison operators.)

These operators are sometimes called as functions as e.g. `\texttt{\langle}(x, y)`: see the description of how argument-matching is done in Ops.

References


Collation of character strings is a complex topic. For an introduction see https://en.wikipedia.org/wiki/Collating_sequence. The Unicode Collation Algorithm (https://unicode.org/reports/tr10/) is likely to be increasingly influential. Where available R by default makes use of ICU (https://icu.unicode.org/) for collation (except in a C locale).
See Also

Logic on how to combine results of comparisons, i.e., logical vectors.
factor for the behaviour with factor arguments.
Syntax for operator precedence.
capabilities for whether ICU is available, and icuSetCollate to tune the string collation algorithm when it is.

Examples

```r
x <- stats::rnorm(20)
x < 1
x[x > 0]

x1 <- 0.5 - 0.3
x2 <- 0.3 - 0.1
x1 == x2  # FALSE on most machines
isTRUE(all.equal(x1, x2))  # TRUE everywhere
```

# range of most 8-bit charsets, as well as of Latin-1 in Unicode
z <- c(32:126, 160:255)
x <- if(l10n_info()$MBCS) {
  intToUtf8(z, multiple = TRUE)
} else rawToChar(as.raw(z), multiple = TRUE)
# by number
writeLines(strwrap(paste(x, collapse=" "), width = 60))
# by locale collation
writeLines(strwrap(paste(sort(x), collapse=" "), width = 60))
```

complex

Complex Numbers and Basic Functionality

Description

Basic functions which support complex arithmetic in R, in addition to the arithmetic operators +, -, *, /, and ^.

Usage

```r
complex(length.out = 0, real = numeric(), imaginary = numeric(),
        modulus = 1, argument = 0)
as.complex(x, ...)
is.complex(x)

Re(z)
Im(z)
Mod(z)
Arg(z)
Conj(z)
```
Arguments

- `length.out` numeric. Desired length of the output vector, inputs being recycled as needed.
- `real` numeric vector.
- `imaginary` numeric vector.
- `modulus` numeric vector.
- `argument` numeric vector.
- `x` an object, probably of mode `complex`.
- `z` an object of mode `complex`, or one of a class for which a methods has been defined.
- `...` further arguments passed to or from other methods.

Details

Complex vectors can be created with `complex`. The vector can be specified either by giving its length, its real and imaginary parts, or modulus and argument. (Giving just the length generates a vector of complex zeroes.)

`as.complex` attempts to coerce its argument to be of complex type: like `as.vector` it strips attributes including names. Up to R versions 3.2.x, all forms of NA and NaN were coerced to a complex NA, i.e., the `NA_complex_` constant, for which both the real and imaginary parts are NA. Since R 3.3.0, typically only objects which are NA in parts are coerced to complex NA, but others with NaN parts, are not. As a consequence, complex arithmetic where only NaN's (but no NA's) are involved typically will not give complex NA but complex numbers with real or imaginary parts of NaN.

Note that `is.complex` and `is.numeric` are never both TRUE.

The functions `Re`, `Im`, `Mod`, `Arg` and `Conj` have their usual interpretation as returning the real part, imaginary part, modulus, argument and complex conjugate for complex values. The modulus and argument are also called the polar coordinates. If \( z = x + iy \) with real \( x \) and \( y \), for \( r = \text{Mod}(z) = \sqrt{x^2 + y^2} \), and \( \phi = \text{Arg}(z) \), \( x = r \cos(\phi) \) and \( y = r \sin(\phi) \). They are all internal generic primitive functions: methods can be defined for them individually or via the `Complex` group generic.

In addition to the arithmetic operators (see Arithmetic) `+`, `-`, `*`, `/`, and `^`, the elementary trigonometric, logarithmic, exponential, square root and hyperbolic functions are implemented for complex values.

Matrix multiplications (`%*%`, `crossprod`, `tcrossprod`) are also defined for complex matrices (`matrix`), and so are `solve`, `eigen` or `svd`.

Internally, complex numbers are stored as a pair of `double` precision numbers, either or both of which can be NaN (including NA, see `NA_complex_` and above) or plus or minus infinity.

S4 methods

`as.complex` is primitive and can have S4 methods set.

`Re`, `Im`, `Mod`, `Arg` and `Conj` constitute the S4 group generic `Complex` and so S4 methods can be set for them individually or via the group generic.

Note

Operations and functions involving complex NaN mostly rely on the C library’s handling of ‘double complex’ arithmetic, which typically returns complex(re=NaN, im=NaN) (but we have not seen a guarantee for that). For + and -, R’s own handling works strictly “coordinate wise”.

Operations involving complex NA, i.e., `NA_complex_`, return `NA_complex_`.
References


See Also

*Arithmetic*: polyroot finds all \(n\) complex roots of a polynomial of degree \(n\).

Examples

```r
require(graphics)

0i ^ (-3:3)

matrix(1i^ (-6:5), nrow = 4) # all columns are the same
0 ^ i # a complex NaN

## create a complex normal vector
z <- complex(real = stats::rnorm(100), imaginary = stats::rnorm(100))
## or also (less efficient)::
z2 <- 1:2 + 1i*(8:9)

## The Arg(.) is an angle:
zz <- (rep(1:4, length.out = 9) + 1i*(9:1))/10
zz.shift <- complex(modulus = Mod(zz), argument = Arg(zz) + pi)
plot(zz, xlim = c(-1,1), ylim = c(-1,1), col = "red", asp = 1,
     main = expression(paste("Rotation by ", " 180^o")))
abline(h = 0, v = 0, col = "blue", lty = 3)
points(zz.shift, col = "orange")

showC <- function(z) noquote(sprintf("(R = %g, I = %g)", Re(z), Im(z)))

## The exact result of this *depends* on the platform, compiler, math-library:
(NpNA <- NaN + NA_complex_); str(NpNA) # behaves as 'cplx NA'
stopifnot(is.na(NpNA), is.na(NA_complex_), is.na(Re(NA_complex_)), is.na(Im(NA_complex_)))
showC(NpNA)# but not always is (shows '(R = NaN, I = NA)' on some platforms)
## and this is not TRUE everywhere:
identical(NpNA, NA_complex_)
showC(NA_complex_) # always == (R = NA, I = NA)
```

## Condition Handling and Recovery

### Description

These functions provide a mechanism for handling unusual conditions, including errors and warnings.

### Usage

```r
tryCatch(expr, ..., finally)
withCallingHandlers(expr, ...)
globalCallingHandlers(...)
```
signalCondition(cond)
simpleCondition(message, call = NULL)
simpleError (message, call = NULL)
simpleWarning (message, call = NULL)
simpleMessage (message, call = NULL)
errorCondition(message, ..., class = NULL, call = NULL)
warningCondition(message, ..., class = NULL, call = NULL)

## S3 method for class 'condition'
as.character(x, ...)
## S3 method for class 'error'
as.character(x, ...)
## S3 method for class 'condition'
print(x, ...)
## S3 method for class 'restart'
print(x, ...)
conditionCall(c)
## S3 method for class 'condition'
conditionCall(c)
conditionMessage(c)
## S3 method for class 'condition'
conditionMessage(c)

withRestarts(expr, ...)
computeRestarts(cond = NULL)
findRestart(name, cond = NULL)
invokeRestart(r, ...)
tryInvokeRestart(r, ...)
invokeRestartInteractively(r)
isRestart(x)
restartDescription(r)
restartFormals(r)
suspendInterrupts(expr)
allowInterrupts(expr)

.signalSimpleWarning(msg, call)
.handleSimpleError(h, msg, call)
.tryResumeInterrupt()

Arguments

  c       a condition object.
  call    call expression.
  cond    a condition object.
  expr    expression to be evaluated.
finally expression to be evaluated before returning or exiting.

h function.

message character string.

msg character string.

name character string naming a restart.

r restart object.

x object.

class character string naming a condition class.

... additional arguments; see details below.

Details

The condition system provides a mechanism for signaling and handling unusual conditions, including errors and warnings. Conditions are represented as objects that contain information about the condition that occurred, such as a message and the call in which the condition occurred. Currently conditions are S3-style objects, though this may eventually change.

Conditions are objects inheriting from the abstract class condition. Errors and warnings are objects inheriting from the abstract subclasses error and warning. The class simpleError is the class used by stop and all internal error signals. Similarly, simpleWarning is used by warning, and simpleMessage is used by message. The constructors by the same names take a string describing the condition as argument and an optional call. The functions conditionMessage and conditionCall are generic functions that return the message and call of a condition.

The function errorCondition can be used to construct error conditions of a particular class with additional fields specified as the ... argument. warningCondition is analogous for warnings.

Conditions are signaled by signalCondition. In addition, the stop and warning functions have been modified to also accept condition arguments.

The function tryCatch evaluates its expression argument in a context where the handlers provided in the ... argument are available. The finally expression is then evaluated in the context in which tryCatch was called; that is, the handlers supplied to the current tryCatch call are not active when the finally expression is evaluated.

Handlers provided in the ... argument to tryCatch are established for the duration of the evaluation of expr. If no condition is signaled when evaluating expr then tryCatch returns the value of the expression.

If a condition is signaled while evaluating expr then established handlers are checked, starting with the most recently established ones, for one matching the class of the condition. When several handlers are supplied in a single tryCatch then the first one is considered more recent than the second. If a handler is found then control is transferred to the tryCatch call that established the handler, the handler found and all more recent handlers are disestablished, the handler is called with the condition as its argument, and the result returned by the handler is returned as the value of the tryCatch call.

Calling handlers are established by withCallingHandlers. If a condition is signaled and the applicable handler is a calling handler, then the handler is called by signalCondition in the context where the condition was signaled but with the available handlers restricted to those below the handler called in the handler stack. If the handler returns, then the next handler is tried; once the last handler has been tried, signalCondition returns NULL.

globalCallingHandlers establishes calling handlers globally. These handlers are only called as a last resort, after the other handlers dynamically registered with withCallingHandlers have been invoked. They are called before the error global option (which is the legacy interface for
global handling of errors). Registering the same handler multiple times moves that handler on top of the stack, which ensures that it is called first. Global handlers are a good place to define a general purpose logger (for instance saving the last error object in the global workspace) or a general recovery strategy (e.g. installing missing packages via the retry_loadNamespace restart).

Like withCallingHandlers and tryCatch, globalCallingHandlers takes named handlers. Unlike these functions, it also has an options-like interface: you can establish handlers by passing a single list of named handlers. To unregister all global handlers, supply a single ‘NULL’. The list of deleted handlers is returned invisibly. Finally, calling globalCallingHandlers without arguments returns the list of currently established handlers, visibly.

User interrupts signal a condition of class interrupt that inherits directly from class condition before executing the default interrupt action.

Restarts are used for establishing recovery protocols. They can be established using withRestarts. One pre-established restart is an abort restart that represents a jump to top level. findRestart and computeRestarts find the available restarts. findRestart returns the most recently established restart of the specified name. computeRestarts returns a list of all restarts. Both can be given a condition argument and will then ignore restarts that do not apply to the condition.

invokeRestart transfers control to the point where the specified restart was established and calls the restart's handler with the arguments, if any, given as additional arguments to invokeRestart. The restart argument to invokeRestart can be a character string, in which case findRestart is used to find the restart. If no restart is found, an error is thrown.

tryInvokeRestart is a variant of invokeRestart that returns silently when the restart cannot be found with findRestart. Because a condition of a given class might be signalled with arbitrary protocols (error, warning, etc), it is recommended to use this permissive variant whenever you are handling conditions signalled from a foreign context. For instance, invocation of a "muffleWarning" restart should be optional because the warning might have been signalled by the user or from a different package with the stop or message protocols. Only use invokeRestart when you have control of the signalling context, or when it is a logical error if the restart is not available.

New restarts for withRestarts can be specified in several ways. The simplest is in name = function form where the function is the handler to call when the restart is invoked. Another simple variant is as name = string where the string is stored in the description field of the restart object returned by findRestart; in this case the handler ignores its arguments and returns NULL. The most flexible form of a restart specification is as a list that can include several fields, including handler, description, and test. The test field should contain a function of one argument, a condition, that returns TRUE if the restart applies to the condition and FALSE if it does not; the default function returns TRUE for all conditions.

One additional field that can be specified for a restart is interactive. This should be a function of no arguments that returns a list of arguments to pass to the restart handler. The list could be obtained by interacting with the user if necessary. The function invokeRestartInteractively calls this function to obtain the arguments to use when invoking the restart. The default interactive method queries the user for values for the formal arguments of the handler function.

Interrupts can be suspended while evaluating an expression using suspendInterrupts. Subexpression can be evaluated with interrupts enabled using allowInterrupts. These functions can be used to make sure cleanup handlers cannot be interrupted.

.signalSimpleWarning, .handleSimpleError, and .tryResumeInterrupt are used internally and should not be called directly.
The tryCatch mechanism is similar to Java error handling. Calling handlers are based on Common Lisp and Dylan. Restarts are based on the Common Lisp restart mechanism.

See Also

stop and warning signal conditions, and try is essentially a simplified version of tryCatch. assertCondition in package tools tests that conditions are signalled and works with several of the above handlers.

Examples

tryCatch(1, finally = print("Hello"))
e <- simpleError("test error")
## Not run:
  stop(e)
  tryCatch(stop(e), finally = print("Hello"))
  tryCatch(stop("fred"), finally = print("Hello"))

## End(Not run)
tryCatch(stop(e), error = function(e) e, finally = print("Hello"))
tryCatch(stop("fred"), error = function(e) e, finally = print("Hello"))
withCallingHandlers({ warning("A"); 1+2 }, warning = function(w) {})
## Not run:
  { withRestarts(stop("A"), abort = function() {}); 1 }

## End(Not run)
withRestarts(invokeRestart("foo", 1, 2), foo = function(x, y) {x + y})

### More examples are part of
demo(error.catching)
Value

If `detail = FALSE`, a character vector of masked objects. If `detail = TRUE`, a list of character vectors giving the masked or masking objects in that member of the search path. Empty vectors are omitted.

Examples

```r
lm <- 1:3
counters(, TRUE)
## gives something like
# $GlobalEnv
# [1] "lm"
#
# $package:base
# [1] "lm"
## Remove things from your "workspace" that mask others:
remove(list = conflicts(detail = TRUE)$GlobalEnv)
```

connections

Functions to Manipulate Connections (Files, URLs, ...)

Description

Functions to create, open and close connections, i.e., “generalized files”, such as possibly compressed files, URLs, pipes, etc.

Usage

```
file(description = "", open = "", blocking = TRUE,
     encoding = getOption("encoding"), raw = FALSE,
     method = getOption("url.method", "default"))

url(description, open = "", blocking = TRUE,
     encoding = getOption("encoding"),
     method = getOption("url.method", "default"),
     headers = NULL)

gzfile(description, open = "", encoding = getOption("encoding"),
        compression = 6)

bzfile(description, open = "", encoding = getOption("encoding"),
       compression = 9)

xzfile(description, open = "", encoding = getOption("encoding"),
       compression = 6)

unz(description, filename, open = "", encoding = getOption("encoding"))

pipe(description, open = "", encoding = getOption("encoding"))

fifo(description, open = "", blocking = FALSE,
      encoding = getOption("encoding"))
```
encoding = getOption("encoding")

socketConnection(host = "localhost", port, server = FALSE,
    blocking = FALSE, open = "a+",
    encoding = getOption("encoding"),
    timeout = getOption("timeout"),
    options = getOption("socketOptions"))

serverSocket(port)

socketAccept(socket, blocking = FALSE, open = "a+",
    encoding = getOption("encoding"),
    timeout = getOption("timeout"),
    options = getOption("socketOptions"))

open(con, ...)
## S3 method for class 'connection'
open(con, open = "r", blocking = TRUE, ...)

close(con, ...)
## S3 method for class 'connection'
close(con, type = "rw", ...)

flush(con)

isOpen(con, rw = "")
isIncomplete(con)

socketTimeout(socket, timeout = -1)

Arguments

description character string. A description of the connection: see ‘Details’.
open character string. A description of how to open the connection (if it should be
    opened initially). See section ‘Modes’ for possible values.
blocking logical. See the ‘Blocking’ section.
encoding The name of the encoding to be assumed. See the ‘Encoding’ section.
raw logical. If true, a ‘raw’ interface is used which will be more suitable for argu-
    ments which are not regular files, e.g. character devices. This suppresses the
    check for a compressed file when opening for text-mode reading, and asserts
    that the ‘file’ may not be seekable.
method character string, partially matched to c("default", "internal", "wininet",
    "libcurl"): see ‘Details’.
headers named character vector of HTTP headers to use in HTTP requests. It is
    ignored for non-HTTP URLs. The User-Agent header, coming from the
HTTPUserAgent option (see options) is used as the first header, automatically.
compression integer in 0–9. The amount of compression to be applied when writing, from
none to maximal available. For xzfile can also be negative: see the ‘Compression’ section.
timeout numeric: the timeout (in seconds) to be used for this connection. Beware that some OSes may treat very large values as zero: however the POSIX standard requires values up to 31 days to be supported.

options optional character vector with options. Currently only "no-delay" is supported on TCP sockets.

filename a filename within a zip file.

host character string. Host name for the port.

port integer. The TCP port number.

server logical. Should the socket be a client or a server?

socket a server socket listening for connections.

con a connection.

type character string. Currently ignored.

rw character string. Empty or "read" or "write", partial matches allowed.

... arguments passed to or from other methods.

Details

The first eleven functions create connections. By default the connection is not opened (except for a socket connection created by socketConnection or socketAccept and for server socket connection created by serverSocket), but may be opened by setting a non-empty value of argument open.

For file the description is a path to the file to be opened (when tilde expansion is done) or a complete URL (when it is the same as calling url), or "" (the default) or "clipboard" (see the ‘Clipboard’ section). Use "stdin" to refer to the C-level ‘standard input’ of the process (which need not be connected to anything in a console or embedded version of R, and is not in RGui on Windows). See also stdin() for the subtly different R-level concept of stdin. See nullfile() for a platform-independent way to get filename of the null device.

For url the description is a complete URL including scheme (such as 'http://', 'https://', 'ftp://' or 'file://'). Method "internal" is that available since connections were introduced but now mainly defunct. Method "wininet" is only available on Windows (it uses the WinINet functions of that OS) and method "libcurl" (using the library of that name: https://curl.se/libcurl/) is nowadays required but was optional on Windows before R 4.2.0. Method "default" currently uses method "internal" for 'file:///' URLs and "libcurl" for all others. Which methods support which schemes has varied by R version – currently "internal" supports only 'file://'; "wininet" supports 'file://', 'http://' and 'https://'. Proxies can be specified: see download.file.

For gzfile the description is the path to a file compressed by gzip: it can also open for reading uncompressed files and those compressed by bzip2, xz or lzma.

For bzfile the description is the path to a file compressed by bzip2.

For xzfile the description is the path to a file compressed by xz (https://en.wikipedia.org/wiki/Xz) or (for reading only) lzma (https://en.wikipedia.org/wiki/LZMA).

unz reads (only) single files within zip files, in binary mode. The description is the full path to the zip file, with ".zip" extension if required.

For pipe the description is the command line to be piped to or from. This is run in a shell, on Windows that specified by the COMSPEC environment variable.

For fifo the description is the path of the fifo. (Support for fifo connections is optional but they are available on most Unix platforms and on Windows.)
The intention is that file and gzfile can be used generally for text input (from files, 'http:///' and 'https:///' URLs) and binary input respectively.

open, close and seek are generic functions: the following applies to the methods relevant to connections.

open opens a connection. In general functions using connections will open them if they are not open, but then close them again, so to leave a connection open call open explicitly.

close closes and destroys a connection. This will happen automatically in due course (with a warning) if there is no longer an R object referring to the connection.

A maximum of 128 connections can be allocated (not necessarily open) at any one time. Three of these are pre-allocated (see stdout). The OS will impose limits on the numbers of connections of various types, but these are usually larger than 125.

flush flushes the output stream of a connection open for write/append (where implemented, currently for file and clipboard connections, stdout and stderr).

If for a file or (on most platforms) a fifo connection the description is "", the file/fifo is immediately opened (in "w+" mode unless open = "w+b" is specified) and unlinked from the file system. This provides a temporary file/fifo to write to and then read from.

socketConnection(server=TRUE) creates a new temporary server socket listening on the given port. As soon as a new socket connection is accepted on that port, the server socket is automatically closed. serverSocket creates a listening server socket which can be used for accepting multiple socket connections by socketAccept. To stop listening for new connections, a server socket needs to be closed explicitly by close.

socketConnection and socketAccept support setting of socket-specific options. Currently only "no-delay" is implemented which enables the TCP_NODELAY socket option, causing the socket to flush send buffers immediately (instead of waiting to collect all output before sending). This option is useful for protocols that need fast request/response turn-around times.

socketTimeout sets connection timeout of a socket connection. A negative timeout can be given to query the old value.

Value

file, pipe, fifo, url, gzfile, bzfile, xzfile, unz, socketConnection, socketAccept and serverSocket return a connection object which inherits from class "connection" and has a first more specific class.

open and flush return NULL, invisibly.

close returns either NULL or an integer status, invisibly. The status is from when the connection was last closed and is available for some types of connections (e.g., pipes, files and fifos): typically zero values indicate success. Negative values will result in a warning; if writing, these may indicate write failures and should not be ignored.

isOpen returns a logical value, whether the connection is currently open.

isIncomplete returns a logical value, whether the last read attempt was blocked, or for an output text connection whether there is unflushed output.

socketTimeout returns the old timeout value of a socket connection.

URLs

url and file support URL schemes 'file:///', 'http:///', 'https:///' and 'ftp:///'.

method = "libcurl" allows more schemes: exactly which schemes is platform-dependent (see libcurlVersion), but all platforms will support 'https:///' and most platforms will support 'ftps:///.'
Support for the ‘ftp://’ scheme by the “internal” method was deprecated in R 4.1.1 and removed in R 4.2.0.

Most methods do not percent-encode special characters such as spaces in ‘http://’ URLs (see `URLencode`), but it seems the “wininet” method does.

A note on ‘file://’ URLs (which are handled by the same internal code irrespective of argument method). The most general form (from RFC1738) is ‘file://host/path/to/file’, but R only accepts the form with an empty host field referring to the local machine.

On a Unix-alike, this is then ‘file:///path/to/file’, where ‘path/to/file’ is relative to ‘/’. So although the third slash is strictly part of the specification not part of the path, this can be regarded as a way to specify the file ‘/path/to/file’. It is not possible to specify a relative path using a file URL.

In this form the path is relative to the root of the filesystem, not a Windows concept. The standard form on Windows is ‘file:///d:/R/repos’: for compatibility with earlier versions of R and Unix versions, any other form is parsed as R as ‘file://’ plus path_to_file. Also, backslashes are accepted within the path even though RFC1738 does not allow them.

No attempt is made to decode a percent-encoded ‘file:’ URL: call `URLdecode` if necessary.

All the methods attempt to follow redirected HTTP and HTTPS URLs.

Server-side cached data is always accepted.

Function `download.file` and several contributed packages provide more comprehensive facilities to download from URLs.

### Modes

Possible values for the argument `open` are

- "r" or "rt" Open for reading in text mode.
- "w" or "wt" Open for writing in text mode.
- "a" or "at" Open for appending in text mode.
- "rb" Open for reading in binary mode.
- "wb" Open for writing in binary mode.
- "ab" Open for appending in binary mode.
- "r+", "r+b" Open for reading and writing.
- "w+", "w+b" Open for reading and writing, truncating file initially.
- "a+", "a+b" Open for reading and appending.

Not all modes are applicable to all connections: for example URLs can only be opened for reading. Only file and socket connections can be opened for both reading and writing. An unsupported mode is usually silently substituted.

If a file or fifo is created on a Unix-alike, its permissions will be the maximal allowed by the current setting of umask (see `Sys.umask`).

For many connections there is little or no difference between text and binary modes. For file-like connections on Windows, translation of line endings (between LF and CRLF) is done in text mode only (but text read operations on connections such as `readLines`, `scan` and `source` work for any form of line ending). Various R operations are possible in only one of the modes: for example `pushBack` is text-oriented and is only allowed on connections open for reading in text mode, and binary operations such as `readBin`, `load` and `save` can only be done on binary-mode connections.

The mode of a connection is determined when actually opened, which is deferred if `open = ""` is given (the default for all but socket connections). An explicit call to `open` can specify the mode,
but otherwise the mode will be "r". (gzfile, bzfile and xzfile connections are exceptions, as the compressed file always has to be opened in binary mode and no conversion of line-endings is done even on Windows, so the default mode is interpreted as "rb".) Most operations that need write access or text-only or binary-only mode will override the default mode of a non-yet-open connection.

Append modes need to be considered carefully for compressed-file connections. They do not produce a single compressed stream on the file, but rather append a new compressed stream to the file. Readers may or may not read beyond end of the first stream: currently R does so for gzfile, bzfile and xzfile connections.

**Compression**

R supports gzip, bzip2 and xz compression (also read-only support for its precursor, lzma compression).

For reading, the type of compression (if any) can be determined from the first few bytes of the file. Thus for file(raw = FALSE) connections, if open is "", "r" or "rt" the connection can read any of the compressed file types as well as uncompressed files. (Using "rb" will allow compressed files to be read byte-by-byte.) Similarly, gzfile connections can read any of the forms of compression and uncompressed files in any read mode.

(The type of compression is determined when the connection is created if open is unspecified and a file of that name exists. If the intention is to open the connection to write a file with a different form of compression under that name, specify open = "w" when the connection is created or unlink the file before creating the connection.)

For write-mode connections, compress specifies how hard the compressor works to minimize the file size, and higher values need more CPU time and more working memory (up to ca 800Mb for xzfile(compress = 9)). For xzfile negative values of compress correspond to adding the xz argument '-e': this takes more time (double?) to compress but may achieve (slightly) better compression. The default (6) has good compression and modest (100Mb memory) usage: but if you are using xz compression you are probably looking for high compression.

Choosing the type of compression involves tradeoffs: gzip, bzip2 and xz are successively less widely supported, need more resources for both compression and decompression, and achieve more compression (although individual files may buck the general trend). Typical experience is that bzip2 compression is 15% better on text files than gzip compression, and xz with maximal compression 30% better. The experience with R save files is similar, but on some large `.rda` files xz compression is much better than the other two. With current computers decompression times even with compress = 9 are typically modest and reading compressed files is usually faster than uncompressed ones because of the reduction in disc activity.

**Encoding**

The encoding of the input/output stream of a connection can be specified by name in the same way as it would be given to `iconv`: see that help page for how to find out what encoding names are recognized on your platform. Additionally, "" and "native.enc" both mean the ‘native’ encoding, that is the internal encoding of the current locale and hence no translation is done.

When writing to a text connection, the connections code always assumes its input is in native encoding, so e.g. `writeLines` has to convert text to native encoding. The native encoding is UTF-8 on most systems (since R 4.2 also on recent Windows) and can represent all characters. `writeLines` does not do the conversion when useBytes=TRUE (for expert use only, only useful on systems with native encoding other than UTF-8), but the connections code still behaves as if the text was in native encoding, so any attempt to convert encoding (encoding argument other than "" and "native.enc") in connections will produce incorrect results.
When reading from a text connection, the connections code re-encodes the input to native encoding (from the encoding given by the encoding argument). On systems where UTF-8 is not the native encoding, one can read text not representable in the native encoding using `readLines` and `scan` by providing them with an unopened connection that has been created with the encoding argument specifying the input encoding. `readLines` and `scan` would then instruct the connections code to convert the text to UTF-8 (instead of native encoding) and they will return it marked (aka declared, see Encoding) as "UTF-8". Finally and for expert use only, one may disable re-encoding of input by specifying "" or "native.enc" as encoding for the connection, but then mark the text as being "UTF-8" or "latin1" via the encoding argument of `readLines` and `scan`.

Re-encoding only works for connections in text mode: reading from a connection with re-encoding specified in binary mode will read the stream of bytes, but mixing text and binary mode reads (e.g., mixing calls to `readLines` and `readChar`) is likely to lead to incorrect results.

The encodings "UCS-2LE" and "UTF-16LE" are treated specially, as they are appropriate values for Windows 'Unicode' text files. If the first two bytes are the Byte Order Mark \x{0FEFF} then these are removed as some implementations of `iconv` do not accept BOMs. Note that whereas most implementations will handle BOMs using encoding "UCS-2" and choose the appropriate byte order, some (including earlier versions of glibc) will not. There is a subtle distinction between "UTF-16" and "UCS-2" (see [https://en.wikipedia.org/wiki/UTF-16](https://en.wikipedia.org/wiki/UTF-16)): the use of characters in the 'Supplementary Planes' which need surrogate pairs is very rare so "UCS-2LE" is an appropriate first choice (as it is more widely implemented).

The encoding "UTF-8-BOM" is accepted for reading and will remove a Byte Order Mark if present (which it often is for files and webpages generated by Microsoft applications). If a BOM is required (it is not recommended) when writing it should be written explicitly, e.g. by `writeChar("\u{FEFF}", con, eos = NULL)` or `writeBin(as.raw(c(0xef, 0xbb, 0xbf)), binary_con)`.

Encoding names "utf8", "mac" and "macroman" are not portable, and not supported on all current R platforms. "UTF-8" is portable and "macintosh" is the official (and most widely supported) name for 'Mac Roman'. (R maps "utf8" to "UTF-8" internally.)

Requesting a conversion that is not supported is an error, reported when the connection is opened. Exactly what happens when the requested translation cannot be done for invalid input is in general undocumented. On output the result is likely to be that up to the error, with a warning. On input, it will most likely be all or some of the input up to the error.

It may be possible to deduce the current native encoding from `Sys.getlocale("LC_CTYPE")`, but not all OSes record it.

### Blocking

Whether or not the connection blocks can be specified for file, url (default yes), fifo and socket connections (default not).

In blocking mode, functions using the connection do not return to the R evaluator until the read/write is complete. In non-blocking mode, operations return as soon as possible, so on input they will return with whatever input is available (possibly none) and for output they will return whether or not the write succeeded.

The function `readLines` behaves differently in respect of incomplete last lines in the two modes: see its help page.

Even when a connection is in blocking mode, attempts are made to ensure that it does not block the event loop and hence the operation of GUI parts of R. These do not always succeed, and the whole R process will be blocked during a DNS lookup on Unix, for example.

Most blocking operations on HTTP/FTP URLs and on sockets are subject to the timeout set by `options("timeout")`. Note that this is a timeout for no response, not for the whole operation. The
timeout is set at the time the connection is opened (more precisely, when the last connection of that
type – 'http:', 'ftp:' or socket – was opened).

Fifos
Fifos default to non-blocking. That follows S version 4 and is probably most natural, but it does
have some implications. In particular, opening a non-blocking fifo connection for writing (only)
will fail unless some other process is reading on the fifo.

Opening a fifo for both reading and writing (in any mode: one can only append to fifos) connects
both sides of the fifo to the R process, and provides an similar facility to file().

Clipboard
file can be used with description = "clipboard" in mode "r" only. This reads the
X11 primary selection (see https://specifications.freedesktop.org/clipboards-spec/
clipboards-latest.txt), which can also be specified as "X11_primary" and the secondary se-
lection as "X11_secondary". On most systems the clipboard selection (that used by 'Copy' from
an 'Edit' menu) can be specified as "X11_clipboard".

When a clipboard is opened for reading, the contents are immediately copied to internal storage in
the connection.

Unix users wishing to write to one of the X11 selections may be able to do so via xclip (https://
github.com/astrand/xclip) or xsel (https://www.vergenet.net/~conrad/software/
xsel/), for example by pipe("xclip -i", "w") for the primary selection.

macOS users can use pipe("pbpaste") and pipe("pbcopy", "w") to read from and write to that
system’s clipboard.

File paths
In most cases these are translated to the native encoding.

The exceptions are file and pipe on Windows, where a description which is marked as being
in UTF-8 is passed to Windows as a ‘wide’ character string. This allows files with names not in the
native encoding to be opened on file systems which use Unicode file names (such as NTFS but not
FAT32).

ftp:// URLs
Most modern browsers do not support such URLs, and https:// ones are much preferred for use
in R.

It is intended that R will continue to allow such URLs for as long as libcurl does, but as they
become rarer this is increasingly untested. What ‘protocols’ the version of libcurl being used
supports can be seen by calling libcurlVersion().

Note
R’s connections are modelled on those in S version 4 (see Chambers, 1998). However R goes
well beyond the S model, for example in output text connections and URL, compressed and socket
connections. The default open mode in R is "r" except for socket connections. This differs from S,
where it is the equivalent of "r+", known as "*".

On (rare) platforms where vsnprintf does not return the needed length of output there is a 100,000
byte output limit on the length of a line for text output on fifo, gzfile, bzfile and xzfile
connections: longer lines will be truncated with a warning.
connections

References


See Also
textConnection, seek, showConnections, pushBack.

Functions making direct use of connections are (text-mode) readLines, writeLines, cat, sink, scan, parse, read.dcf, dput, dump and (binary-mode) readBin, readChar, writeBin, writeChar, load and save.
capabilities to see if fifo connections are supported by this build of R.
gzcon to wrap gzip (de)compression around a connection.
options HTTPUserAgent, internet.info and timeout are used by some of the methods for URL connections.
memCompress for more ways to (de)compress and references on data compression.
extSoftVersion for the versions of the zlib (for gzfile), bzip2 and xz libraries in use.

To flush output to the Windows and macOS consoles, see flush.console.

Examples

zzfil <- tempfile(fileext=".data")
zz <- file(zzfil, "w") # open an output file connection
cat("TITLE extra line", "2 3 5 7", ", "11 13 17", file = zz, sep = "\n")
cat("One more line\n", file = zz)
close(zz)
readLines(zzfil)
unlink(zzfil)

zzfil <- tempfile(fileext=".gz")
zz <- gzfile(zzfil, "w") # compressed file
cat("TITLE extra line", "2 3 5 7", ", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzfile(zzfil))
close(zz)
unlink(zzfil)
zz # an invalid connection

zzfil <- tempfile(fileext=".bz2")
zz <- bzfile(zzfil, "w") # bzip2-ed file

cat("TITLE extra line", "2 3 5 7", ", "11 13 17", file = zz, sep = "\n")
close(zz)
zz # print() method: invalid connection
print(readLines(zz <- bzfile(zzfil))))
close(zz)
unlink(zzfil)

# An example of a file open for reading and writing
Tpath <- tempfile("test")
Tfile <- file(Tpath, "r")
c(isOpen(Tfile, "r"), isOpen(Tfile, "w")) # both TRUE
cat("abc\ndef\n", file = Tfile)
connections

readLines(Tfile)
seek(Tfile, 0, rw = "r")  # reset to beginning
readLines(Tfile)
cat("ghi\n", file = Tfile)
readLines(Tfile)

Tfile # -> print(): "valid" connection
close(Tfile)
Tfile # -> print(): "invalid" connection
unlink(Tpath)

## We can do the same thing with an anonymous file.
Tfile <- file()
cat("abc\n\ndef\n", file = Tfile)
readLines(Tfile)
close(Tfile)

## Not run:  ## fifo example -- may hang even with OS support for fifos
if(capabilities("fifo")) {
  zzfil <- tempfile(fileext="-fifo")
  zz <- fifo(zzfil, "w+")
  writeLines("abc", zz)
  print(readLines(zz))
  close(zz)
  unlink(zzfil)
}
## End(Not run)

## Unix examples of use of pipes

# read listing of current directory
readLines(pipe("ls -1"))

# remove trailing commas. Suppose

## Not run:  % cat data2_
450, 390, 467, 654, 30, 542, 334, 432, 421,
357, 497, 493, 550, 549, 467, 575, 578, 342,
446, 547, 534, 495, 979, 479
## End(Not run)

# Then read this by
scan(pipe("sed -e s/,$/// data2_
"), sep = ",")

# convert decimal point to comma in output: see also write.table
# both R strings and (probably) the shell need \ doubled
zzfil <- tempfile("outfile")
zz <- pipe(paste("sed s/\\./,/ >", zzfil), "w")
cat(format(round(stats::rnorm(48), 4)), fill = 70, file = zz)
close(zz)
file.show(zzfil, delete.file = TRUE)

## Not run:
## example for a machine running a finger daemon

con <- socketConnection(port = 79, blocking = TRUE)
writeLines(paste0(system("whoami", intern = TRUE), "\r"), con)
## End(Not run)

### Not run:

### Two R processes communicating via non-blocking sockets

# R process 1

con1 <- socketConnection(port = 6011, server = TRUE)
writeLines(LETTERS, con1)
close(con1)

# R process 2

con2 <- socketConnection(Sys.info()["nodename"], port = 6011)
# as non-blocking, may need to loop for input
readLines(con2)
while(isIncomplete(con2)) {
  Sys.sleep(1)
  z <- readLines(con2)
  if(length(z)) print(z)
}
close(con2)

### examples of use of encodings

# write a file in UTF-8

cat(x, file = (con <- file("foo", "w", encoding = "UTF-8"))); close(con)

# read a 'Windows Unicode' file

A <- read.table(con <- file("students", encoding = "UCS-2LE")); close(con)

### End(Not run)

<table>
<thead>
<tr>
<th>Constants</th>
<th>Built-in Constants</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Description

Constants built into R.

### Usage

LETTERS
letters
month.abb
month.name
pi

### Details

R has a small number of built-in constants.

The following constants are available:

- LETTERS: the 26 upper-case letters of the Roman alphabet;
- letters: the 26 lower-case letters of the Roman alphabet;
• `month.abb`: the three-letter abbreviations for the English month names;
• `month.name`: the English names for the months of the year;
• `pi`: the ratio of the circumference of a circle to its diameter.

These are implemented as variables in the base namespace taking appropriate values.

References


See Also

data, DateTimeClasses.

Quotes for the parsing of character constants, NumericConstants for numeric constants.

Examples

```r
## John Machin (ca 1706) computed pi to over 100 decimal places
## using the Taylor series expansion of the second term of
## pi - 4*(4*atan(1/5) - atan(1/239))

## months in English
month.name

## months in your current locale
format(ISOdate(2000, 1:12, 1), "%B")
format(ISOdate(2000, 1:12, 1), "%b")
```

---

**contributors**  

The **R Project Contributors**

**Description**

The R Who-is-who, describing who made significant contributions to the development of R.

**Usage**

`contributors()`
Description

These are the basic control-flow constructs of the R language. They function in much the same way as control statements in any Algol-like language. They are all reserved words.

Usage

\[
\begin{align*}
\text{if}(&\text{cond}) \text{ expr} \\
\text{if}(&\text{cond}) \text{ cons.expr} \text{ else alt.expr} \\
\text{for}(&\text{var} \text{ in seq}) \text{ expr} \\
\text{while}(&\text{cond}) \text{ expr} \\
\text{repeat expr} \\
\text{break} \\
\text{next}
\end{align*}
\]

Arguments

- **cond**: A length-one logical vector that is not NA. Other types are coerced to logical if possible, ignoring any class. (Conditions of length greater than one are an error.)
- **var**: A syntactical name for a variable.
- **seq**: An expression evaluating to a vector (including a list and an expression) or to a pairlist or NULL. A factor value will be coerced to a character vector. This can be a long vector.
- **expr, cons.expr, alt.expr**: An expression in a formal sense. This is either a simple expression or a so-called compound expression, usually of the form \{ expr1 ; expr2 \}.

Details

- **break** breaks out of a for, while or repeat loop; control is transferred to the first statement outside the inner-most loop. next halts the processing of the current iteration and advances the looping index. Both break and next apply only to the innermost of nested loops.

Note that it is a common mistake to forget to put braces (( . . )) around your statements, e.g., after if(...) or for(. . . ). In particular, you should not have a newline between } and else to avoid a syntax error in entering a if . . . else construct at the keyboard or via source. For that reason, one (somewhat extreme) attitude of defensive programming is to always use braces, e.g., for if clauses.

The seq in a for loop is evaluated at the start of the loop; changing it subsequently does not affect the loop. If seq has length zero the body of the loop is skipped. Otherwise the variable var is assigned in turn the value of each element of seq. You can assign to var within the body of the loop, but this will not affect the next iteration. When the loop terminates, var remains as a variable containing its latest value.
Value

if returns the value of the expression evaluated, or NULL invisibly if none was (which may happen if there is no else).

for, while and repeat return NULL invisibly. for sets var to the last used element of seq, or to NULL if it was of length zero.

break and next do not return a value as they transfer control within the loop.

References


See Also

Syntax for the basic R syntax and operators, Paren for parentheses and braces.

ifelse, switch for other ways to control flow.

Examples

```r
for(i in 1:5) print(1:i)
for(n in c(2,5,10,20,50)) {
  x <- stats::rnorm(n)
  cat(n, " : ", sum(x^2), " \n", sep = "")
}
f <- factor(sample(letters[1:5], 10, replace = TRUE))
for(i in unique(f)) print(i)
```

Description

R is released under the ‘GNU Public License’: see license for details. The license describes your right to use R. Copyright is concerned with ownership of intellectual rights, and some of the software used has conditions that the copyright must be explicitly stated: see the ‘Details’ section. We are grateful to these people and other contributors (see contributors) for the ability to use their work.

Details

The file ‘R_HOME/COPYRIGHTS’ lists the copyrights in full detail.
Given matrices \( x \) and \( y \) as arguments, return a matrix cross-product. This is formally equivalent to (but usually slightly faster than) the call \( t(x) %*% y \) (\texttt{crossprod}) or \( x %*% t(y) \) (\texttt{tcrossprod}).

### Usage

\begin{verbatim}
crossprod(x, y = NULL)
tcrossprod(x, y = NULL)
\end{verbatim}

### Arguments

\( x, y \) numeric or complex matrices (or vectors); \( y = \text{NULL} \) is taken to be the same matrix as \( x \). Vectors are promoted to single-column or single-row matrices, depending on the context.

### Value

A double or complex matrix, with appropriate \texttt{dimnames} taken from \( x \) and \( y \).

### Note

When \( x \) or \( y \) are not matrices, they are treated as column or row matrices, but their \texttt{names} are usually not promoted to \texttt{dimnames}. Hence, currently, the last example has empty \texttt{dimnames}.

In the same situation, these matrix products (also \texttt{%%}) are more flexible in promotion of vectors to row or column matrices, such that more cases are allowed, since R 3.2.0.

The propagation of NaN/Inf values, precision, and performance of matrix products can be controlled by \texttt{options("matprod")}.

### References


### See Also

\texttt{%%} and outer product \texttt{%%}.

### Examples

\begin{verbatim}
(z <- crossprod(1:4)) # = sum(1 + 2^2 + 3^2 + 4^2)
drop(z) # scalar
x <- 1:4; names(x) <- letters[1:4]; x
tcrossprod(as.matrix(x)) # is identical(tcrossprod(as.matrix(x)),
crossprod(t(x)))
tcrossprod(x) # no dimnames

m <- matrix(1:6, 2,3) ; v <- 1:3; v2 <- 2:1
\end{verbatim}
Cstack_info

Description

Report information on the C stack size and usage (if available).

Usage

Cstack_info()

Details

On most platforms, C stack information is recorded when R is initialized and used for stack-checking. If this information is unavailable, the size will be returned as NA, and stack-checking is not performed.

The information on the stack base address is thought to be accurate on Windows, Linux (using glibc), macOS and FreeBSD but a heuristic is used on other platforms. Because this might be slightly inaccurate, the current usage could be estimated as negative. (The heuristic is not used on embedded uses of R on platforms where the stack base information is not thought to be accurate.)

The 'evaluation depth' is the number of nested R expressions currently under evaluation: this has a limit controlled by options("expressions").

Value

An integer vector. This has named elements

size The size of the stack (in bytes), or NA if unknown.
current The estimated current usage (in bytes), possibly NA.
direction 1 (stack grows down, the usual case) or -1 (stack grows up).
eval_depth The current evaluation depth (including two calls for the call to Cstack_info).

Examples

Cstack_info()
**cumsum**  

*Cumulative Sums, Products, and Extremes*

**Description**

Returns a vector whose elements are the cumulative sums, products, minima or maxima of the elements of the argument.

**Usage**

```r
cumsum(x)  
cumprod(x)  
cummax(x)  
cummin(x)
```

**Arguments**

- `x` a numeric or complex (not `cummin` or `cummax`) object, or an object that can be coerced to one of these.

**Details**

These are generic functions: methods can be defined for them individually or via the `Math` group generic.

**Value**

A vector of the same length and type as `x` (after coercion), except that `cumprod` returns a numeric vector for integer input (for consistency with `*`). Names are preserved.

An `NA` value in `x` causes the corresponding and following elements of the return value to be `NA`, as does integer overflow in `cumsum` (with a warning).

**S4 methods**

`cumsum` and `cumprod` are S4 generic functions: methods can be defined for them individually or via the `Math` group generic. `cummax` and `cummin` are individually S4 generic functions.

**References**


**Examples**

```r
cumsum(1:10)  
cumprod(1:10)  
cummin(c(3:1, 2:0, 4:2))  
cummax(c(3:1, 2:0, 4:2))
```
curlGetHeaders  

Retrieve Headers from URLs

Description

Retrieve the headers for a URL for a supported protocol such as http://, ftp://, https:// and ftpp://.

Usage

curlGetHeaders(url, redirect = TRUE, verify = TRUE,
               timeout = 0L, TLS = "")

Arguments

url character string specifying the URL.
redirect logical: should redirections be followed?
verify logical: should certificates be verified as valid and applying to that host?
timeout integer: the maximum time in seconds the request is allowed to take. Non-positive and invalid values are ignored (including the default). (Added in \texttt{R 4.1.0}.)
TLS character: the minimum version of the TLS protocol to be used for https:// URLs: the default (""") is no restriction beyond that of the underlying \texttt{libcurl} (usually 1.0). Other valid values are "1.1", "1.2" (both for \texttt{libcurl 7.34.0} and later) and "1.3" (7.52.0 and later), if supported by the underlying version of \texttt{libcurl} and the SSL library it uses.

Details

This reports what \texttt{curl -I -L} or \texttt{curl -I} would report. For a \texttt{ftp://} URL the ‘headers’ are a record of the conversation between client and server before data transfer.

Only 500 header lines will be reported: there is a limit of 20 redirections so this should suffice (and even 20 would indicate problems).

If argument \texttt{timeout} is not set to a positive integer this uses \texttt{getOption("timeout")} which defaults to 60 seconds. As the request cannot be interrupted you may want to consider a shorter value.

To see all the details of the interaction with the server(s) set \texttt{options(internet.info = 1)}.

HTTP[S] servers are allowed to refuse requests to read the headers and some do: this will result in a status of 405.

For possible issues with secure URLs (especially on Windows) see \texttt{download.file}.

There is a security risk in not verifying certificates, but as only the headers are captured it is slight. Usually looking at the URL in a browser will reveal what the problem is (and it may well be machine-specific).

Value

A character vector with integer attribute "status" (the last-received 'status' code). If redirection occurs this will include the headers for all the URLs visited.


A successful FTP connection will usually have status 250, 257 or 350.
See Also

capabilities("libcurl") to see if this is supported. libcurlVersion for the version of libcurl in use.

options HTTPUserAgent and timeout are used.

Examples

## needs Internet access, results vary
curlGetHeaders("http://bugs.r-project.org")  ## this redirects to https://
## 2023-04: replaces slow and unreliable https://httpbin.org/status/404
curlGetHeaders("https://developer.R-project.org/inet-tests/not-found")
## returns status

---

cut  

Convert Numeric to Factor

Description

cut divides the range of x into intervals and codes the values in x according to which interval they fall. The leftmost interval corresponds to level one, the next leftmost to level two and so on.

Usage

cut(x, ...)

## Default S3 method:
cut(x, breaks, labels = NULL,
  include.lowest = FALSE, right = TRUE, dig.lab = 3,
  ordered_result = FALSE, ...)

Arguments

- **x**: a numeric vector which is to be converted to a factor by cutting.
- **breaks**: either a numeric vector of two or more unique cut points or a single number (greater than or equal to 2) giving the number of intervals into which x is to be cut.
- **labels**: labels for the levels of the resulting category. By default, labels are constructed using "(a,b]" interval notation. If labels = FALSE, simple integer codes are returned instead of a factor.
- **include.lowest**: logical, indicating if an 'x[i]' equal to the lowest (or highest, for right = FALSE) ‘breaks’ value should be included.
- **right**: logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
- **dig.lab**: integer which is used when labels are not given. It determines the number of digits used in formatting the break numbers.
- **ordered_result**: logical: should the result be an ordered factor?
- **...**: further arguments passed to or from other methods.
When `breaks` is specified as a single number, the range of the data is divided into `breaks` pieces of equal length, and then the outer limits are moved away by 0.1% of the range to ensure that the extreme values both fall within the break intervals. (If `x` is a constant vector, equal-length intervals are created, one of which includes the single value.)

If a `labels` parameter is specified, its values are used to name the factor levels. If none is specified, the factor level labels are constructed as "(b1, b2]", "(b2, b3]" etc. for `right = TRUE` and as "[b1, b2)"...if `right = FALSE`. In this case, `dig.lab` indicates the minimum number of digits should be used in formatting the numbers `b1`, `b2`, .... A larger value (up to 12) will be used if needed to distinguish between any pair of endpoints: if this fails labels such as "Range3" will be used. Formatting is done by `formatC`.

The default method will sort a numeric vector of `breaks`, but other methods are not required to and `labels` will correspond to the intervals after sorting.

As from R 3.2.0, `getOption("OutDec")` is consulted when labels are constructed for `labels = NULL`.

A `factor` is returned, unless `labels = FALSE` which results in an integer vector of level codes. Values which fall outside the range of `breaks` are coded as `NA`, as are `NaN` and `NA` values.

Instead of `table(cut(x, br))`, `hist(x, br, plot = FALSE)` is more efficient and less memory hungry. Instead of `cut(*, labels = FALSE)`, `findInterval()` is more efficient.


`split` for splitting a variable according to a group factor; `factor`, `tabulate`, `table`, `findInterval`.

`quantile` for ways of choosing breaks of roughly equal content (rather than length).

`.bincode` for a bare-bones version.

```
Z <- stats::rnorm(10000)
table(cut(Z, breaks = -6:6))
sum(table(cut(Z, breaks = -6:6, labels = FALSE)))
sum(graphics::hist(Z, breaks = -6:6, plot = FALSE)$counts)

cut(rep(1.5), 4) #-- dummy
tx0 <- c(9, 4, 6, 5, 3, 10, 5, 3, 5)
x <- rep(0:8, tx0)
stopifnot(table(x) == tx0)

table( cut(x, breaks = 8) )
table( cut(x, breaks = 3 * (-2:5)) )
```
```r
table( cut(x, breaks = 3*(-2:5), right = FALSE))

##--- some values OUTSIDE the breaks :
table(cx <- cut(x, breaks = 2*(0:4)))
table(cx1 <- cut(x, breaks = 2*(0:4), right = FALSE))
which(is.na(cx)); x[is.na(cx)]  ##-- the first 9 values 0
which(is.na(cx1)); x[is.na(cx1)]  ##-- the last 5 values 8

## Label construction:
y <- stats::rnorm(100)
table(cut(y, breaks = pi/3*(-3:3)))
table(cut(y, breaks = pi/3*(-3:3), dig.lab = 4))
# extra digits don't "harm" here
table(cut(y, breaks = 1*(-3:3), right = FALSE))
#- the same, since no exact INT!

## sometimes the default dig.lab is not enough to be avoid confusion:
aaa <- c(1,2,3,4,5,2,3,4,5,6,7)
cut(aaa, 3)
cut(aaa, 3, dig.lab = 4, ordered_result = TRUE)

## one way to extract the breakpoints
labs <- levels(cut(aaa, 3))
cbind(lower = as.numeric( sub("\((.+),.*", "\1", labs) ),
               upper = as.numeric( sub("[^,]*,([^\]]*\]\]\), "\1", labs )))
```

### cut.POSIXt

Convert a Date or Date-Time Object to a Factor

**Description**

Method for `cut` applied to date-time objects.

**Usage**

```r
## S3 method for class 'POSIXt'
cut(x, breaks, labels = NULL, start.on.monday = TRUE,
    right = FALSE, ...)

## S3 method for class 'Date'
cut(x, breaks, labels = NULL, start.on.monday = TRUE,
    right = FALSE, ...)
```

**Arguments**

- `x` an object inheriting from class "POSIXt" or "Date".
- `breaks` a vector of cut points or number giving the number of intervals which `x` is to be cut into or an interval specification, one of "sec", "min", "hour", "day", "DSTday", "week", "month", "quarter" or "year", optionally preceded by an integer and a space, or followed by "s". (For "Date" objects only interval specifications using "day", "week", "month", "quarter" and "year" are allowed.)
labels labels for the levels of the resulting category. By default, labels are constructed from the left-hand end of the intervals (which are included for the default value of right). If labels = FALSE, simple integer codes are returned instead of a factor.

start.on.monday logical. If breaks = "weeks", should the week start on Mondays or Sundays?

right, ... arguments to be passed to or from other methods.

Details

Note that the default for right differs from the default method. Using include.lowest = TRUE will include both ends of the range of dates.

Using breaks = "quarter" will create intervals of 3 calendar months, with the intervals beginning on January 1, April 1, July 1 or October 1 (based upon min(x)) as appropriate.

A vector of breaks will be sorted before use: labels should correspond to the sorted vector.

Value

A factor is returned, unless labels = FALSE which returns the integer level codes.

Values which fall outside the range of breaks are coded as NA, as are and NA values.

See Also

seq.POSIXt, seq.Date, cut

Examples

## random dates in a 10-week period
cut(ISOdate(2001, 1, 1) + 70*86400*stats::runif(100), "weeks")
cut(as.Date("2001/1/1") + 70*stats::runif(100), "weeks")

# The standards all have midnight as the start of the day, but some # people incorrectly interpret it at the end of the previous day ...
tm <- seq(as.POSIXct("2012-06-01 06:00"), by = "6 hours", length.out = 24)
aggregate(1:24, list(day = cut(tm, "days")), mean)
# and a version with midnight included in the previous day: aggregate(1:24, list(day = cut(tm, "days", right = TRUE)), mean)

---

data.class Object Classes

Description

Determine the class of an arbitrary R object.

Usage

data.class(x)

Arguments

x an R object.
Value

character string giving the class of x.

The class is the (first element) of the class attribute if this is non-NULL, or inferred from the object’s dim attribute if this is non-NULL, or mode(x).

Simply speaking, data.class(x) returns what is typically useful for method dispatching. (Or, what the basic creator functions already and maybe eventually all will attach as a class attribute.)

Note

For compatibility reasons, there is one exception to the rule above: When x is integer, the result of data.class(x) is "numeric" even when x is classed.

See Also

class

Examples

x <- LETTERS
data.class(factor(x)) # has a class attribute
data.class(matrix(x, ncol = 13)) # has a dim attribute
data.class(list(x)) # the same as mode(x)
data.class(x) # the same as mode(x)

stopifnot(data.class(1:2) == "numeric") # compatibility "rule"

data.frame

Data Frames

Description

The function data.frame() creates data frames, tightly coupled collections of variables which share many of the properties of matrices and of lists, used as the fundamental data structure by most of R’s modeling software.

Usage

data.frame(..., row.names = NULL, check.rows = FALSE,
check.names = TRUE, fix.empty.names = TRUE,
stringsAsFactors = FALSE)

Arguments

... these arguments are of either the form value or tag = value. Component names are created based on the tag (if present) or the deparsed argument itself.
row.names NULL or a single integer or character string specifying a column to be used as row names, or a character or integer vector giving the row names for the data frame.
check.rows if TRUE then the rows are checked for consistency of length and names.
check.names logical. If TRUE then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names and are not duplicated. If necessary they are adjusted (by make.names) so that they are.

fix.empty.names logical indicating if arguments which are “unnamed” (in the sense of not being formally called as someName = arg) get an automatically constructed name or rather name “". Needs to be set to FALSE even when check.names is false if “" names should be kept.

stringsAsFactors logical: should character vectors be converted to factors? The ‘factory-fresh’ default has been TRUE previously but has been changed to FALSE for R 4.0.0.

Details

A data frame is a list of variables of the same number of rows with unique row names, given class "data.frame". If no variables are included, the row names determine the number of rows.

The column names should be non-empty, and attempts to use empty names will have unsupported results. Duplicate column names are allowed, but you need to use check.names = FALSE for data.frame to generate such a data frame. However, not all operations on data frames will preserve duplicated column names: for example matrix-like subsetting will force column names in the result to be unique.

data.frame converts each of its arguments to a data frame by calling as.data.frame(optional = TRUE). As that is a generic function, methods can be written to change the behaviour of arguments according to their classes: R comes with many such methods. Character variables passed to data.frame are converted to factor columns if not protected by I and argument stringsAsFactors is true. If a list or data frame or matrix is passed to data.frame it is as if each component or column had been passed as a separate argument (except for matrices protected by I).

Objects passed to data.frame should have the same number of rows, but atomic vectors (see is.vector), factors and character vectors protected by I will be recycled a whole number of times if necessary (including as elements of list arguments).

If row names are not supplied in the call to data.frame, the row names are taken from the first component that has suitable names, for example a named vector or a matrix with rownames or a data frame. (If that component is subsequently recycled, the names are discarded with a warning.) If row.names was supplied as NULL or no suitable component was found the row names are the integer sequence starting at one (and such row names are considered to be ‘automatic’, and not preserved by as.matrix).

If row names are supplied of length one and the data frame has a single row, the row.names is taken to specify the row names and not a column (by name or number).

Names are removed from vector inputs not protected by I.

Value

A data frame, a matrix-like structure whose columns may be of differing types (numeric, logical, factor and character and so on).

How the names of the data frame are created is complex, and the rest of this paragraph is only the basic story. If the arguments are all named and simple objects (not lists, matrices of data frames) then the argument names give the column names. For an unnamed simple argument, a deparsed version of the argument is used as the name (with an enclosing I(...) removed). For a named matrix/list/data frame argument with more than one named column, the names of the columns are the name of the argument followed by a dot and the column name inside the argument: if the argument
is unnamed, the argument's column names are used. For a named or unnamed matrix/list/data frame argument that contains a single column, the column name in the result is the column name in the argument. Finally, the names are adjusted to be unique and syntactically valid unless check.names = FALSE.

**Note**

In versions of R prior to 2.4.0 row.names had to be character: to ensure compatibility with such versions of R, supply a character vector as the row.names argument.

**References**


**See Also**

I, plot.data.frame, print.data.frame, row.names, names (for the column names), [.data.frame for subsetting methods and I(matrix(.)) examples; Math.data.frame etc, about Group methods for dataframes; read.table, make.names, list2DF for creating data frames from lists of variables.

**Examples**

```r
L3 <- LETTERS[1:3]
char <- sample(L3, 10, replace = TRUE)
(d <- data.frame(x = 1, y = 1:10, char = char))
## The "same" with automatic column names:
data.frame(1, 1:10, sample(L3, 10, replace = TRUE))

is.data.frame(d)
## enable automatic conversion of character arguments to factor columns:
(dd <- data.frame(d, fac = letters[1:10], stringsAsFactors = TRUE))
rbind(class = sapply(dd, class), mode = sapply(dd, mode))
stopifnot(1:10 == row.names(d)) # {coercion}
(d0 <- d[, FALSE]) # data frame with 0 columns and 10 rows
(d_0 <- d[FALSE, ]) # <0 rows> data frame (3 named cols)
(d00 <- d0[FALSE, ]) # data frame with 0 columns and 0 rows
```

---

**Description**

Return the matrix obtained by converting all the variables in a data frame to numeric mode and then binding them together as the columns of a matrix. Factors and ordered factors are replaced by their internal codes.

**Usage**

```r
data.matrix(frame, rownames.force = NA)
```
Arguments

frame a data frame whose components are logical vectors, factors or numeric or character vectors.

rownames.force logical indicating if the resulting matrix should have character (rather than NULL) rownames. The default, NA, uses NULL rownames if the data frame has 'automatic' row.names or for a zero-row data frame.

Details

Logical and factor columns are converted to integers. Character columns are first converted to factors and then to integers. Any other column which is not numeric (according to is.numeric) is converted by as.numeric or, for S4 objects, as(, "numeric"). If all columns are integer (after conversion) the result is an integer matrix, otherwise a numeric (double) matrix.

Value

If frame inherits from class "data.frame", an integer or numeric matrix of the same dimensions as frame, with dimnames taken from the row.names (or NULL, depending on rownames.force) and names.

Otherwise, the result of as.matrix.

Note

The default behaviour for data frames differs from R < 2.5.0 which always gave the result character rownames.

References


See Also

as.matrix, data.frame, matrix.

Examples

DF <- data.frame(a = 1:3, b = letters[10:12],
c = seq(as.Date("2004-01-01"), by = "week", length.out = 3),
stringsAsFactors = TRUE)
data.matrix(DF[1:2])
data.matrix(DF)
Description

Returns a character string of the current system date and time.

Usage

date()

Value

The string has the form "Fri Aug 20 11:11:00 1999", i.e., length 24, since it relies on POSIX's ctime ensuring the above fixed format. Timezone and Daylight Saving Time are taken account of, but not indicated in the result.

The day and month abbreviations are always in English, irrespective of locale.

References


See Also

Sys.Date and Sys.time; Date and DateTimeClasses for objects representing date and time.

Examples

(d <- date())
nchar(d) == 24

## something similar in the current locale
## depending on ctime; e.g. %e could be %d:
format(Sys.time(), "%a %b %e %H:%M:%S %Y")

Dates

Description

Description of the class "Date" representing calendar dates.

Usage

## S3 method for class 'Date'
summary(object, digits = 12, ...)

## S3 method for class 'Date'
print(x, max = NULL, ...)
Dates

Arguments

object, x  a Date object to be summarized or printed.
digits    number of significant digits for the computations.
max       numeric or NULL, specifying the maximal number of entries to be printed. By
default, when NULL, getOption("max.print") used.
...       further arguments to be passed from or to other methods.

Details

Dates are represented as the number of days since 1970-01-01, with negative values for earlier
dates. They are always printed following the rules of the current Gregorian calendar, even though
that calendar was not in use long ago (it was adopted in 1752 in Great Britain and its colonies).
When printing there is assumed to be a year zero.
It is intended that the date should be an integer value, but this is not enforced in the internal repre-
sentation. Fractional days will be ignored when printing. It is possible to produce fractional days
via the mean method or by adding or subtracting (see Ops.Date).

When a date is converted to a date-time (for example by as.POSIXct or as.POSIXlt its time is
taken as midnight in UTC.

Printing dates involves conversion to class "POSIXlt" which treats dates of more than about 780
million years from present as NA.
For the many methods see methods(class = "Date"). Several are documented separately, see
below.

See Also

Sys.Date for the current date.
weekdays for convenience extraction functions.

Methods with extra arguments and documentation:

Ops.Date for operators on "Date" objects.
format.Date for conversion to and from character strings.
axis.Date and hist.Date for plotting.
seq.Date, cut.Date, and round.Date for utility operations.

See DateTimeClasses for date-time classes.

Examples

(today <- Sys.Date())
format(today, "%d %b %Y")  # with month as a word
(tenweeks <- seq(today, length.out=10, by="1 week")). # next ten weeks
weekdays(today)
months(tenweeks)

(Dls <- as.Date(.leap.seconds))

# Show use of year zero:
(z <- as.Date("01-01-01"). # how it is printed depends on the OS
z - 365 # so year zero was a leap year.
as.Date("00-02-29")
# if you want a different format, consider something like (if supported)
## Not run: format(z, "%04Y-%m-%d") # "0001-01-01"
format(z, "%4Y-%m-%d") # "1-01-01"
format(z, "%Y-%m-%d") # "1-01-01"

## End(Not run)

## length(<Date>) <- n now works
ls <- Dls; length(ls) <- 12
l2 <- Dls; length(l2) <- 5 + length(Dls)
stopifnot(exprs = {
  ## length(.) <- * is compatible to subsetting/indexing:
  identical(ls, Dls[seq_along(ls)])
  identical(l2, Dls[seq_along(l2)])
  ## has filled with NA's
  is.na(l2[(length(Dls)+1):length(l2)])
})

---

**DateTimeClasses**

**Date-Time Classes**

### Description

Description of the classes "POSIXlt" and "POSIXct" representing calendar dates and times.

### Usage

#### S3 method for class 'POSIXct'

```r
print(x, tz = "", usetz = TRUE, max = NULL, ...)
```

#### S3 method for class 'POSIXct'

```r
summary(object, digits = 15, ...)
```

time + z
z + time
time - z
time1 lop time2

### Arguments

- **x, object**: an object to be printed or summarized from one of the date-time classes.
- **tz, usetz**: for timezone formatting, passed to `format.POSIXct`.
- **max**: numeric or NULL, specifying the maximal number of entries to be printed. By default, when NULL, `getOption("max.print")` used.
- **digits**: number of significant digits for the computations: should be high enough to represent the least important time unit exactly.
- **lop**: one of `==`, `!=`, `<`, `<=`, `>`, `>=`.

---

**DateTimeClasses**

**Date-Time Classes**

### Description

Description of the classes "POSIXlt" and "POSIXct" representing calendar dates and times.

### Usage

#### S3 method for class 'POSIXct'

```r
print(x, tz = "", usetz = TRUE, max = NULL, ...)
```

#### S3 method for class 'POSIXct'

```r
summary(object, digits = 15, ...)
```

time + z
z + time
time - z
time1 lop time2

### Arguments

- **x, object**: an object to be printed or summarized from one of the date-time classes.
- **tz, usetz**: for timezone formatting, passed to `format.POSIXct`.
- **max**: numeric or NULL, specifying the maximal number of entries to be printed. By default, when NULL, `getOption("max.print")` used.
- **digits**: number of significant digits for the computations: should be high enough to represent the least important time unit exactly.
- **lop**: one of `==`, `!=`, `<`, `<=`, `>`, `>=`. 

Details

There are two basic classes of date/times. Class "POSIXct" represents the (signed) number of seconds since the beginning of 1970 (in the UTC time zone) as a numeric vector. Class "POSIXlt" is internally a list of vectors with components named sec, min, hour for the time, mday, mon, and year, for the date, wday, yday for the day of the week and day of the year, isdst, a Daylight Saving Time flag, and sometimes (both optional) zone, a string for the time zone, and gmt0ff, offset in seconds from GMT, see the section ‘Details on POSIXlt’ below for more details.

The classes correspond to the POSIX/C99 constructs of ‘calendar time’ (the time_t data type, “ct”), and ‘local time’ (or broken-down time, the ‘struct tm’ data type, “lt”), from which they also inherit their names.

"POSIXct" is more convenient for including in data frames, and "POSIXlt" is closer to human-readable forms. A virtual class "POSIXt" exists from which both of the classes inherit: it is used to allow operations such as subtraction to mix the two classes.

Logical comparisons and some arithmetic operations are available for both classes. One can add or subtract a number of seconds from a date-time object, but not add two date-time objects. Subtraction of two date-time objects is equivalent to using difftime. Be aware that "POSIXlt" objects will be interpreted as being in the current time zone for these operations unless a time zone has been specified.

Both classes may have an attribute "tzone", specifying the time zone. Note however that their meaning differ, see the section ‘Time Zones’ below for more details.

Unfortunately, the conversion is complicated by the operation of time zones and leap seconds (according to this version of R’s data, 27 days have been 86401 seconds long so far, the last being on (actually, immediately before) 2017-01-01: the times of the extra seconds are in the object .leap.seconds). The details of this are entrusted to the OS services where possible. It seems that some rare systems used to use leap seconds, but all known current platforms ignore them (as required by POSIX). This is detected and corrected for at build time, so "POSIXct" times used by R do not include leap seconds on any platform.

Using c on "POSIXlt" objects converts them to the current time zone, and on "POSIXct" objects drops "tzone" attributes if they are not all the same.

A few times have specific issues. First, the leap seconds are ignored, and real times such as "2005-12-31 23:59:60" are (probably) treated as the next second. However, they will never be generated by R, and are unlikely to arise as input. Second, on some OSes there is a problem in the POSIX/C99 standard with "1969-12-31 23:59:59 UTC", which is -1 in calendar time and that value is on those OSes also used as an error code. Thus as.POSIXct("1969-12-31 23:59:59", format = "%Y-%m-%d %H:%M:%S", tz = "UTC") may give NA, and hence as.POSIXct("1969-12-31 23:59:59", tz = "UTC") will give "1969-12-31 23:59:00". Other OSes (including the code used by R on Windows) report errors separately and so are able to handle that time as valid.

The print methods respect options("max.print").

Time zones

"POSIXlt" objects will often have an attribute "tzone", a character vector of length 3 giving the time zone name (from the TZ environment variable or argument tz of functions creating "POSIXlt" objects; "" marks the current time zone) and the names of the base time zone and the alternate (daylight-saving) time zone. Sometimes this may just be of length one, giving the time zone name.

"POSIXct" objects may also have an attribute "tzone", a character vector of length one. If set to a non-empty value, it will determine how the object is converted to class "POSIXlt" and in particular how it is printed. This is usually desirable, but if you want to specify an object in a particular time zone but to be printed in the current time zone you may want to remove the "tzone" attribute.
Details on POSIXlt

Class "POSIXlt" is internally a named list of vectors representing date-times, with the following list components:

- **sec** 0–61: seconds, allowing for leap seconds.
- **min** 0–59: minutes.
- **hour** 0–23: hours.
- **mday** 1–31: day of the month
- **mon** 0–11: months after the first of the year.
- **year** years since 1900.
- **wday** 0–6 day of the week, starting on Sunday.
- **yday** 0–365: day of the year (365 only in leap years).
- **isdst** Daylight Saving Time flag. Positive if in force, zero if not, negative if unknown.
- **zone** (Optional.) The abbreviation for the time zone in force at that time: "" if unknown (but "" might also be used for UTC).
- **gmtoff** (Optional.) The offset in seconds from GMT: positive values are East of the meridian. Usually NA if unknown, but 0 could mean unknown.

The components must be in this order: that was only minimally checked prior to R 4.3.0. All objects created in R 4.3.0 have the optional components. From earlier versions of R, he last two components will not be present for times in UTC and are platform-dependent. Currently gmtoff is set on almost all current platforms: those based on BSD or glibc (including Linux and macOS) and those using the tzcode implementation shipped with R (including Windows and by default macOS).

Note that the internal list structure is somewhat hidden, as many methods (including `length(x)`, `print()` and `str()`) apply to the abstract date-time vector, as for "POSIXct". One can extract and replace single components via `[]` indexing with two indices (see the examples).

The components of "POSIXlt" are integer vectors, except **sec** (double) and zone (character). However most users will coerce numeric values for the first to real and the rest bar zone to integer.

Components **wday** and **yday** are for information, and are not used in the conversion to calendar time nor for printing, `format()`, or in `as.character()`.

However, component **isdst** is needed to distinguish times at the end of DST: typically 1am to 2am occurs twice, first in DST and then in standard time. At all other times **isdst** can be deduced from the first six values, but the behaviour if it is set incorrectly is platform-dependent. For example Linux/glibc when checked fixed up incorrect values in time zones which support DST but gave an error on value 1 in those without DST.

For “ragged” and out-of-range vs “balanced” "POSIXlt" objects, see `balancePOSIXlt()`.

Sub-second Accuracy

Classes "POSIXct" and "POSIXlt" are able to express fractions of a second where the latter allows for higher accuracy. Consequently, conversion of fractions between the two forms may not be exact, but will have better than microsecond accuracy.

Fractional seconds are printed only if `options("digits.secs")` is set: see `strftime`.
Valid ranges for times

The "POSIXt" class can represent a very wide range of times (up to billions of years), but such times can only be interpreted with reference to a time zone.

The concept of time zones was first adopted in the nineteenth century, and the Gregorian calendar was introduced in 1582 but not universally adopted until 1927. OS services almost invariably assume the Gregorian calendar and may assume that the time zone that was first enacted for the location was in force before that date. (The earliest legislated time zone seems to have been London on 1847-12-01.) Some OSes assume the previous use of ‘local time’ based on the longitude of a location within the time zone.

Most operating systems represent POSIXct times as C type long. This means that on 32-bit OSes this covers the period 1902 to 2037. On all known 64-bit platforms and for the code we use on 32-bit Windows, the range of representable times is billions of years: however, not all can convert correctly times before 1902 or after 2037. A few benighted OSes used a unsigned type and so cannot represent times before 1970.

Where possible the platform limits are detected, and outside the limits we use our own C code. This uses the offset from GMT in use either for 1902 (when there was no DST) or that predicted for one of 2030 to 2037 (chosen so that the likely DST transition days are Sundays), and uses the alternate (daylight-saving) time zone only if isdst is positive or (if -1) if DST was predicted to be in operation in the 2030s on that day.

Note that there are places (e.g., Rome) whose offset from UTC varied in the years prior to 1902, and these will be handled correctly only where there is OS support.

There is no reason to assume that the DST rules will remain the same in the future: the US legislated in 2005 to change its rules as from 2007, with a possible future reversion. So conversions for times more than a year or two ahead are speculative. Other countries have changed their rules (and indeed, if DST is used at all) at a few days’ notice. So representations and conversion of future dates are tentative. This also applies to dates after the in-use version of the time-zone database – not all platforms keep it up to date, which includes that shipped with older versions of R where used (which it is by default on Windows and macOS).

Warnings

Some Unix-like systems (especially Linux ones) do not have environment variable TZ set, yet have internal code that expects it (as does POSIX). We have tried to work around this, but if you get unexpected results try setting TZ. See Sys.timezone for valid settings.

Great care is needed when comparing objects of class "POSIXt". Not only are components and attributes optional; several components may have values meaning ‘not yet determined’ and the same time represented in different time zones will look quite different.

The order of the list components of "POSIXt" objects must not be changed, as several C-based conversion methods rely on the order for efficiency.

References


See Also

Dates for dates without times.

as.POSIXct and as.POSIXlt for conversion between the classes.

strptime for conversion to and from character representations.
Sys.time for clock time as a "POSIXct" object.
difftime for time intervals.
balancePOSIXt() for balancing or filling “ragged” POSIXt objects.
cut.POSIXt, seq.POSIXt, round.POSIXt and trunc.POSIXt for methods for these classes.
weekdays for convenience extraction functions.

Examples

```r
## IGNORE_RDIFF_BEGIN
(z <- Sys.time()) # the current date, as class "POSIXct"
Sys.time() - 3600 # an hour ago
as.POSIXlt(Sys.time(), "GMT") # the current time in GMT
print(.leap.seconds, tz = "PST8PDT") # and in Seattle’s
## IGNORE_RDIFF_END

## look at *internal* representation of "POSIXlt":
leapS <- as.POSIXlt(.leap.seconds)
names(unclass(leapS)) ; is.list(leapS)
## str() on inner structure needs unclass(.):
utils::str(unclass(leapS), vec.len = 7)
## show all (apart from "tzone" attr):
data.frame(unclass(leapS))

## Extracting *single* components of POSIXlt objects:
leapS[1:5, "year"]
leapS[17:22, "mon"]

## length(.) <- n now works for "POSIXct" and "POSIXlt":
for(lpS in list(.leap.seconds, leapS)) {
  ls <- lpS; length(ls) <- 12
  l2 <- lpS; length(l2) <- 5 + length(lpS)
  stopifnot(exprs = {
    ## length(.) <- * is compatible to subsetting/indexing:
    identical(ls, lpS[seq_along(ls)])
    identical(l2, lpS[seq_along(l2)])
    ## has filled with NA’s
    is.na(l2[(length(lpS)+1):length(l2)])
  })
}
```


dcf

Read and Write Data in DCF Format

Description

Reads or writes an R object from/to a file in Debian Control File format.
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dcf

Usage
read.dcf(file, fields = NULL, all = FALSE, keep.white = NULL)
write.dcf(x, file = "", append = FALSE, useBytes = FALSE,
indent = 0.1 * getOption("width"),
width = 0.9 * getOption("width"),
keep.white = NULL)
Arguments
file

either a character string naming a file or a connection. "" indicates output to the
console. For read.dcf this can name a compressed file (see gzfile).

fields

Fields to read from the DCF file. Default is to read all fields.

all

a logical indicating whether in case of multiple occurrences of a field in a record,
all these should be gathered. If all is false (default), only the last such occurrence is used.

keep.white

a character string with the names of the fields for which whitespace should be
kept as is, or NULL (default) indicating that there are no such fields. Coerced
to character if possible. For fields where whitespace is not to be kept as is,
read.dcf removes leading and trailing whitespace, and write.dcf folds using
strwrap.

x

the object to be written, typically a data frame. If not, it is attempted to coerce x
to a data frame.

append

logical. If TRUE, the output is appended to the file. If FALSE, any existing file of
the name is destroyed.

useBytes

logical to be passed to writeLines(), see there: “for expert use”.

indent

a positive integer specifying the indentation for continuation lines in output entries.

width

a positive integer giving the target column for wrapping lines in the output.

Details
DCF is a simple format for storing databases in plain text files that can easily be directly read and
written by humans. DCF is used in various places to store R system information, like descriptions
and contents of packages.
The DCF rules as implemented in R are:
1. A database consists of one or more records, each with one or more named fields. Not every
record must contain each field. Fields may appear more than once in a record.
2. Regular lines start with a non-whitespace character.
3. Regular lines are of form tag:value, i.e., have a name tag and a value for the field, separated
by : (only the first : counts). The value can be empty (i.e., whitespace only).
4. Lines starting with whitespace are continuation lines (to the preceding field) if at least one
character in the line is non-whitespace. Continuation lines where the only non-whitespace
character is a ‘.’ are taken as blank lines (allowing for multi-paragraph field values).
5. Records are separated by one or more empty (i.e., whitespace only) lines.
6. Individual lines may not be arbitrarily long; prior to R 3.0.2 the length limit was approximately
8191 bytes per line.


Note that read.dcf(all = FALSE) reads the file byte-by-byte. This allows a 'DESCRIPTION' file to be read and only its ASCII fields used, or its 'Encoding' field used to re-encode the remaining fields.

write.dcf does not write NA fields.

Value

The default read.dcf(all = FALSE) returns a character matrix with one row per record and one column per field. Leading and trailing whitespace of field values is ignored unless a field is listed in keep.white. If a tag name is specified in the file, but the corresponding value is empty, then an empty string is returned. If the tag name of a field is specified in fields but never used in a record, then the corresponding value is NA. If fields are repeated within a record, the last one encountered is returned. Malformed lines lead to an error.

For read.dcf(all = TRUE) a data frame is returned, again with one row per record and one column per field. The columns are lists of character vectors for fields with multiple occurrences, and character vectors otherwise.

Note that an empty file is a valid DCF file, and read.dcf will return a zero-row matrix or data frame.

For write.dcf, invisible NULL.

Note

As from R 3.4.0, ‘whitespace’ in all cases includes newlines.

References


Note that R does not require encoding in UTF-8, which is a recent Debian requirement. Nor does it use the Debian-specific sub-format which allows comment lines starting with ‘#’.

See Also

write.table.

available.packages, which uses read.dcf to read the indices of package repositories.

Examples

```r
## Create a reduced version of the DESCRIPTION file in package 'splines'
x <- read.dcf(file = system.file("DESCRIPTION", package = "splines"),
              fields = c("Package", "Version", "Title"))
write.dcf(x)

## An online DCF file with multiple records
con <- url("https://cran.r-project.org/src/contrib/PACKAGES")
y <- read.dcf(con, all = TRUE)
close(con)
utils::str(y)
```
**debug**  
*Debug a Function*

**Description**
Set, unset or query the debugging flag on a function. The `text` and `condition` arguments are the same as those that can be supplied via a call to `browser`. They can be retrieved by the user once the browser has been entered, and provide a mechanism to allow users to identify which breakpoint has been activated.

**Usage**

```r
debug(fun, text = "", condition = NULL, signature = NULL)
debugonce(fun, text = "", condition = NULL, signature = NULL)
unddebug(fun, signature = NULL)
isdebugged(fun, signature = NULL)
debuggingState(on = NULL)
```

**Arguments**

- `fun` any interpreted R function.
- `text` a text string that can be retrieved when the browser is entered.
- `condition` a condition that can be retrieved when the browser is entered.
- `signature` an optional method signature. If specified, the method is debugged, rather than its generic.
- `on` logical; a call to the support function `debuggingState` returns `TRUE` if debugging is globally turned on, `FALSE` otherwise. An argument of one or the other of those values sets the state. If the debugging state is `FALSE`, none of the debugging actions will occur (but explicit `browser` calls in functions will continue to work).

**Details**
When a function flagged for debugging is entered, normal execution is suspended and the body of function is executed one statement at a time. A new `browser` context is initiated for each step (and the previous one destroyed).

At the debug prompt the user can enter commands or R expressions, followed by a newline. The commands are described in the `browser` help topic.

To debug a function which is defined inside another function, single-step through to the end of its definition, and then call debug on its name.

If you want to debug a function not starting at the very beginning, use `trace(..., at = *)` or `setBreakpoint`.

Using debug is persistent, and unless debugging is turned off the debugger will be entered on every invocation (note that if the function is removed and replaced the debug state is not preserved). Use `debugonce()` to enter the debugger only the next time the function is invoked.

To debug an S4 method by explicit signature, use `signature`. When specified, signature indicates the method of `fun` to be debugged. Note that debugging is implemented slightly differently for this case, as it uses the trace machinery, rather than the debugging bit. As such, `text` and `condition`
cannot be specified in combination with a non-null signature. For methods which implement the .local rematching mechanism, the .local closure itself is the one that will be ultimately debugged (see isRematched).

isdebugged returns TRUE if a) signature is NULL and the closure fun has been debugged, or b) signature is not NULL, fun is an S4 generic, and the method of fun for that signature has been debugged. In all other cases, it returns FALSE.

The number of lines printed for the deparsed call when a function is entered for debugging can be limited by setting options(deparse.max.lines).

When debugging is enabled on a byte compiled function then the interpreted version of the function will be used until debugging is disabled.

Value

depbug and undebug invisibly return NULL.

isdebugged returns TRUE if the function or method is marked for debugging, and FALSE otherwise.

See Also

ddebugcall for conveniently debugging methods, browser notably for its 'commands', trace; traceback to see the stack after an Error: ... message; recover for another debugging approach.

Examples

## Not run:
depbug(library)
library(methods)

## Not run
## Not run:
depbugonce(sample)
## only the first call will be debugged
sample(10, 1)
sample(10, 1)

## End(Not run)

Defunct

Marking Objects as Defunct

Description

When a function is removed from R it should be replaced by a function which calls .Defunct.

Usage

. Defunct(new, package = NULL, msg)
Arguments

- **new** character string: A suggestion for a replacement function.
- **package** character string: The package to be used when suggesting where the defunct function might be listed.
- **msg** character string: A message to be printed, if missing a default message is used.

Details

.DEfunct is called from defunct functions. Functions should be listed in help("pkg-defunct") for an appropriate pkg, including base (with the alias added to the respective Rd file).

.DEfunct signals an error of class defunctError with fields old, new, and package.

See Also

Deprecated.

base-defunct and so on which list the defunct functions in the packages.

delayedAssign

Delay Evaluation and Promises

Description

delayedAssign creates a promise to evaluate the given expression if its value is requested. This provides direct access to the lazy evaluation mechanism used by R for the evaluation of (interpreted) functions.

Usage

delayedAssign(x, value, eval.env = parent.frame(1),
               assign.env = parent.frame(1))

Arguments

- **x** a variable name (given as a quoted string in the function call)
- **value** an expression to be assigned to x
- **eval.env** an environment in which to evaluate value
- **assign.env** an environment in which to assign x

Details

Both eval.env and assign.env default to the currently active environment.

The expression assigned to a promise by delayedAssign will not be evaluated until it is eventually ‘forced’. This happens when the variable is first accessed.

When the promise is eventually forced, it is evaluated within the environment specified by eval.env (whose contents may have changed in the meantime). After that, the value is fixed and the expression will not be evaluated again, where the promise still keeps its expression.
Value

This function is invoked for its side effect, which is assigning a promise to evaluate value to the variable x.

See Also

`substitute`, to see the expression associated with a promise, if `assign.env` is not the `.GlobalEnv`.

Examples

```r
msg <- "old"
delayedAssign("x", msg)
substitute(x) # shows only 'x', as it is in the global env.
msg <- "new!"
x # new!

delayedAssign("x", {
  for(i in 1:3)
    cat("yippee!\n")
  10
})
x^2 #= yippee
x^2 #= simple number

ne <- new.env()
delayedAssign("x", pi + 2, assign.env = ne)
## See the promise (without "forcing" (i.e. evaluating) it):
substitute(x, ne) # 'pi + 2'

### Promises in an environment [for advanced users]:  ---------------------

e <- (function(x, y = 1, z) environment())(cos, "y", {cat(" HO!\n"); pi+2})
## How can we look at all promises in an env (w/o forcing them)?
gete <- function(e_)
{  
  ne <- names(e_)
  names(ne) <- ne
  lapply(lapply(ne, as.name),
    function(n) eval(substitute(substitute(X, e_), list(X=n))))
}
(exps <- gete(e))
sapply(exps, typeof)

(le <- as.list(e)) # evaluates ("force"s) the promises
stopifnot(identical(le, lapply(exps, eval))) # and another "Ho!"
```

deparse

Expression Deparsing

Description

Turn unevaluated expressions into character strings.
Usage

deparse(expr, width.cutoff = 60L,
    backtick = mode(expr) %in% c("call", "expression", "(", "function"),
    control = c("keepNA", "keepInteger", "niceNames", "showAttributes"),
    nlines = -1L)

deparse1(expr, collapse = " ", width.cutoff = 500L, ...)

Arguments

expr any R expression.
width.cutoff integer in [20, 500] determining the cutoff (in bytes) at which line-breaking is tried.
backtick logical indicating whether symbolic names should be enclosed in backticks if they do not follow the standard syntax.
control character vector (or NULL) of deparsing options. control = "all" is thorough, see .deparse0pts.
nlines integer: the maximum number of lines to produce. Negative values indicate no limit.
collapse a string, passed to paste().
... further arguments passed to deparse().

details

These functions turn unevaluated expressions (where 'expression' is taken in a wider sense than the strict concept of a vector of mode and type (typeof) "expression" used in expression) into character strings (a kind of inverse to parse).

A typical use of this is to create informative labels for data sets and plots. The example shows a simple use of this facility. It uses the functions deparse and substitute to create labels for a plot which are character string versions of the actual arguments to the function myplot.

The default for the backtick option is not to quote single symbols but only composite expressions. This is a compromise to avoid breaking existing code.

width.cutoff is a lower bound for the line lengths: deparsing a line proceeds until at least width.cutoff bytes have been output and e.g. arg = value expressions will not be split across lines.

deparse1() is a simple utility added in R 4.0.0 to ensure a string result (character vector of length one), typically used in name construction, as deparse1(substitute(.)).

note

To avoid the risk of a source attribute out of sync with the actual function definition, the source attribute of a function will never be deparsed as an attribute.

Deparsing internal structures may not be accurate: for example the graphics display list recorded by recordPlot is not intended to be deparsed and .Internal calls will be shown as primitive calls.

References

See Also

."deparseOpts" for available control settings; dput() and dump() for related functions using identical internal deparsing functionality.

substitute, parse, expression.

Quotes for quoting conventions, including backticks.

Examples

require(stats); require(graphics)

deparse(args(lm))
deparse(args(lm), width.cutoff = 500)

myplot <- function(x, y) {
  plot(x, y, xlab = deparse1(substitute(x)),
       ylab = deparse1(substitute(y)))
}

e <- quote("foo bar")
deparse(e)
deparse(e, backtick = TRUE)
e <- quote("foo bar"+1)
deparse(e)
deparse(e, control = "all") # wraps it w/ quote(. )

deparseOpts

Options for Expression Deparsing

Description

Process the deparsing options for deparse, dput and dump.

Usage

."deparseOpts"(control)

..deparseOpts

Arguments

control character vector of deparsing options.

Details

..deparseOpts is the character vector of possible deparsing options used by .deparseOpts().
..deparseOpts() is called by deparse, dput and dump to process their control argument.

The control argument is a vector containing zero or more of the following strings (exactly those in ..deparseOpts). Partial string matching is used.
"keepInteger": Either surround integer vectors by as.integer() or use suffix L, so they are not converted to type double when parsed. This includes making sure that integer NAs are preserved (via NA_integer_ if there are no non-NA values in the vector, unless "S_compatible" is set).

"quoteExpressions": Surround unevaluated expressions, but not formulas, with quote(), so they are not evaluated when re-parsed.

"showAttributes": If the object has attributes (other than a source attribute, see srcref), use structure() to display them as well as the object value unless the only such attribute is names and the "niceNames" option is set. This ("showAttributes") is the default for deparse and dput.

"useSource": If the object has a source attribute (srcref), display that instead of deparsing the object. Currently only applies to function definitions.

"warnIncomplete": Some exotic objects such as environments, external pointers, etc. cannot be deparsed properly. This option causes a warning to be issued if the deparser recognizes one of these situations.

Also, the parser in \texttt{R < 2.7.0} would only accept strings of up to 8192 bytes, and this option gives a warning for longer strings.

"keepNA": Integer, real and character NAs are surrounded by coercion functions where necessary to ensure that they are parsed to the same type. Since e.g. \texttt{NA_real_} can be output in \texttt{R}, this is mainly used in connection with \texttt{S_compatible}.

"niceNames": If true, lists and atomic vectors with non-NA names (see \texttt{names}) are deparsed as e.g., \texttt{c(A = 1)} instead of \texttt{structure(1, names = \"A\")}, independently of the "showAttributes" setting.

"all": An abbreviated way to specify all of the options listed above plus "digits17". This is the default for dump, and, without "digits17", the options used by edit (which are fixed).

"delayPromises": Deparse promises in the form \texttt{<promise: expression>} rather than evaluating them. The value and the environment of the promise will not be shown and the deparsed code cannot be sourced.

"S_compatible": Make deparsing as far as possible compatible with S and \texttt{R < 2.5.0}. For compatibility with S, integer values of double vectors are deparsed with a trailing decimal point. Backticks are not used.

"hexNumeric": Real and finite complex numbers are output in \texttt{"%a"} format as binary fractions (coded as hexadecimal: see sprintf) with maximal opportunity to be recorded exactly to full precision. Complex numbers with one or both non-finite components are output as if this option were not set.

(This relies on that format being correctly supported: known problems on Windows are worked around as from \texttt{R 3.1.2}.)

"digits17": Real and finite complex numbers are output using format \texttt{"%.17g"} which may give more precision than the default (but the output will depend on the platform and there may be loss of precision when read back). Complex numbers with one or both non-finite components are output as if this option were not set.

"exact": An abbreviated way to specify control = c("all", "hexNumeric") which is guaranteed to be exact for numbers, see also below.

For the most readable (but perhaps incomplete) display, use control = NULL. This displays the object’s value, but not its attributes. The default in \texttt{deparse} is to display the attributes as well, but not to use any of the other options to make the result parseable. (\texttt{dump} uses more default options via control = "all", and printing of functions without sources uses c("keepInteger", "keepNA") to which one may add "warnIncomplete".)
Using control = "exact" (short for control = c("all", "hexNumeric")) comes closest to making `deparse()` an inverse of `parse()` (but we have not yet seen an example where "all", now including "digits17", would not have been as good). However, not all objects are deparse-able even with these options, and a warning will be issued if the function recognizes that it is being asked to do the impossible.

Only one of "hexNumeric" and "digits17" can be specified.

**Value**

An integer value corresponding to the control options selected.

**Examples**

```R
stopifnot(.deparseOpts("exact") == .deparseOpts(c("all", "hexNumeric")))
(iOpt.all <- .deparseOpts("all")) # a four digit integer

## one integer --> vector binary bits
int2bits <- function(x, base = 2L, 
  ndigits = 1 + floor(1e-9 + log(max(x,1), base))) {
  r <- numeric(ndigits)
  for (i in ndigits:1) {
    r[i] <- x%%base
    if (i > 1L)
      x <- x%/%base
  }
  rev(r) # smallest bit at left
}
int2bits(iOpt.all)

## What options does "all" contain ? =========
(dep0.indiv <- setdiff(.deparseOpts, c("all", "exact")))
(oa <- dep0.indiv[int2bits(iOpt.all) == 1])# 8 strings
stopifnot(identical(iOpt.all, .deparseOpts(oa)))

## ditto for "exact" instead of "all":
(iOpt.X <- .deparseOpts("exact"))
data.frame(opts = dep0.indiv, 
  all = int2bits(iOpt.all),
  exact= int2bits(iOpt.X))
(oX <- dep0.indiv[int2bits(iOpt.X) == 1]) # 8 strings, too
diffXall <- oa != oX
stopifnot(identical(iOpt.X, .deparseOpts(oX)),
  identical(oX[diffXall], "hexNumeric"),
  identical(oa[diffXall], "digits17"))
```

### Deprecated Marking Objects as Deprecated

**Description**

When an object is about to be removed from R it is first deprecated and should include a call to `.Deprecated.`
Usage

`.Deprecated(new, package=NULL, msg, old = as.character(sys.call(sys.parent()))[1L])`

Arguments

- `new` character string: A suggestion for a replacement function.
- `package` character string: The package to be used when suggesting where the deprecated function might be listed.
- `msg` character string: A message to be printed, if missing a default message is used.
- `old` character string specifying the function (default) or usage which is being deprecated.

Details

`.Deprecated("<new name>")` is called from deprecated functions. The original help page for these functions is often available at `help("oldName-deprecated")` (note the quotes). Functions should be listed in `help("pkg-deprecated")` for an appropriate `pkg`, including `base`.

`.Deprecated` signals a warning of class `deprecatedWarning` with fields `old`, `new`, and `package`.

See Also

- `Defunct`
- `base-deprecated` and so on which list the deprecated functions in the packages.

---

### det

**Calculate the Determinant of a Matrix**

**Description**

det calculates the determinant of a matrix. `determinant` is a generic function that returns separately the modulus of the determinant, optionally on the logarithm scale, and the sign of the determinant.

**Usage**

- `det(x, ...)`
- `determinant(x, logarithm = TRUE, ...)`

**Arguments**

- `x` numeric matrix: logical matrices are coerced to numeric.
- `logarithm` logical; if TRUE (default) return the logarithm of the modulus of the determinant.
- `...` Optional arguments. At present none are used. Previous versions of `det` allowed an optional `method` argument. This argument will be ignored but will not produce an error.
The determinant function uses an LU decomposition and the `det` function is simply a wrapper around a call to `determinant`.

Often, computing the determinant is not what you should be doing to solve a given problem.

For `det`, the determinant of `x`. For `determinant`, a list with components

- `modulus`: a numeric value. The modulus (absolute value) of the determinant if `logarithm` is `FALSE`; otherwise the logarithm of the modulus.
- `sign`: integer; either +1 or −1 according to whether the determinant is positive or negative.

Examples

```r
(x <- matrix(1:4, ncol = 2))
unlist(determinant(x))
det(x)
det(print(cbind(1, 1:3, c(2,0,1))))
```

Detach a database, i.e., remove it from the `search()` path of available R objects. Usually this is either a `data.frame` which has been `attached` or a package which was attached by `library`.

Usage

```r
detach(name, pos = 2L, unload = FALSE, character.only = FALSE, force = FALSE)
```

Arguments

- `name`: The object to detach. Defaults to `search()[pos]`. This can be an unquoted name or a character string but not a character vector. If a number is supplied this is taken as `pos`.
- `pos`: Index position in `search()` of the database to detach. When `name` is a number, `pos = name` is used.
- `unload`: A logical value indicating whether or not to attempt to unload the namespace when a package is being detached. If the package has a namespace and `unload` is `TRUE`, then `detach` will attempt to unload the namespace via `unloadNamespace`: if the namespace is imported by another namespace or `unload` is `FALSE`, no unloading will occur.
- `character.only`: a logical indicating whether `name` can be assumed to be a character string.
- `force`: logical: should a package be detached even though other attached packages depend on it?
Details

This is most commonly used with a single number argument referring to a position on the search list, and can also be used with a unquoted or quoted name of an item on the search list such as package:tools.

If a package has a namespace, detaching it does not by default unload the namespace (and may not even with unload = TRUE), and detaching will not in general unload any dynamically loaded compiled code (DLLs); see getLoadedDLLs and library.dynam.unload. Further, registered S3 methods from the namespace will not be removed, and because S3 methods are not tagged to their source on registration, it is in general not possible to safely un-register the methods associated with a given package. If you use library on a package whose namespace is loaded, it attaches the exports of the already loaded namespace. So detaching and re-attaching a package may not refresh some or all components of the package, and is inadvisable. The most reliable way to completely detach a package is to restart R.

Value

The return value is invisible. It is NULL when a package is detached, otherwise the environment which was returned by attach when the object was attached (incorporating any changes since it was attached).

Good practice

detach() without an argument removes the first item on the search path after the workspace. It is all too easy to call it too many or too few times, or to not notice that the search path has changed since an attach call.

Use of attach/detach is best avoided in functions (see the help for attach) and in interactive use and scripts it is prudent to detach by name.

Note

You cannot detach either the workspace (position 1) nor the base package (the last item in the search list), and attempting to do so will throw an error.

Unloading some namespaces has undesirable side effects: e.g. unloading grid closes all graphics devices, and on some systems tcltk cannot be reloaded once it has been unloaded and may crash R if this is attempted.

References


See Also

attach, library, search, objects, unloadNamespace, library.dynam.unload.

Examples

require(splines) # package
detach(package:splines)
## or also
library(splines)
 pkg <- "package:splines"
## careful: do not do this unless 'splines' is not already attached.
library(splines)
detach(2) # 'pos' used for 'name'

## an example of the name argument to attach
## and of detaching a database named by a character vector
attach_and_detach <- function(db, pos = 2)
{
  name <- deparse1(substitute(db))
  attach(db, pos = pos, name = name)
  print(search()[pos])
  detach(name, character.only = TRUE)
}

attach_and_detach(women, pos = 3)

---

**diag**  

**Matrix Diagonals**

**Description**

Extract or replace the diagonal of a matrix, or construct a diagonal matrix.

**Usage**

diag(x = 1, nrow, ncol, names = TRUE)
diag(x) <- value

**Arguments**

- **x**
  a matrix, vector or 1D array, or missing.

- **nrow, ncol**
  optional dimensions for the result when x is not a matrix.

- **names**
  (when x is a matrix) logical indicating if the resulting vector, the diagonal of x, should inherit names from dimnames(x) if available.

- **value**
  either a single value or a vector of length equal to that of the current diagonal. Should be of a mode which can be coerced to that of x.

**Details**

diag has four distinct usages:

1. x is a matrix, when it extracts the diagonal.
2. x is missing and nrow is specified, it returns an identity matrix.
3. x is a scalar (length-one vector) and the only argument, it returns a square identity matrix of size given by the scalar.
4. x is a ‘numeric’ (complex, numeric, integer, logical, or raw) vector, either of length at least 2 or there were further arguments. This returns a matrix with the given diagonal and zero off-diagonal entries.

It is an error to specify nrow or ncol in the first case.
Value

If x is a matrix then diag(x) returns the diagonal of x. The resulting vector will have names if names is true and if the matrix x has matching column and rownames.

The replacement form sets the diagonal of the matrix x to the given value(s).

In all other cases the value is a diagonal matrix with nrow rows and ncol columns (if ncol is not given the matrix is square). Here nrow is taken from the argument if specified, otherwise inferred from x: if that is a vector (or 1D array) of length two or more, then its length is the number of rows, but if it is of length one and neither nrow nor ncol is specified, nrow = as.integer(x).

When a diagonal matrix is returned, the diagonal elements are one except in the fourth case, when x gives the diagonal elements: it will be recycled or truncated as needed, but fractional recycling and truncation will give a warning.

Note

Using diag(x) can have unexpected effects if x is a vector that could be of length one. Use diag(x, nrow = length(x)) for consistent behaviour.

References


See Also

upper.tri, lower.tri, matrix.

Examples

dim(diag(3))
diag(10, 3, 4) # guess what?
all(diag(1:3) == (m <- matrix(0,3,3); diag(m) <- 1:3; m))

## other "numeric"-like diagonal matrices :
diag(c(1i,2i)) # complex
diag(TRUE, 3) # logical
diag(as.raw(1:3)) # raw
(D2 <- diag(2:1, 4)); typeof(D2) # "integer"

require(stats)
## diag(<var-cov-matrix>) = variances
diag(var(M <- cbind(X = 1:5, Y = rnorm(5))))
#-> vector with names "X" and "Y"
rownames(M) <- c(colnames(M), rep(“,", 3))
M; diag(M) # named as well
diag(M, names = FALSE) # w/o names
**diff**

* Lagged Differences*

**Description**

Returns suitably lagged and iterated differences.

**Usage**

```r
diff(x, ...)  
## Default S3 method:  
diff(x, lag = 1, differences = 1, ...)  
## S3 method for class 'POSIXt'  
diff(x, lag = 1, differences = 1, ...)  
## S3 method for class 'Date'  
diff(x, lag = 1, differences = 1, ...)  
```

**Arguments**

- `x`: a numeric vector or matrix containing the values to be differenced.
- `lag`: an integer indicating which lag to use.
- `differences`: an integer indicating the order of the difference.
- `...`: further arguments to be passed to or from methods.

**Details**

`diff` is a generic function with a default method and ones for classes "ts", "POSIXt" and "Date". NA's propagate.

**Value**

If `x` is a vector of length `n` and `differences = 1`, then the computed result is equal to the successive differences `x[(1+lag):n] - x[1:(n-lag)]`. If `differences` is larger than one this algorithm is applied recursively to `x`. Note that the returned value is a vector which is shorter than `x`. If `x` is a matrix then the difference operations are carried out on each column separately.

**References**


**See Also**

diff.ts, diffinv.
**Examples**

```r
diff(1:10, 2)
diff(1:10, 2, 2)
x <- cumsum(cumsum(1:10))
diff(x, lag = 2)
diff(x, differences = 2)
diff(.leap.seconds)
```

**Description**

Time intervals creation, printing, and some arithmetic. The `print()` method calls these “time differences”.

**Usage**

```r
time1 - time2

difftime(time1, time2, tz, units = c("auto", "secs", "mins", "hours", "days", "weeks"))
as.difftime(tim, format = "%X", units = "auto", tz = "UTC")
```

### S3 method for class 'difftime'

```r
format(x, ...)
```

### S3 method for class 'difftime'

```r
units(x)
```

### S3 replacement method for class 'difftime'

```r
units(x) <- value
```

### S3 method for class 'difftime'

```r
as.double(x, units = "auto", ...)
```

### Group methods, notably for round(), signif(), floor(), ceiling(), trunc(), abs(); called directly, *not* as Math():

```r
Math(x, ...)
```

**Arguments**

- `time1, time2`: date-time or date objects.
- `tz`: an optional time zone specification to be used for the conversion, mainly for "POSIXlt" objects.
- `units`: character string. Units in which the results are desired. Can be abbreviated.
- `value`: character string. Like units, except that abbreviations are not allowed.
- `tim`: character string or numeric value specifying a time interval.
difftime

format character specifying the format of tim: see strptime. The default is a locale-specific time format.

x an object inheriting from class "difftime".

... arguments to be passed to or from other methods.

Details

Function difftime calculates a difference of two date/time objects and returns an object of class "difftime" with an attribute indicating the units. The Math group method provides round, signif, floor, ceiling, trunc, abs, and sign methods for objects of this class, and there are methods for the group-generic (see Ops) logical and arithmetic operations.

If units = "auto", a suitable set of units is chosen, the largest possible (excluding "weeks") in which all the absolute differences are greater than one.

Subtraction of date-time objects gives an object of this class, by calling difftime with units = "auto". Alternatively, as.difftime() works on character-coded or numeric time intervals; in the latter case, units must be specified, and format has no effect.

Limited arithmetic is available on "difftime" objects: they can be added or subtracted, and multiplied or divided by a numeric vector. In addition, adding or subtracting a numeric vector by a "difftime" object implicitly converts the numeric vector to a "difftime" object with the same units as the "difftime" object. There are methods for mean and sum (via the Summary group generic), and diff via diff.default building on the "difftime" method for arithmetic, notably -.

The units of a "difftime" object can be extracted by the units function, which also has a replacement form. If the units are changed, the numerical value is scaled accordingly. The replacement version keeps attributes such as names and dimensions.

Note that units = "days" means a period of 24 hours, hence takes no account of Daylight Savings Time. Differences in objects of class "Date" are computed as if in the UTC time zone.

The as.double method returns the numeric value expressed in the specified units. Using units = "auto" means the units of the object.

The format method simply formats the numeric value and appends the units as a text string.

Warning

Because R follows POSIX (and almost all computer clocks) in ignoring leap seconds, so do time differences. So in a UTC time zone

```r
z <- as.POSIXct(c("2016-12-31 23:59:59", "2017-01-01 00:00:01"))
```

reports 'Time difference of 2 secs' but 3 seconds elapsed while the computer clock advanced by 2 seconds.

If you want the elapsed time interval, you need to add in any leap seconds for yourself.

Note

Units such as "months" are not possible as they are not of constant length. To create intervals of months, quarters or years use seq.Date or seq.POSIXt.

See Also

DateTimeClasses.
Examples

(z <- Sys.time() - 3600)
Sys.time() - z  # just over 3600 seconds.

## time interval between release days of R 1.2.2 and 1.2.3.

as.difftime(c("0:3:20", "11:23:15"))
as.difftime(c("3:20", "23:15", "2:"), format = "%H:%M") # 3rd gives NA
(z <- as.difftime(c(0,30,60), units = "mins"))
as.numeric(z, units = "secs")
as.numeric(z, units = "hours")
format(z)

---

**dim**

**Dimensions of an Object**

Description

Retrieve or set the dimension of an object.

Usage

\[
\text{dim}(x) \\
\text{dim}(x) \leftarrow \text{value}
\]

Arguments

- **x**: an R object, for example a matrix, array or data frame.
- **value**: For the default method, either NULL or a numeric vector, which is coerced to integer (by truncation).

Details

The functions `dim` and `dim<`- are internal generic primitive functions.

`dim` has a method for data.frames, which returns the lengths of the row.names attribute of x and of x (as the numbers of rows and columns respectively).

Value

For an array (and hence in particular, for a matrix) `dim` retrieves the `dim` attribute of the object. It is `NULL` or a vector of mode integer.

The replacement method changes the "dim" attribute (provided the new value is compatible) and removes any "dimnames" and "names" attributes.

References

See Also
  ncol, nrow and dimnames.

Examples
  x <- 1:12; dim(x) <- c(3,4)
  x

  # simple versions of nrow and ncol could be defined as follows
  nrow0 <- function(x) dim(x)[1]
  ncol0 <- function(x) dim(x)[2]
For a 1D matrix the names are the same thing as the (only) component of the dimnames.

Both are primitive functions.

provideDimnames(x) provides dimnames where "missing", such that its result has character dimnames for each component. If unique is true as by default, they are unique within each component via make.unique(*, sep=sep).

---

**Value**

The dimnames of a matrix or array can be NULL (which is not stored) or a list of the same length as dim(x). If a list, its components are either NULL or a character vector with non-negative length of the appropriate dimension of x. The list can have names. It is possible that all components are NULL: such dimnames may get converted to NULL.

For the "data.frame" method both dimnames are character vectors, and the rownames must contain no duplicates nor missing values.

provideDimnames(x) returns x, with "NULL - free" dimnames, i.e. each component a character vector of correct length.

---

**Note**

Setting components of the dimnames, e.g., dimnames(A)[[1]] <- value is a common paradigm, but note that it will not work if the value assigned is NULL. Use rownames instead, or (as it does) manipulate the whole dimnames list.

---

**References**


---

**See Also**

rownames, colnames; array, matrix, data.frame.

---

**Examples**

```r
## simple versions of rownames and colnames
## could be defined as follows
rownames0 <- function(x) dimnames(x)[[1]]
colnames0 <- function(x) dimnames(x)[[2]]

(dn <- dimnames(A <- provideDimnames(N <- array(1:24, dim = 2:4))))
A0 <- A; dimnames(A)[2:3] <- list(NULL)
stopifnot(identical(A0, provideDimnames(A)))
strd <- function(x) utils::str(dimnames(x))
strd(provideDimnames(A, base= list(letters[-(1:9)], tail(LETTERS))))
strd(provideDimnames(N, base= list(letters[-(1:9)], tail(LETTERS)))) # recycling
strd(provideDimnames(A, base= list(c("AA","BB")))) # recycling on both levels
## set "empty dimnames"
provideDimnames(rbind(1, 2:3), base = list(""), unique=FALSE)
```
**do.call**

**Execute a Function Call**

**Description**

`do.call` constructs and executes a function call from a name or a function and a list of arguments to be passed to it.

**Usage**

```r
do.call(what, args, quote = FALSE, envir = parent.frame())
```

**Arguments**

- **what**: either a function or a non-empty character string naming the function to be called.
- **args**: a list of arguments to the function call. The names attribute of `args` gives the argument names.
- **quote**: a logical value indicating whether to quote the arguments.
- **envir**: an environment within which to evaluate the call. This will be most useful if `what` is a character string and the arguments are symbols or quoted expressions.

**Details**

If `quote` is `FALSE`, the default, then the arguments are evaluated (in the calling environment, not in `envir`). If `quote` is `TRUE` then each argument is quoted (see `quote`) so that the effect of argument evaluation is to remove the quotes – leaving the original arguments unevaluated when the call is constructed.

The behavior of some functions, such as `substitute`, will not be the same for functions evaluated using `do.call` as if they were evaluated from the interpreter. The precise semantics are currently undefined and subject to change.

**Value**

The result of the (evaluated) function call.

**Warning**

This should not be used to attempt to evade restrictions on the use of `.Internal` and other non-API calls.

**References**


**See Also**

`call` which creates an unevaluated call.
Examples

do.call("complex", list(imaginary = 1:3))

## if we already have a list (e.g., a data frame)
## we need c() to add further arguments
tmp <- expand.grid(letters[1:2], 1:3, c("+", "-"))
do.call("paste", c(tmp, sep = \\

do.call(paste, list(as.name("A"), as.name("B"))), quote = TRUE))

## examples of where objects will be found.
A <- 2
f <- function(x) print(x^2)
env <- new.env()
assign("A", 10, envir = env)
assign("f", f, envir = env)
f <- function(x) print(x)
f(A) # 2  
do.call("f", list(A)) # 2

do.call("f", list(A), envir = env) # 4

do.call( f, list(A), envir = env) # 2

do.call("f", list(quote(A)), envir = env) # 100

do.call( f, list(quote(A)), envir = env) # 10

do.call("f", list(as.name("A")), envir = env) # 100


eval(call("f", A)) # 2  
eval(call("f", quote(A))) # 2

eval(call("f", A), envir = env) # 4

eval(call("f", quote(A)), envir = env) # 100

dontCheck

Identity Function to Suppress Checking

Description

The `dontCheck` function is the same as `identity`, but is interpreted by R CMD check code analysis as a directive to suppress checking of x. Currently this is only used by `checkFF(registration = TRUE)` when checking the `.NAME` argument of foreign function calls.

Usage

dontCheck(x)

Arguments

x  
an R object.

See Also

`suppressForeignCheck` which explains why that and `dontCheck` are undesirable and should be avoided if at all possible.
Description

... and .1, .2 etc are used to refer to arguments passed down from a calling function. These (and the following) can only be used inside a function which has ... among its formal arguments.

...elt(n) is a functional way to get .<n> and basically the same as eval(paste0("..", n)), just more elegant and efficient. Note that switch(n, ...) is very close, differing by returning NULL invisibly instead of an error when n is zero or too large.

...length() returns the number of expressions in ..., and ...names() the names. These are the same as length(list(...)) or names(list(...)) but without evaluating the expressions in ... (which happens with list(...)).

Evaluating elements of ... with .1, .2, ...elt(n), etc. propagates visibility. This is consistent with the evaluation of named arguments which also propagates visibility.

Usage

...length()
...names()
...elt(n)

Arguments

n a positive integer, not larger than the number of expressions in ..., which is the same as ...length() which is the same as length(list(...)), but the latter evaluates all expressions in ....

See Also

... and ..1, ..2 are reserved words in R, see Reserved.

For more, see the 'Introduction to R' manual for usage of these syntactic elements, and dotsMethods for their use in formal (S4) methods.

Examples

tst <- function(n, ...) ...elt(n)
tst(1, pi=pi*0:1, 2:4) ## [1] 0.000000 3.141593
tst(2, pi=pi*0:1, 2:4) ## [1] 2 3 4
try(tst(1)) # -> Error about '...' not containing an element.

ellt <- function(x, ...) ...length()
tst.dls <- function(x, ...) ...names()
tst.dls(1:10) # 0 (because the first argument is 'x')
tst.dls(4, 5) # 1
tst.dls(4, 5, 6) # 2 namely '5, 6'
tst.dls(4, 5, 6, 7, sin(1:10), "foo"/"bar") # 5. Note: no evaluation!
tst.dns(4, foo=5, 6, bar=7, sini = sin(1:10), "foo"/"bar")
## "foo" "bar" "sini"
## From R 4.1.0 to 4.1.2, ...names() sometimes did not match names(list(...));
## check and show (these examples all would've failed):
chk.n2 <- function(...) stopifnot(identical(print(...names()), names(list(...))))
chk.n2(4, foo=5, 6, bar=7, sini = sin(1:10), "bar")
chk.n2()
chk.n2(1,2)

double

### Double-Precision Vectors

**Description**
Create, coerce to or test for a double-precision vector.

**Usage**
double(length = 0)
as.double(x, ...)
is.double(x)
single(length = 0)
as.single(x, ...)

**Arguments**

- **length**
  A non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.

- **x**
  object to be coerced or tested.

- **...**
  further arguments passed to or from other methods.

**Details**
double creates a double-precision vector of the specified length. The elements of the vector are all equal to 0. It is identical to numeric.
as.double is a generic function. It is identical to as.numeric. Methods should return an object of base type "double".
is.double is a test of double type.

R has no single precision data type. All real numbers are stored in double precision format. The functions as.single and single are identical to as.double and double except they set the attribute Csingle that is used in the .C and .Fortran interface, and they are intended only to be used in that context.

**Value**
double creates a double-precision vector of the specified length. The elements of the vector are all equal to 0.
as.double attempts to coerce its argument to be of double type: like as.vector it strips attributes including names. (To ensure that an object is of double type without stripping attributes, use storage.mode.) Character strings containing optional whitespace followed by either a decimal representation or a hexadecimal representation (starting with 0x or 0X) can be converted, as can special values such as "NA", "NaN", "Inf" and "infinity", irrespective of case.
as.double for factors yields the codes underlying the factor levels, not the numeric representation of the labels, see also factor.

is.double returns TRUE or FALSE depending on whether its argument is of double type or not.

Double-precision values

All R platforms are required to work with values conforming to the IEC 60559 (also known as IEEE 754) standard. This basically works with a precision of 53 bits, and represents to that precision a range of absolute values from about $2 \times 10^{-308}$ to $2 \times 10^{308}$. It also has special values NaN (many of them), plus and minus infinity and plus and minus zero (although R acts as if these are the same). There are also denormalized (or subnormal) numbers with values below the range given above but represented to less precision.

See .Machine for precise information on these limits. Note that ultimately how double precision numbers are handled is down to the CPU/FPU and compiler.

In IEEE 754-2008/IEC60559:2011 this is called ‘binary64’ format.

Note on names

It is a historical anomaly that R has two names for its floating-point vectors, double and numeric (and formerly had real).

double is the name of the type. numeric is the name of the mode and also of the implicit class. As an S4 formal class, use "numeric".

The potential confusion is that R has used mode "numeric" to mean ‘double or integer’, which conflicts with the S4 usage. Thus is.numeric tests the mode, not the class, but as.numeric (which is identical to as.double) coerces to the class.

References


See Also

integer, numeric, storage.mode.

Examples

is.double(1)
all(double(3) == 0)
dput Write an Object to a File or Recreate it

Description

Writes an ASCII text representation of an R object to a file, the R console, or a connection, or uses one to recreate the object.

Usage

dput(x, file = "", control = c("keepNA", "keepInteger", "niceNames", "showAttributes"))
dget(file, keep.source = FALSE)

Arguments

x an object.
file either a character string naming a file or a connection. "" indicates output to the console.
control character vector (or NULL) of deparsing options. control = "all" is thorough, see .deparseOpts.
keep.source logical: should the source formatting be retained when parsing functions, if possible?

Details

dput opens file and deparses the object x into that file. The object name is not written (unlike dump). If x is a function the associated environment is stripped. Hence scoping information can be lost.

Deparsing an object is difficult, and not always possible. With the default control, dput() attempts to deparse in a way that is readable, but for more complex or unusual objects (see dump), not likely to be parsed as identical to the original. Use control = "all" for the most complete deparsing; use control = NULL for the simplest deparsing, not even including attributes.

dput will warn if fewer characters were written to a file than expected, which may indicate a full or corrupt file system.

To display saved source rather than deparsing the internal representation include "useSource" in control. R currently saves source only for function definitions. If you do not care about source representation (e.g., for a data object), for speed set options(keep.source = FALSE) when calling source.

Value

For dput, the first argument invisibly.

For dget, the object created.
Note

This is **not** a good way to transfer objects between R sessions. `dump` is better, but the functions `save` and `saveRDS` are designed to be used for transporting R data, and will work with R objects that `dput` does not handle correctly as well as being much faster.

To avoid the risk of a source attribute out of sync with the actual function definition, the source attribute of a function will never be written as an attribute.

References


See Also

deparse, .deparseOpts, dump, write.

Examples

```r
fil <- tempfile()
## Write an ASCII version of the 'base' function mean() to our temp file, ..
dput(base::mean, fil)
## ... read it back into 'bar' and confirm it is the same
bar <- dget(fil)
stopifnot(all.equal(bar, base::mean, check.environment = FALSE))

## Create a function with comments
baz <- function(x) {
  # Subtract from one
  1-x
}
## and display it
dput(baz)
## and now display the saved source
dput(baz, control = "useSource")

## Numeric values:
xx <- pi^(1:3)
dput(xx)
dput(xx, control = "digits17")
dput(xx, fil); dget(fil) - xx # slight rounding on all platforms
dput(xx, fil, control = "digits17")
dget(fil) - xx # slight rounding on some platforms
dput(xx, fil, control = "hexNumeric"); dget(fil) - xx
unlink(fil)

xn <- setNames(xx, paste0("pi^",1:3))
dput(xn) # nicer, now "niceNames" being part of default 'control'
dput(xn, control = "S_compat") # no names
## explicitly asking for output as in R < 3.5.0:
dput(xn, control = c("keepNA", "keepInteger", "showAttributes"))
```
### drop

**Drop Redundant Extent Information**

**Description**
Delete the dimensions of an array which have only one level.

**Usage**

drop(x)

**Arguments**

- **x**: an array (including a matrix).

**Value**
If `x` is an object with a `dim` attribute (e.g., a matrix or `array`), then `drop` returns an object like `x`, but with any extents of length one removed. Any accompanying `dimnames` attribute is adjusted and returned with `x`: if the result is a vector the names are taken from the `dimnames` (if any). If the result is a length-one vector, the names are taken from the first dimension with a `dimname`.

Array subsetting ([]) performs this reduction unless used with `drop = FALSE`, but sometimes it is useful to invoke `drop` directly.

**See Also**

- `drop1` which is used for dropping terms in models, and `droplevels` used for dropping unused levels from a `factor`.

**Examples**

```r
dim(drop(array(1:12, dim = c(1,3,1,1,2,1,2)))) # = 3 2 2
drop(1:3 %*% 2:4) # scalar product
```

### droplevels

**Drop Unused Levels from Factors**

**Description**
The function `droplevels` is used to drop unused levels from a `factor` or, more commonly, from factors in a data frame.

**Usage**

```r
droplevels(x, ...)  # S3 method for class 'factor'
droplevels(x, exclude = if(anyNA(levels(x))) NULL else NA, ...)  # S3 method for class 'data.frame'
droplevels(x, except, exclude, ...)
```
Arguments

- **x**: an object from which to drop unused factor levels.
- **exclude**: passed to `factor()`: factor levels which should be excluded from the result even if present. Note that this was implicitly NA in R <= 3.3.1 which did drop NA levels even when present in x, contrary to the documentation. The current default is compatible with x[, drop=TRUE].
- **...**: further arguments passed to methods
- **except**: indices of columns from which not to drop levels

Details

The method for class "factor" is currently equivalent to `factor(x, exclude=exclude)`. For the data frame method, you should rarely specify exclude “globally” for all factor columns; rather the default uses the same factor-specific exclude as the factor method itself.

The except argument follows the usual indexing rules.

Value

droplevels returns an object of the same class as x

Note

This function was introduced in R 2.12.0. It is primarily intended for cases where one or more factors in a data frame contains only elements from a reduced level set after subsetting. (Notice that subsetting does not in general drop unused levels). By default, levels are dropped from all factors in a data frame, but the except argument allows you to specify columns for which this is not wanted.

See Also

- `subset` for subsetting data frames.
- `factor` for definition of factors.
- `drop` for dropping array dimensions.
- `drop1` for dropping terms from a model.
- `[.factor` for subsetting of factors.

Examples

```r
aq <- transform(airquality, Month = factor(Month, labels = month.abb[5:9]))
aq <- subset(aq, Month != "Jul")
table(aq$Month)
table(droplevels(aq)$Month)
```

Description

This function takes a vector of names of R objects and produces text representations of the objects on a file or connection. A dump file can usually be sourced into another R session.

Usage

dump(list, file = "dumpdata.R", append = FALSE,
      control = "all", envir = parent.frame(), evaluate = TRUE)
Arguments

- **list**: character vector (or **NULL**). The names of R objects to be dumped.
- **file**: either a character string naming a file or a connection. "" indicates output to the console.
- **append**: if TRUE and file is a character string, output will be appended to file; otherwise, it will overwrite the contents of file.
- **control**: character vector (or NULL) indicating deparsing options. See **.deparseOpts** for their description.
- **envir**: the environment to search for objects.
- **evaluate**: logical. Should promises be evaluated?

Details

If some of the objects named do not exist (in scope), they are omitted, with a warning. If file is a file and no objects exist then no file is created. 

**source**ing may not produce an identical copy of dumped objects. A warning is issued if it is likely that problems will arise, for example when dumping exotic or complex objects (see the Note).

**dump** will also warn if fewer characters were written to a file than expected, which may indicate a full or corrupt file system.

A dump file can be **sourced** into another R (or perhaps S) session, but the functions **save** and **saveRDS** are designed to be used for transporting R data, and will work with R objects that **dump** does not handle. For maximal reproducibility use **control = "exact"**.

To produce a more readable representation of an object, use **control = NULL**. This will skip attributes, and will make other simplifications that make **source** less likely to produce an identical copy. See **.deparseOpts** for details.

To deparse the internal representation of a function rather than displaying the saved source, use **control = c("keepInteger", "warnIncomplete", "keepNA")**. This will lose all formatting and comments, but may be useful in those cases where the saved source is no longer correct.

Promises will normally only be encountered by users as a result of lazy-loading (when the default **evaluate = TRUE** is essential) and after the use of **delayedAssign**, when **evaluate = FALSE** might be intended.

Value

An invisible character vector containing the names of the objects which were dumped.

Note

As **dump** is defined in the base namespace, the **base** package will be searched before the global environment unless **dump** is called from the top level prompt or the **envir** argument is given explicitly.

To avoid the risk of a source attribute becoming out of sync with the actual function definition, the source attribute of a function will never be dumped as an attribute.

Currently environments, external pointers, weak references and objects of type S4 are not deparsed in a way that can be **source**d. In addition, **language objects** are deparsed in a simple way whatever the value of **control**, and this includes not dumping their attributes (which will result in a warning).

References

duplicated

See Also

.deparseOpts for available control settings; dput(), dget() and deparse() for related functions using identical internal deparsing functionality.

write, write.table, etc for “dumping” data to (text) files.

save and saveRDS for a more reliable way to save R objects.

Examples

```r
x <- 1; y <- 1:10
fil <- tempfile(fileext=".Rdmped")
dump(ls(pattern = '^\[xyz\]', fil)
print(.Last.value)
unlink(fil)
```

---

**duplicated**  
**Determine Duplicate Elements**

**Description**

duplicated() determines which elements of a vector or data frame are duplicates of elements with smaller subscripts, and returns a logical vector indicating which elements (rows) are duplicates.

anyDuplicated(.) is a “generalized” more efficient version any(duplicated(.)), returning positive integer indices instead of just TRUE.

**Usage**

duplicated(x, incomparables = FALSE, ...)

```r
## Default S3 method:
duplicated(x, incomparables = FALSE,
  fromLast = FALSE, nmax = NA, ...)
```

```r
## S3 method for class 'array'
duplicated(x, incomparables = FALSE, MARGIN = 1,
  fromLast = FALSE, ...)
```

```r
anyDuplicated(x, incomparables = FALSE, ...)

## Default S3 method:
anyDuplicated(x, incomparables = FALSE,
  fromLast = FALSE, ...)

## S3 method for class 'array'
anyDuplicated(x, incomparables = FALSE,
  MARGIN = 1, fromLast = FALSE, ...)
```

**Arguments**

- **x** a vector or a data frame or an array or NULL.
- **incomparables** a vector of values that cannot be compared. FALSE is a special value, meaning that all values can be compared, and may be the only value accepted for methods other than the default. It will be coerced internally to the same type as x.
duplicated

fromLast logical indicating if duplication should be considered from the reverse side, i.e.,
the last (or rightmost) of identical elements would correspond to duplicated =
FALSE.
nmax the maximum number of unique items expected (greater than one).
... arguments for particular methods.
MARGIN the array margin to be held fixed: see apply, and note that MARGIN = 0 may be
useful.

Details

These are generic functions with methods for vectors (including lists), data frames and arrays (in-
cluding matrices).

For the default methods, and whenever there are equivalent method definitions for duplicated
and anyDuplicated, anyDuplicated(x, ...) is a “generalized” shortcut for any(duplicated(x,
...)), in the sense that it returns the index i of the first duplicated entry x[i] if there is one, and 0
otherwise. Their behaviours may be different when at least one of duplicated and anyDuplicated
has a relevant method.

duplicated(x, fromLast = TRUE) is equivalent to but faster than rev(duplicated(rev(x))).
The array method calculates for each element of the sub-array specified by MARGIN if the remaining
dimensions are identical to those for an earlier (or later, when fromLast = TRUE) element (in row-
major order). This would most commonly be used to find duplicated rows (the default) or columns
(with MARGIN = 2). Note that MARGIN = 0 returns an array of the same dimensionality attributes as x.

Missing values ("NA") are regarded as equal, numeric and complex ones differing from NaN; char-
acter strings will be compared in a “common encoding”; for details, see match (and unique) which
use the same concept.

Values in incomparables will never be marked as duplicated. This is intended to be used for a
fairly small set of values and will not be efficient for a very large set.

Except for factors, logical and raw vectors the default nmax = NA is equivalent to nmax = length(x).
Since a hash table of size 8*nmax bytes is allocated, setting nmax suitably can save large amounts
of memory. For factors it is automatically set to the smaller of length(x) and the number of levels
plus one (for NA). If nmax is set too small there is liable to be an error: nmax = 1 is silently ignored.

Long vectors are supported for the default method of duplicated, but may only be usable if nmax
is supplied.

Value

duplicated(): For a vector input, a logical vector of the same length as x. For a data frame, a
logical vector with one element for each row. For a matrix or array, and when MARGIN = 0, a logical
array with the same dimensions and dimnames.

anyDuplicated(): an integer or real vector of length one with value the 1-based index of the first
duplicate if any, otherwise 0.

Warning

Using this for lists is potentially slow, especially if the elements are not atomic vectors (see vector)
or differ only in their attributes. In the worst case it is $O(n^2)$.

References

Brooks/Cole.
See Also

unique.

Examples

```r
x <- c(9:20, 1:5, 3:7, 0:8)
## extract unique elements
(xu <- x[!duplicated(x)])
## similar, same elements but different order:
(xu2 <- x[!duplicated(x, fromLast = TRUE)])

## xu == unique(x) but unique(x) is more efficient
stopifnot(identical(xu, unique(x)),
          identical(xu2, unique(x, fromLast = TRUE)))
```

duplicated(iris)[140:143]
duplicated(iris3, MARGIN = c(1, 3))
anyDuplicated(iris) ## 143

Arguments

- `x`: a character string giving the pathname to a DLL, also known as a dynamic shared object. (See 'Details' for what these terms mean.)
- `local`: a logical value controlling whether the symbols in the DLL are stored in their own local table and not shared across DLLs, or added to the global symbol table. Whether this has any effect is system-dependent.
- `now`: a logical controlling whether all symbols are resolved (and relocated) immediately the library is loaded or deferred until they are used. This control is useful for developers testing whether a library is complete and has all the necessary symbols, and for users to ignore missing symbols. Whether this has any effect is system-dependent.
- `...`: other arguments for future expansion.
symbol  a character string giving a symbol name.

PACKAGE  if supplied, confine the search for the name to the DLL given by this argument (plus the conventional extension, ".so", ".s1", ".dll", ...). This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols. This is used in the same way as in 

type  The type of symbol to look for: can be any ("", the default), "Fortran", "Call" or "External".

Details

The objects `dyn.load` loads are called ‘dynamically loadable libraries’ (abbreviated to ‘DLL’) on all platforms except macOS, which uses the term for a different sort of object. On Unix-alikes they are also called ‘dynamic shared objects’ (‘DSO’), or ‘shared objects’ for short. (The POSIX standards use ‘executable object file’, but no one else does.)

See ‘See Also’ and the ‘Writing R Extensions’ and ‘R Installation and Administration’ manuals for how to create and install a suitable DLL.

Unfortunately a very few platforms (e.g., Compaq Tru64) do not handle the PACKAGE argument correctly, and may incorrectly find symbols linked into R.

The additional arguments to `dyn.load` mirror the different aspects of the mode argument to the `dlopen()` routine on POSIX systems. They are available so that users can exercise greater control over the loading process for an individual library. In general, the default values are appropriate and you should override them only if there is good reason and you understand the implications.

The local argument allows one to control whether the symbols in the DLL being attached are visible to other DLLs. While maintaining the symbols in their own namespace is good practice, the ability to share symbols across related ‘chapters’ is useful in many cases. Additionally, on certain platforms and versions of an operating system, certain libraries must have their symbols loaded globally to successfully resolve all symbols.

One should be careful of the potential side-effect of using lazy loading via the now argument as FALSE. If a routine is called that has a missing symbol, the process will terminate immediately. The intended use is for library developers to call with value TRUE to check that all symbols are actually resolved and for regular users to call with FALSE so that missing symbols can be ignored and the available ones can be called.

The initial motivation for adding these was to avoid such termination in the _init() routines of the Java virtual machine library. However, symbols loaded locally may not be (read probably) available to other DLLs. Those added to the global table are available to all other elements of the application and so can be shared across two different DLLs.

Some (very old) systems do not provide (explicit) support for local/global and lazy/eager symbol resolution. This can be the source of subtle bugs. One can arrange to have warning messages emitted when unsupported options are used. This is done by setting either of the options verbose or warn to be non-zero via the options function.

There is a short discussion of these additional arguments with some example code available at https://www.stat.ucdavis.edu/~duncan/R/dynload/.

Value

The function `dyn.load` is used for its side effect which links the specified DLL to the executing R image. Calls to .C, .Call, .Fortran and .External can then be used to execute compiled C functions or Fortran subroutines contained in the library. The return value of `dyn.load` is an object of class `DLLInfo`. See `getLoadedDLLs` for information about this class.
The function `dyn.unload` unlinks the DLL. Note that unloading a DLL and then re-loading a DLL of the same name may or may not work: on Solaris it used the first version loaded. Note also that some DLLs cannot be safely unloaded at all: unloading a DLL which implements C finalizers but does not unregister them on unload causes R to crash.

`is.loaded` checks if the symbol name is loaded and searchable and hence available for use as a character string value for argument `.NAME` in `.C` or `.Fortran` or `.Call` or `.External`. It will succeed if any one of the four calling functions would succeed in using the entry point unless type is specified. (See `.Fortran` for how Fortran symbols are mapped.) Note that symbols in base packages are not searchable, and other packages can be so marked.

**Warning**

Do not use `dyn.unload` on a DLL loaded by `library.dynam`: use `library.dynam.unload`. This is needed for system housekeeping.

**Note**

`is.loaded` requires the name you would give to `.C` etc. It must be a character string and so cannot be an R object as used for registered native symbols (see “Writing R Extensions” section 5.4.). Some registered symbols are available by name but most are not, including those in the examples below.

By default, the maximum number of DLLs that can be loaded is now 614 when the OS limit on the number of open files allows or can be increased, but less otherwise (but it will be at least 100). A specific maximum can be requested via the environment variable `R_MAX_NUM_DLLS`, which has to be set (to a value between 100 and 1000 inclusive) before starting an R session. If the OS limit on the number of open files does not allow using this maximum and cannot be increased, R will fail to start with an error. The maximum is not allowed to be greater than 60% of the OS limit on the number of open files (essentially unlimited on Windows, on Unix typically 1024, but 256 on macOS). The limit can sometimes (including on macOS) be modified using command `ulimit -n` (sh, bash) or `limit descriptors` (csh) in the shell used to launch R. Increasing `R_MAX_NUM_DLLS` comes with some memory overhead.

If the OS limit on the number of open files cannot be determined, the DLL limit is 100 and cannot be changed via `R_MAX_NUM_DLLS`.

The creation of DLLs and the runtime linking of them into executing programs is very platform dependent. In recent years there has been some simplification in the process because the C subroutine call `dlopen` has become the POSIX standard for doing this. Under Unix-alikes `dyn.load` uses the `dlopen` mechanism and should work on all platforms which support it. On Windows it uses the standard mechanism (LoadLibrary) for loading DLLs.

The original code for loading DLLs in Unix-alikes was provided by Heiner Schwarte.

**References**


**See Also**

`library.dynam` to be used inside a package’s `.onLoad` initialization.

`SHLIB` for how to create suitable DLLs.

eapply

Apply a Function Over Values in an Environment

eapply applies FUN to the named values from an environment and returns the results as a list. The user can request that all named objects are used (normally names that begin with a dot are not). The output is not sorted and no enclosing environments are searched.

Usage

eapply(env, FUN, ..., all.names = FALSE, USE.NAMES = TRUE)

Arguments

eval          environment to be used.
FUN           the function to be applied, found via match.fun. In the case of functions like +, %%, etc., the function name must be backquoted or quoted.
...           optional arguments to FUN.
all.names     a logical indicating whether to apply the function to all values.
USE.NAMES     logical indicating whether the resulting list should have names.

Value

A named (unless USE.NAMES = FALSE) list. Note that the order of the components is arbitrary for hashed environments.

See Also

evironment, lapply.

Examples

require(stats)

env <- new.env(hash = FALSE) # so the order is fixed
env$a <- 1:10
env$beta <- exp(-3:3)
env$logic <- c(TRUE, FALSE, FALSE, TRUE)
# what have we there?
utils::ls.str(env)

# compute the mean for each list element
eapply(env, mean)
eigen

Spectral Decomposition of a Matrix

Description
Computes eigenvalues and eigenvectors of numeric (double, integer, logical) or complex matrices.

Usage
eigen(x, symmetric, only.values = FALSE, EISPACK = FALSE)

Arguments
x
a numeric or complex matrix whose spectral decomposition is to be computed. Logical matrices are coerced to numeric.
symmetric
if TRUE, the matrix is assumed to be symmetric (or Hermitian if complex) and only its lower triangle (diagonal included) is used. If symmetric is not specified, isSymmetric(x) is used.
only.values
if TRUE, only the eigenvalues are computed and returned, otherwise both eigenvalues and eigenvectors are returned.
EISPACK
logical. Defunct and ignored.

Details
If symmetric is unspecified, isSymmetric(x) determines if the matrix is symmetric up to plausible numerical inaccuracies. It is surer and typically much faster to set the value yourself.
Computing the eigenvectors is the slow part for large matrices.
Computing the eigendecomposition of a matrix is subject to errors on a real-world computer: the definitive analysis is Wilkinson (1965). All you can hope for is a solution to a problem suitably close to x. So even though a real asymmetric x may have an algebraic solution with repeated real eigenvalues, the computed solution may be of a similar matrix with complex conjugate pairs of eigenvalues.
Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code (most often 1): these can only be interpreted by detailed study of the FORTRAN code. Missing, NaN or infinite values in x will given an error.

Value
The spectral decomposition of x is returned as a list with components
values
a vector containing the p eigenvalues of x, sorted in decreasing order, according to Mod(values) in the asymmetric case when they might be complex (even for real matrices). For real asymmetric matrices the vector will be complex only if complex conjugate pairs of eigenvalues are detected.
eigen
eigen vectors

either a $p \times p$ matrix whose columns contain the eigenvectors of $x$, or NULL if only.values is TRUE. The vectors are normalized to unit length.

Recall that the eigenvectors are only defined up to a constant: even when the length is specified they are still only defined up to a scalar of modulus one (the sign for real matrices).

When only.values is not true, as by default, the result is of S3 class "eigen".

If $r \leftarrow \text{eigen}(A)$, and $V \leftarrow r$\text{$vectors$}; $\lambda$ $\leftarrow r$\text{$values$}, then

$$A = V \Lambda V^{-1}$$

(up to numerical fuzz), where $\Lambda = \text{diag}(\lambda)$.

Source

eigen uses the LAPACK routines DSYEVR, DGEEV, ZHEEV and ZGEEV.

LAPACK is from https://netlib.org/lapack/ and its guide is listed in the references.

References


See Also

svd, a generalization of eigen; qr, and chol for related decompositions.

To compute the determinant of a matrix, the qr decomposition is much more efficient: det.

Examples

eigen(cbind(c(1,-1), c(-1,1)))
eigen(cbind(c(1,-1), c(-1,1)), symmetric = FALSE)
# same (different algorithm).

eigen(cbind(1, c(1,-1)), only.values = TRUE)
eigen(cbind(-1, 2:1)) # complex values
eigen(print(cbind(c(0, i1), c(-i1, 0)))) # Hermite ==> real Eigenvalues
## 3 x 3:
eigen(cbind(1, 3:1, 1:3))
eigen(cbind(-1, c(1:2,0), 0:2)) # complex values
encodeString

**Encode Character Vector as for Printing**

**Description**

encodeString escapes the strings in a character vector in the same way print.default does, and optionally fits the encoded strings within a field width.

**Usage**

```
encodeString(x, width = 0, quote = "", na.encode = TRUE, justify = c("left", "right", "centre", "none"))
```

**Arguments**

- `x` A character vector, or an object that can be coerced to one by `as.character`.
- `width` integer: the minimum field width. If `NULL` or `NA`, this is taken to be the largest field width needed for any element of `x`.
- `quote` character: quoting character, if any.
- `na.encode` logical: should `NA` strings be encoded?
- `justify` character: partial matches are allowed. If padding to the minimum field width is needed, how should spaces be inserted? `justify == "none"` is equivalent to `width = 0`, for consistency with `format.default`.

**Details**

This escapes backslash and the control characters `'\a'` (bell), `'\b'` (backspace), `'\f'` (formfeed), `'\n'` (line feed, aka “newline”), `'\r'` (carriage return), `'\t'` (tab) and `'\v'` (vertical tab) as well as any non-printable characters in a single-byte locale, which are printed in octal notation (`\xyz` with leading zeroes).

Which characters are non-printable depends on the current locale. Windows’ reporting of printable characters is unreliable, so there all other control characters are regarded as non-printable, and all characters with codes 32–255 as printable in a single-byte locale. See `print.default` for how non-printable characters are handled in multi-byte locales.

If `quote` is a single or double quote any embedded quote of the same type is escaped. Note that justification is of the quoted string, hence spaces are added outside the quotes.

**Value**

A character vector of the same length as `x`, with the same attributes (including names and dimensions) but with no class set.

Marked UTF-8 encodings are preserved.

**Note**

The default for `width` is different from `format.default`, which does similar things for character vectors but without encoding using escapes.
Encoding

Read or Set the Declared Encodings for a Character Vector

Description

Read or set the declared encodings for a character vector.

Usage

Encoding(x)

Encoding(x) <- value

enc2native(x)

enc2utf8(x)

Arguments

x
A character vector.

value
A character vector of positive length.

Details

Character strings in R can be declared to be encoded in "latin1" or "UTF-8" or as "bytes". These declarations can be read by Encoding, which will return a character vector of values "latin1", "UTF-8" "bytes" or "unknown", or set, when value is recycled as needed and other values are silently treated as "unknown". ASCII strings will never be marked with a declared encoding, since their representation is the same in all supported encodings. Strings marked as "bytes" are intended to be non-ASCII strings which should be manipulated as bytes, and never converted to a character encoding (so writing them to a text file is supported only by writeLines(useBytes = TRUE)).
enc2native and enc2utf8 convert elements of character vectors to the native encoding or UTF-8 respectively, taking any marked encoding into account. They are primitive functions, designed to do minimal copying.

There are other ways for character strings to acquire a declared encoding apart from explicitly setting it (and these have changed as R has evolved). The parser marks strings containing ‘\u’ or ‘\U’ escapes. Functions scan, read.table, readlines, and parse have an encoding argument that is used to declare encodings. iconv declares encodings from its to argument, and console input in suitable locales is also declared. intToUtf8 declares its output as “UTF-8”, and output text connections (see textConnection) are marked if running in a suitable locale. Under some circumstances (see its help page) source(encoding=) will mark encodings of character strings it outputs.

Most character manipulation functions will set the encoding on output strings if it was declared on the corresponding input. These include chartr, strsplit(useBytes = FALSE), tolower and toupper as well as sub(useBytes = FALSE) and gsub(useBytes = FALSE). Note that such functions do not preserve the encoding, but if they know the input encoding and that the string has been successfully re-encoded (to the current encoding or UTF-8), they mark the output.

substr does preserve the encoding, and chartr, tolower and toupper preserve UTF-8 encoding on systems with Unicode wide characters. With their fixed and perl options, strsplit, sub and gsub will give a marked UTF-8 result if any of the inputs are UTF-8.

paste and sprintf return elements marked as bytes if any of the corresponding inputs is marked as bytes, and otherwise marked as UTF-8 if any of the inputs is marked as UTF-8.

match, pmatch, charmatch, duplicated and unique all match in UTF-8 if any of the elements are marked as UTF-8.

Changing the current encoding from a running R session may lead to confusion (see Sys.setlocale).

There is some ambiguity as to what is meant by a ‘Latin-1’ locale, since some OSes (notably Windows) make use of character positions undefined (or used for control characters) in the ISO 8859-1 character set. How such characters are interpreted is system-dependent but as from R 3.5.0 they are if possible interpreted as per Windows codepage 1252 (which Microsoft calls ‘Windows Latin 1 (ANSI)’) when converting to e.g. UTF-8.

Value
A character vector.

For enc2utf8 encodings are always marked: they are for enc2native in UTF-8 and Latin-1 locales.

Examples

```r
## x is intended to be in latin1
x. <- x <- "fa\xE7ile"
Encoding(x.) # unknown (UTF-8 loc.) | latin1 (8859-1/CP-1252 loc.) | ....
Encoding(x) <- "latin1"
x
xx <- iconv(x, "latin1", "UTF-8")
Encoding(c(x., x, xx))
c(x, xx)
xb <- xx; Encoding(xb) <- "bytes"
xb # will be encoded in hex
cat("x = ", x, ", xx = ", xx, ", xb = ", xb, ",\n", sep = "")
(Ex <- Encoding(c(x., x, xx, xb)))
stopifnot(identical(Ex, c(Encoding(x.), Encoding(x),
      Encoding(xx), Encoding(xb))))
```
environment

Environments consist of a frame, or collection of named objects, and a pointer to an enclosing environment. The most common example is the frame of variables local to a function call; its enclosure is the environment where the function was defined (unless changed subsequently). The enclosing environment is distinguished from the parent frame: the latter (returned by parent.frame) refers to the environment of the caller of a function. Since confusion is so easy, it is best never to use ‘parent’ in connection with an environment (despite the presence of the function parent.env).
When `get` or `exists` search an environment with the default `inherits = TRUE`, they look for the variable in the frame, then in the enclosing frame, and so on.

The global environment `.GlobalEnv`, more often known as the user’s workspace, is the first item on the search path. It can also be accessed by `globalenv()`. On the search path, each item’s enclosure is the next item.

The object `.BaseNamespaceEnv` is the namespace environment for the base package. The environment of the base package itself is available as `baseenv()`.

If one follows the chain of enclosures found by repeatedly calling `parent.env` from any environment, eventually one reaches the empty environment `emptyenv()`, into which nothing may be assigned.

The replacement function `parent.env<-` is extremely dangerous as it can be used to destructively change environments in ways that violate assumptions made by the internal C code. It may be removed in the near future.

The replacement form of `environment`, `is.environment`, `baseenv`, `emptyenv` and `globalenv` are primitive functions.

System environments, such as the base, global and empty environments, have names as do the package and namespace environments and those generated by `attach()`. Other environments can be named by giving a "name" attribute, but this needs to be done with care as environments have unusual copying semantics.

### Value

If `fun` is a function or a formula then `environment(fun)` returns the environment associated with that function or formula. If `fun` is NULL then the current evaluation environment is returned.

The replacement form sets the environment of the function or formula `fun` to the value given.

- `is.environment(obj)` returns TRUE if and only if `obj` is an environment.
- `new.env` returns a new (empty) environment with (by default) enclosure the parent frame.
- `parent.env` returns the enclosing environment of its argument.
- `parent.env<-` sets the enclosing environment of its first argument.
- `environmentName` returns a character string, that given when the environment is printed or "" if it is not a named environment.
- `env.profile` returns a list with the following components: size the number of chains that can be stored in the hash table, nchains the number of non-empty chains in the table (as reported by `HASHPRI`), and counts an integer vector giving the length of each chain (zero for empty chains). This function is intended to assess the performance of hashed environments. When `env` is a non hashed environment, NULL is returned.

### See Also

For the performance implications of hashing or not, see https://en.wikipedia.org/wiki/Hash_table.

The `envir` argument of `eval`, `get`, and `exists`.

`ls` may be used to view the objects in an environment, and hence `ls.str` may be useful for an overview.

`sys.source` can be used to populate an environment.
Examples

\begin{verbatim}
f <- function() "top level function"

##-- all three give the same:
environment()
environment(f)
.GlobalEnv

ls(envir = environment(stats::approxfun(1:2, 1:2, method = "const")))
is.environment(.GlobalEnv) # TRUE

e1 <- new.env(parent = baseenv()) # this one has enclosure package:base.
e2 <- new.env(parent = e1)
assign("a", 3, envir = e1)
ls(e1)
ls(e2)
exists("a", envir = e2) # this succeeds by inheritance
exists("a", envir = e2, inherits = FALSE)
exists("+", envir = e2) # this succeeds by inheritance

eh <- new.env(hash = TRUE, size = NA)
with(env.profile(eh), stopifnot(size == length(counts)))
\end{verbatim}

<table>
<thead>
<tr>
<th>EnvVar</th>
<th>Environment Variables</th>
</tr>
</thead>
</table>

Description

Details of some of the environment variables which affect an \texttt{R} session.

Details

It is impossible to list all the environment variables which can affect an \texttt{R} session: some affect the OS system functions which \texttt{R} uses, and others will affect add-on packages. But here are notes on some of the more important ones. Those that set the defaults for options are consulted only at startup (as are some of the others).

\textbf{HOME}: The user's 'home' directory.

\textbf{LANGUAGE}: Optional. The language(s) to be used for message translations. This is consulted when needed.

\textbf{LC\_ALL}: (etc) Optional. Use to set various aspects of the locale – see \texttt{Sys.getlocale}. Consulted at startup.

\textbf{MAKEINDEX}: The path to \texttt{makeindex}. If unset to a value determined when \texttt{R} was built. Used by the emulation mode of \texttt{texi2dvi} and \texttt{texi2pdf}.

\textbf{R\_BATCH}: Optional – set in a batch session, that is one started by \texttt{R CMD BATCH}. Most often set to "," so test by something like \texttt{!is.na(Sys.getenv("R\_BATCH", NA))}.

\textbf{R\_BROWSER}: The path to the default browser. Used to set the default value of \texttt{options("browser")}.

\textbf{R\_COMPLETION}: Optional. If set to \texttt{FALSE}, command-line completion is not used. (Not used by the macOS GUI.)
R_DEFAULT_PACKAGES: A comma-separated list of packages which are to be attached in every session. See options.
R_DOC_DIR: The location of the R ‘doc’ directory. Set by R.
R_ENVIRON: Optional. The path to the site environment file: see Startup. Consulted at startup.
R_GSCMD: Optional. The path to Ghostscript, used by dev2bitmap, bitmap and embedFonts. Consulted when those functions are invoked. Since it will be treated as if passed to system, spaces and shell metacharacters should be escaped.
R_HISTFILE: Optional. The path of the history file: see Startup. Consulted at startup and when the history is saved.
R_HISTSIZE: Optional. The maximum size of the history file, in lines. Exactly how this is used depends on the interface.

On Unix-alikes, for the readline command-line interface it takes effect when the history is saved (by savehistory or at the end of a session).

On Windows, for Rgui it controls the number of lines saved to the history file: the size of the history used in the session is controlled by the console customization: see Rconsole.
R_HOME: The top-level directory of the R installation: see R.home. Set by R.
R_INCLUDE_DIR: The location of the R ‘include’ directory. Set by R.
R_LIBS: Optional. Used for initial setting of .libPaths.
R_LIBS_SITE: Optional. Used for initial setting of .libPaths.
R_LIBS_USER: Optional. Used for initial setting of .libPaths.
R_PAPERSIZE: Optional. Used to set the default for options("papersize"), e.g. used by pdf and postscript.
R_PCRE_JIT_STACK_MAXSIZE: Optional. Consulted when PCRE’s JIT pattern compiler is first used. See grep.
R_PDFVIEWER: The path to the default PDF viewer. Used by R CMD Rd2pdf.
R_PLATFORM: The platform – a string of the form cpu-vendor-os, see R.Version.
R_PROFILE: Optional. The path to the site profile file: see Startup. Consulted at startup.
R_RD4PDF: Options for pdflatex processing of Rd files. Used by R CMD Rd2pdf.
R_SHARE_DIR: The location of the R ‘share’ directory. Set by R.
R_TEXI2DVCMD: The path to texi2dvi. Defaults to the value of TEXI2DVI, and if that is unset to a value determined when R was built.

Only on Unix-alikes:
Consulted at startup to set the default for options("texi2dvi"), used by texi2dvi and texi2pdf in package tools.
R_TIDYCMD: The path to HTML tidy. Used by R CMD check if _R_CHECK_RD_VALIDATE_RD2HTML_ is set to a true value (as it is by '--as-cran').
R_UNZIPCMD: The path to unzip. Sets the initial value for options("unzip") on a Unix-alike when namespace utils is loaded.
R_ZIPCMD: The path to zip. Used by zip and by R CMD INSTALL --build on Windows.
TMPDIR, TMP, TEMP: Consulted (in that order) when setting the temporary directory for the session: see tempdir. TMPDIR is also used by some of the utilities: see the help for build.
TZ: Optional. The current time zone. See Sys.timezone for the system-specific formats. Consulted as needed.
TZDIR: Optional. The top-level directory of the time-zone database. See Sys.timezone.
no_proxy, http_proxy, ftp_proxy: (and more). Optional. Settings for download.file: see its help for further details.
Unix-specific

Some variables set on Unix-alikes, and not (in general) on Windows.

DISPLAY: Optional: used by X11. Tk (in package tcltk), the data editor and various packages.
EDITOR: The path to the default editor: sets the default for options("editor") when namespace utils is loaded.

PAGER: The path to the pager with the default setting of options("pager"). The default value is chosen at configuration, usually as the path to less.
R_PRINTCMD: Sets the default for options("printcmd"), which sets the default print command to be used by postscript.
R_SUPPORT_OLD_TARS logical. Sets the default for the support_old_tars argument of untar. Should be set to TRUE if an old system tar command is used which does not support either xz compression or automagically detecting compression type.

Windows-specific

Some Windows-specific variables are

GSC: Optional: the path to Ghostscript, used if R_GSCMD is not set.
R_USER: The user’s ‘home’ directory. Set by R. (HOME will be set to the same value if not already set.)

See Also

Sys.getenv and Sys.setenv to read and set environmental variables in an R session.

gctorture for environment variables controlling garbage collection.

---

**eval**  
*Evaluate an (Unevaluated) Expression*

**Description**

Evaluate an R expression in a specified environment.

**Usage**

```r
eval(expr, envir = parent.frame(),
     enclos = if(is.list(envir) || is.pairlist(envir))
              parent.frame() else baseenv())

evalq(expr, envir, enclos)
eval.parent(expr, n = 1)
local(expr, envir = new.env())
```

**Arguments**

- `expr` an object to be evaluated. See ‘Details’.
- `envir` the environment in which expr is to be evaluated. May also be NULL, a list, a data frame, a pairlist or an integer as specified to `sys.call`.
- `enclos` Relevant when envir is a (pair)list or a data frame. Specifies the enclosure, i.e., where R looks for objects not found in envir. This can be NULL (interpreted as the base package environment, baseenv()) or an environment.
- `n` number of parent generations to go back
Details

eval evaluates the expr argument in the environment specified by envir and returns the computed value. If envir is not specified, then the default is parent.frame() (the environment where the call to eval was made).

Objects to be evaluated can be of types call or expression or name (when the name is looked up in the current scope and its binding is evaluated), a promise or any of the basic types such as vectors, functions and environments (which are returned unchanged).

The evalq form is equivalent to eval(quote(expr), ...). eval evaluates its first argument in the current scope before passing it to the evaluator: evalq avoids this.

eval.parent(expr, n) is a shorthand for eval(expr, parent.frame(n)).

If envir is a list (such as a data frame) or pairlist, it is copied into a temporary environment (with enclosure enclos), and the temporary environment is used for evaluation. So if expr changes any of the components named in the (pair)list, the changes are lost.

If envir is NULL it is interpreted as an empty list so no values could be found in envir and look-up goes directly to enclos.

local evaluates an expression in a local environment. It is equivalent to evalq except that its default argument creates a new, empty environment. This is useful to create anonymous recursive functions and as a kind of limited namespace feature since variables defined in the environment are not visible from the outside.

Value

The result of evaluating the object: for an expression vector this is the result of evaluating the last element.

Note

Due to the difference in scoping rules, there are some differences between R and S in this area. In particular, the default enclosure in S is the global environment.

When evaluating expressions in a data frame that has been passed as an argument to a function, the relevant enclosure is often the caller’s environment, i.e., one needs eval(x, data, parent.frame()).

References


See Also

evaluation,quote,sys.frame,parent.frame,environment.

Further, force to force evaluation, typically of function arguments.

Examples

eval(2 ^ 2 ^ 3)
mEx <- expression(2^2^3); mEx; 1 + eval(mEx)
eval({ xx <- pi; xx^2}); xx

a <- 3 ; aa <- 4 ; evalq(evalq(a+b+aa, list(a = 1)), list(b = 5)) # == 10
a <- 3 ; aa <- 4 ; evalq(evalq(a+b+aa, -1), list(b = 5)) # == 12
eval <- function() {
  e1 <- parent.frame()
  ## Evaluate a in e1
  aa <- eval(expression(a), e1)
  ## evaluate the expression bound to a in e1
  a <- expression(x+y)
  list(aa = aa, eval = eval(a, e1))
}

tst.ev <- function(a = 7) { x <- pi; y <- 1; ev() }
tst.ev() #-> aa : 7, eval : 4.14

a <- list(a = 3, b = 4)
with(a, a <- 5) # alters the copy of a from the list, discarded.

##
## Example of evalq()
##
N <- 3
env <- new.env()
assign("N", 27, envir = env)
## this version changes the visible copy of N only, since the argument
## passed to eval is '4'.
eval(N <- 4, env)
N
get("N", envir = env)
## this version does the assignment in env, and changes N only there.
evalq(N <- 5, env)
N
get("N", envir = env)

##
## Uses of local()
##
# Mutually recursive.
# gg gets value of last assignment, an anonymous version of f.

gg <- local({
  k <- function(y)f(y)
  f <- function(x) if(x) x*k(x-1) else 1
})
gg(10)
sapply(1:5, gg)

# Nesting locals: a is private storage accessible to k
gg <- local({
  k <- local({
    a <- 1
    function(y)(print(a <<- a+1);f(y))
  })
  f <- function(x) x*k(x-1) else 1
})
sapply(1:5, gg)
exists

Look for an R object of the given name and possibly return it

Usage

```r
exists(x, where = -1, envir = , frame, mode = "any", inherits = TRUE)
get0(x, envir = pos.to.env(-1L), mode = "any", inherits = TRUE, ifnotfound = NULL)
```

Arguments

- `x` a variable name (given as a character string or a symbol).
- `where` where to look for the object (see the details section); if omitted, the function will search as if the name of the object appeared unquoted in an expression.
- `envir` an alternative way to specify an environment to look in, but it is usually simpler to just use the `where` argument.
- `frame` a frame in the calling list. Equivalent to giving `where` as `sys.frame(frame)`. 
- `mode` the mode or type of object sought: see the ‘Details’ section.
- `inherits` should the enclosing frames of the environment be searched?
- `ifnotfound` the return value of `get0(x, *)` when `x` does not exist.

Details

The `where` argument can specify the environment in which to look for the object in any of several ways: as an integer (the position in the `search` list); as the character string name of an element in the search list; or as an `environment` (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily there for back compatibility.

This function looks to see if the name `x` has a value bound to it in the specified environment. If `inherits` is `TRUE` and a value is not found for `x` in the specified environment, the enclosing frames of the environment are searched until the name `x` is encountered. See `environment` and the ‘R Language Definition’ manual for details about the structure of environments and their enclosures.

**Warning:** `inherits = TRUE` is the default behaviour for R but not for S.

If `mode` is specified then only objects of that type are sought. The `mode` may specify one of the collections "numeric" and "function" (see `mode`): any member of the collection will suffice. (This is true even if a member of a collection is specified, so for example `mode = "special"` will seek any type of function.)
exists(): Logical, true if and only if an object of the correct name and mode is found.

get0(): The object—as from get(x, *)—if exists(x, *) is true, otherwise ifnotfound.

Note

With get0(), instead of the easy to read but somewhat inefficient

```r
if (exists(myVarName, envir = myEnvir)) {
  r <- get(myVarName, envir = myEnvir)
  ## ... deal with r ...
}
```

you now can use the more efficient (and slightly harder to read)

```r
if (!is.null(r <- get0(myVarName, envir = myEnvir))) {
  ## ... deal with r ...
}
```

References


See Also

get and hasName. For quite a different kind of “existence” checking, namely if function arguments were specified, missing; and for yet a different kind, namely if a file exists, file.exists.

Examples

```r
## Define a substitute function if necessary:
if(!exists("some.fun", mode = "function"))
  some.fun <- function(x) { cat("some.fun(x)\n"); x }
search()
exists("ls", 2) # true even though ls is in pos = 3
exists("ls", 2, inherits = FALSE) # false

## These are true (in most circumstances):
identical(ls, get0("ls"))
identical(NULL, get0(".foo.bar.")) # default ifnotfound = NULL (!)
```
**expand.grid**

Create a Data Frame from All Combinations of Factor Variables

**Description**

Create a data frame from all combinations of the supplied vectors or factors. See the description of the return value for precise details of the way this is done.

**Usage**

```r
expand.grid(..., KEEP.OUT.ATTRS = TRUE, stringsAsFactors = TRUE)
```

**Arguments**

- `...` vectors, factors or a list containing these.
- `KEEP.OUT.ATTRS` a logical indicating the "out.attrs" attribute (see below) should be computed and returned.
- `stringsAsFactors` logical specifying if character vectors are converted to factors.

**Value**

A data frame containing one row for each combination of the supplied factors. The first factors vary fastest. The columns are labelled by the factors if these are supplied as named arguments or named components of a list. The row names are 'automatic'.

Attribute "out. attr" is a list which gives the dimension and dimnames for use by `predict` methods.

**Note**

Conversion to a factor is done with levels in the order they occur in the character vectors (and not alphabetically, as is most common when converting to factors).

**References**


**See Also**

- `combn` (package `utils`) for the generation of all combinations of n elements, taken m at a time.

**Examples**

```r
require(utils)

expand.grid(height = seq(60, 80, 5), weight = seq(100, 300, 50),
sex = c("Male","Female"))

x <- seq(0, 10, length.out = 100)
y <- seq(-1, 1, length.out = 20)
d1 <- expand.grid(x = x, y = y)
d2 <- expand.grid(x = x, y = y, KEEP.OUT.ATTRS = FALSE)
```
expression

object.size(d1) - object.size(d2)
##-> 5992 or 8832 (on 32- / 64-bit platform)

expression  Unevaluated Expressions

Description

Creates or tests for objects of mode and class "expression".

Usage

expression(...)

is.expression(x)

as.expression(x, ...)

Arguments

...  expression: R objects, typically calls, symbols or constants.
     as.expression: arguments to be passed to methods.
     x  an arbitrary R object.

Details

‘Expression’ here is not being used in its colloquial sense, that of mathematical expressions. Those are calls (see call) in R, and an R expression vector is a list of calls, symbols etc, for example as returned by parse.

As an object of mode "expression" is a list, it can be subsetted by [, [[ or $, the latter two extracting individual calls etc. The replacement forms of these operators can be used to replace or delete elements.

expression and is.expression are primitive functions. expression is ‘special’: it does not evaluate its arguments.

Value

expression returns a vector of type "expression" containing its arguments (unevaluated).

is.expression returns TRUE if expr is an expression object and FALSE otherwise.

as.expression attempts to coerce its argument into an expression object. It is generic, and only the default method is described here. (The default method calls as.vector(type = "expression") and so may dispatch methods for as.vector.) NULL, calls, symbols (see as.symbol) and pairlists are returned as the element of a length-one expression vector. Atomic vectors are placed element-by-element into an expression vector (without using any names): lists have their type (typeof) changed to an expression vector (keeping all attributes). Other types are not currently supported.

References

See Also
call, eval, function. Further, text, legend, and plotmath for plotting mathematical expressions.

Examples

length(ex1 <- expression(1 + 0:9)) # 1
ex1
  # 1:10
eval(ex1) # 1:10

length(ex3 <- expression(u, 2, u + 0:9)) # 3
mode(ex3[3]) # expression
mode(ex3[[3]]) # call
## but not all components are 'call's:
sapply(ex3, mode) # name numeric call
double language
sapply(ex3, typeof) # symbol double language
rm(ex3)

Extract or Replace Parts of an Object

Extract

Extract or Replace Parts of an Object

Description

Operators acting on vectors, matrices, arrays and lists to extract or replace parts.

Usage

x[i]
x[i, j, ...], drop = TRUE]
x[[i, exact = TRUE]]
x[[i, j, ...], exact = TRUE]]
x$name
ggetElement(object, name)

Arguments

x, object
  object from which to extract element(s) or in which to replace element(s).

i, j, ...
  indices specifying elements to extract or replace. Indices are numeric or character vectors or empty (missing) or NULL. Numeric values are coerced to integer or whole numbers as by as.integer or for large values by trunc (and hence truncated towards zero). Character vectors will be matched to the names of the object (or for matrices/arrays, the dimnames): see ‘Character indices’ below for further details.
  For [-indexing only: i, j... can be logical vectors, indicating elements/slices to select. Such vectors are recycled if necessary to match the corresponding extent. i, j... can also be negative integers, indicating elements/slices to leave out of the selection.
When indexing arrays by \([ \) a single argument \(i\) can be a matrix with as many columns as there are dimensions of \(x\); the result is then a vector with elements corresponding to the sets of indices in each row of \(i\).

An index value of \(\text{NULL}\) is treated as if it were \(\text{integer}(0)\).

**name**
A literal character string or a name (possibly backtick quoted). For extraction, this is normally (see under ‘Environments’) partially matched to the names of the object.

**drop**
For matrices and arrays. If \(\text{TRUE}\) the result is coerced to the lowest possible dimension (see the examples). This only works for extracting elements, not for the replacement. See drop for further details.

**exact**
Controls possible partial matching of \([ [\) when extracting by a character vector (for most objects, but see under ‘Environments’). The default is no partial matching. Value \(\text{NA}\) allows partial matching but issues a warning when it occurs. Value \(\text{FALSE}\) allows partial matching without any warning.

**value**
Typically an array-like \(\text{R}\) object of a similar class as \(x\).

**Details**

These operators are generic. You can write methods to handle indexing of specific classes of objects, see \(\text{InternalMethods}\) as well as \(\text{.data.frame}\) and \(\text{.factor}\). The descriptions here apply only to the default methods. Note that separate methods are required for the replacement functions \(\text{<-}\), \([ [\) and \(\$\) for use when indexing occurs on the assignment side of an expression.

The most important distinction between \([\), \([ [\) and \(\$\) is that the \([\) can select more than one element whereas the other two select a single element.

Note that \(x[[[]]]\) is always erroneous.

The default methods work somewhat differently for atomic vectors, matrices/arrays and for recursive (list-like, see \text{is.recursive}) objects. \(\$\) is only valid for recursive objects (and \(\text{NULL}\)), and is only discussed in the section below on recursive objects.

Subsetting (except by an empty index) will drop all attributes except names, \text{dim} and \text{dimnames}.

Indexing can occur on the right-hand-side of an expression for extraction, or on the left-hand-side for replacement. When an index expression appears on the left side of an assignment (known as subassignment) then that part of \(x\) is set to the value of the right hand side of the assignment. In this case no partial matching of character indices is done, and the left-hand-side is coerced as needed to accept the values. For vectors, the answer will be of the higher of the types of \(x\) and value in the hierarchy \text{raw} < \text{logical} < \text{integer} < \text{double} < \text{complex} < \text{character} < \text{list} < \text{expression}. Attributes are preserved (although names, \text{dim} and \text{dimnames} will be adjusted suitably). Subassignment is done sequentially, so if an index is specified more than once the latest assigned value for an index will result.

It is an error to apply any of these operators to an object which is not subsettable (e.g., a function).

**Atomic vectors**

The usual form of indexing is \([\), \([ [\) can be used to select a single element dropping names, whereas \([\) keeps them, e.g., in \(c(abc = 123)[1]\).

The index object \(i\) can be numeric, logical, character or empty. Indexing by factors is allowed and is equivalent to indexing by the numeric codes (see \text{factor}) and not by the character values which are printed (for which use \(\text{as.character}(i)\)).

An empty index selects all values: this is most often used to replace all the entries but keep the attributes.
Matrices and arrays

Matrices and arrays are vectors with a dimension attribute and so all the vector forms of indexing can be used with a single index. The result will be an unnamed vector unless x is one-dimensional when it will be a one-dimensional array.

The most common form of indexing a k-dimensional array is to specify k indices to [. As for vector indexing, the indices can be numeric, logical, character, empty or even factor. And again, indexing by factors is equivalent to indexing by the numeric codes, see ‘Atomic vectors’ above.

An empty index (a comma separated blank) indicates that all entries in that dimension are selected. The argument drop applies to this form of indexing.

A third form of indexing is via a numeric matrix with the one column for each dimension: each row of the index matrix then selects a single element of the array, and the result is a vector. Negative indices are not allowed in the index matrix. NA and zero values are allowed: rows of an index matrix containing a zero are ignored, whereas rows containing an NA produce an NA in the result.

Indexing via a character matrix with one column per dimensions is also supported if the array has dimension names. As with numeric matrix indexing, each row of the index matrix selects a single element of the array. Indices are matched against the appropriate dimension names. NA is allowed and will produce an NA in the result. Unmatched indices as well as the empty string ("") are not allowed and will result in an error.

A vector obtained by matrix indexing will be unnamed unless x is one-dimensional when the row names (if any) will be indexed to provide names for the result.

Recursive (list-like) objects

Indexing by [ is similar to atomic vectors and selects a list of the specified element(s).

Both [[ and $ select a single element of the list. The main difference is that $ does not allow computed indices, whereas [[ does. x$name is equivalent to x[["name", exact = FALSE]]. Also, the partial matching behavior of [[ can be controlled using the exact argument.

gElement(x, name) is a version of x[[name, exact = TRUE]] which for formally classed (S4) objects returns slot(x, name), hence providing access to even more general list-like objects.

[ and [[ are sometimes applied to other recursive objects such as calls and expressions. Pairlists (such as calls) are coerced to lists for extraction by [, but all three operators can be used for replacement.

[[ can be applied recursively to lists, so that if the single index i is a vector of length p, alist[[i]] is equivalent to alist[[i1]]...[[ip]] providing all but the final indexing results in a list.

Note that in all three kinds of replacement, a value of NULL deletes the corresponding item of the list. To set entries to NULL, you need x[i] <- list(NULL).

When $<- is applied to a NULL x, it first coerces x to list(). This is what also happens with [[<- where in R versions less than 4.y.z, a length one value resulted in a length one (atomic) vector.

Environments

Both $ and [[ can be applied to environments. Only character indices are allowed and no partial matching is done. The semantics of these operations are those of get(i, env = x, inherits = FALSE). If no match is found then NULL is returned. The replacement versions, $<- and [[<- can also be used. Again, only character arguments are allowed. The semantics in this case are those of assign(i, value, env = x, inherits = FALSE). Such an assignment will either create a new binding or change the existing binding in x.
NAs in indexing

When extracting, a numerical, logical or character NA index picks an unknown element and so returns NA in the corresponding element of a logical, integer, numeric, complex or character result, and NULL for a list. (It returns Ø for a raw result.)

When replacing (that is using indexing on the lhs of an assignment) NA does not select any element to be replaced. As there is ambiguity as to whether an element of the rhs should be used or not, this is only allowed if the rhs value is of length one (so the two interpretations would have the same outcome). (The documented behaviour of S was that an NA replacement index ‘goes nowhere’ but uses up an element of value: Becker et al p. 359. However, that has not been true of other implementations.)

Argument matching

Note that these operations do not match their index arguments in the standard way: argument names are ignored and positional matching only is used. So m[j = 2, i = 1] is equivalent to m[2, 1] and not to m[1, 2].

This may not be true for methods defined for them; for example it is not true for the data.frame methods described in [.data.frame which warn if i or j is named and have undocumented behaviour in that case.

To avoid confusion, do not name index arguments (but drop and exact must be named).

S4 methods

These operators are also implicit S4 generics, but as primitives, S4 methods will be dispatched only on S4 objects x.

The implicit generics for the $ and $<- operators do not have name in their signature because the grammar only allows symbols or string constants for the name argument.

Character indices

Character indices can in some circumstances be partially matched (see pmatch) to the names or dimnames of the object being subsetted (but never for subassignment). Unlike S (Becker et al p. 358), R never uses partial matching when extracting by [, and partial matching is not by default used by [[] (see argument exact).

Thus the default behaviour is to use partial matching only when extracting from recursive objects (except environments) by $. Even in that case, warnings can be switched on by options(warnPartialMatchDollar = TRUE).

Neither empty (""") nor NA indices match any names, not even empty nor missing names. If any object has no names or appropriate dimnames, they are taken as all "" and so match nothing.

Error conditions

Attempting to apply a subsetting operation to objects for which this is not possible signals an error of class notSubsettableError. The object component of the error condition contains the non-subsettable object.

Subscript out of bounds errors are signaled as errors of class subscriptOutOfRangeError. The object component of the error condition contains the object being subsetted. The integer subscript component is zero for vector subscipting, and for multiple subscripts indicates which subscript was out of bounds. The index component contains the erroneous index.
References


See Also

names for details of matching to names, and pmatch for partial matching.
list, array, matrix.
[.data.frame and [.factor for the behaviour when applied to data.frame and factors.
Syntax for operator precedence, and the ‘R Language Definition’ manual about indexing details.
NULL for details of indexing null objects.

Examples

```r
x <- 1:12
m <- matrix(1:6, nrow = 2, dimnames = list(c("a", "b"), LETTERS[1:3]))
li <- list(pi = pi, e = exp(1))
x[10]   # the tenth element of x
x <- x[-1]  # delete the 1st element of x
m[1,]   # the first row of matrix m
m[1,, drop = FALSE]  # is a 1-row matrix
m[cbind(c(TRUE, FALSE, TRUE)),]# logical indexing
m[cbind(c("a", "b", "a"), c("A", "C", "B"))]
# matrix numeric index
m[ci]   # matrix character index
m <- m[,-1]  # delete the first column of m
li[[1]]   # the first element of list li
y <- list(1, 2, a = 4, 5)
y[c(3, 4)] # a list containing elements 3 and 4 of y
y$a  # the element of y named a

## non-integer indices are truncated:
(i <- 3.999999999) # "4" is printed
(1:5)[i]  # 3

## named atomic vectors, compare "][" and "][] :
nx <- c(Abc = 123, pi = pi)
nx[1]; nx["pi"]  # keeps names, whereas "][] does not:
nx[[1]]; nx[["pi"]]

## recursive indexing into lists
z <- list(a = list(b = 9, c = "hello"), d = 1:5)
unlist(z)
z[[c(1, 2)]]
z[[c(1, 2, 1)]]  # both "hello"
z[[c("a", "b")]] <- "new"
unlist(z)

## check $ and [[ for environments
e1 <- new.env()
e1$a <- 10
e1["a"]
e1[["a"]]
e1[["b"]]] <- 20
e1$b
```
ls(e!)

## partial matching - possibly with warning :
stopifnot(identical(li$p, pi))
op <- options(warnPartialMatchDollar = TRUE)
stopifnot(identical(li$p, pi), #-- a warning
    inherits(tryCatch (li$p, warning = identity), "warning")
## revert the warning option:
options(op)

---

Extract.data.frame  

Extract or Replace Parts of a Data Frame

Description

Extract or replace subsets of data frames.

Usage

## S3 method for class 'data.frame'
x[i, j, drop = ]
## S3 replacement method for class 'data.frame'
x[i, j] <- value
## S3 method for class 'data.frame'
x[..., exact = TRUE]
## S3 replacement method for class 'data.frame'
x[[i, j]] <- value
## S3 replacement method for class 'data.frame'
x$name <- value

Arguments

x  
data frame.

i, j, ...  
elements to extract or replace. For [ and [[, these are numeric or character or, for [ only, empty or logical. Numeric values are coerced to integer as if by as.integer. For replacement by [, a logical matrix is allowed.

name  
A literal character string or a name (possibly backtick quoted).

drop  
logical. If TRUE the result is coerced to the lowest possible dimension. The default is to drop if only one column is left, but not to drop if only one row is left.

value  
A suitable replacement value: it will be repeated a whole number of times if necessary and it may be coerced: see the Coercion section. If NULL, deletes the column if a single column is selected.

exact  
logical: see [, and applies to column names.
Details

Data frames can be indexed in several modes. When [] and [[] are used with a single vector index (x[i] or x[[i]]), they index the data frame as if it were a list. In this usage a drop argument is ignored, with a warning.

There is no data.frame method for $, so x$name uses the default method which treats x as a list (with partial matching of column names if the match is unique, see Extract). The replacement method (for $) checks value for the correct number of rows, and replicates it if necessary.

When [] and [[] are used with two indices (x[i, j] and x[[i, j]]) they act like indexing a matrix: [[] can only be used to select one element. Note that for each selected column, xj say, typically (if it is not matrix-like), the resulting column will be xj[i], and hence rely on the corresponding [ method, see the examples section.

If [] returns a data frame it will have unique (and non-missing) row names, if necessary transforming the row names using make.unique. Similarly, if columns are selected column names will be transformed to be unique if necessary (e.g., if columns are selected more than once, or if more than one column of a given name is selected if the data frame has duplicate column names).

When drop = TRUE, this is applied to the subsetting of any matrices contained in the data frame as well as to the data frame itself.

The replacement methods can be used to add whole column(s) by specifying non-existent column(s), in which case the column(s) are added at the right-hand edge of the data frame and numerical indices must be contiguous to existing indices. On the other hand, rows can be added at any row after the current last row, and the columns will be in-filled with missing values. Missing values in the indices are not allowed for replacement.

For [] the replacement value can be a list: each element of the list is used to replace (part of) one column, recycling the list as necessary. If columns specified by number are created, the names (if any) of the corresponding list elements are used to name the columns. If the replacement is not selecting rows, list values can contain NULL elements which will cause the corresponding columns to be deleted. (See the Examples.)

Matrix indexing (x[i] with a logical or a 2-column integer matrix i) using [] is not recommended. For extraction, x is first coerced to a matrix. For replacement, logical matrix indices must be of the same dimension as x. Replacements are done one column at a time, with multiple type coercions possibly taking place.

Both [] and [[] extraction methods partially match row names. By default neither partially match column names, but [[] will if exact = FALSE (and with a warning if exact = NA). If you want to exact matching on row names use match, as in the examples.

Value

For [], a data frame, list or a single column (the latter two only when dimensions have been dropped). If matrix indexing is used for extraction a vector results. If the result would be a data frame an error results if undefined columns are selected (as there is no general concept of a ‘missing’ column in a data frame). Otherwise if a single column is selected and this is undefined the result is NULL.

For [[] a column of the data frame or NULL (extraction with one index) or a length-one vector (extraction with two indices).

For $, a column of the data frame (or NULL).

For [<-, [[]<- and <$>-, a data frame.
Coercion

The story over when replacement values are coerced is a complicated one, and one that has changed during R’s development. This section is a guide only.

When \[ and \[ are used to add or replace a whole column, no coercion takes place but value will be replicated (by calling the generic function rep) to the right length if an exact number of repeats can be used.

When \[ is used with a logical matrix, each value is coerced to the type of the column into which it is to be placed.

When \[ and \[ are used with two indices, the column will be coerced as necessary to accommodate the value.

Note that when the replacement value is an array (including a matrix) it is not treated as a series of columns (as data.frame and as.data.frame do) but inserted as a single column.

Warning

The default behaviour when only one row is left is equivalent to specifying drop = FALSE. To drop from a data frame to a list, drop = TRUE has to be specified explicitly.

Arguments other than drop and exact should not be named: there is a warning if they are and the behaviour differs from the description here.

See Also

subset which is often easier for extraction, data.frame, Extract.

Examples

sw <- swiss[1:5, 1:4]  # select a manageable subset

sw[1:3]  # select columns
sw[, 1:3]  # same
sw[4:5, 1:3]  # select rows and columns
sw[1]  # a one-column data frame
sw[, 1, drop = FALSE]  # the same
sw[, 1]  # a (unnamed) vector
sw[[1]]  # the same
sw$Fert  # the same (possibly w/ warning, see Extract)

sw[1,]  # a one-row data frame
sw[1,, drop = TRUE]  # a list

sw["C", ]  # partially matches
sw[match("C", row.names(sw)), ]  # no exact match
try(sw[, "Ferti"])  # column names must match exactly

sw[sw$Fertility > 90,]  # logical indexing, see also ?subset
sw[cc(1, 1:2), ]  # duplicate row, unique row names are created

sw[sw <= 6] <- 6  # logical matrix indexing

sw

## adding a column
sw["new1"] <- LETTERS[1:5]  # adds a character column
Extract or Replace Parts of a Factor

Description

Extract or replace subsets of factors.

Usage

## S3 method for class 'factor'
x[...], drop = FALSE]
## S3 method for class 'factor'
x[[...]]
## S3 replacement method for class 'factor'
x[[...]] <- value
## S3 replacement method for class 'factor'
x[[...]] <- value
Arguments

- `x`: a factor
- `...`: a specification of indices – see Extract.
- `drop`: logical. If true, unused levels are dropped.
- `value`: character: a set of levels. Factor values are coerced to character.

Details

When unused levels are dropped the ordering of the remaining levels is preserved.
If `value` is not in `levels(x)`, a missing value is assigned with a warning.
Any `contrasts` assigned to the factor are preserved unless `drop = TRUE`.
The `[]` method supports argument `exact`.

Value

A factor with the same set of levels as `x` unless `drop = TRUE`.

See Also

`factor`, `Extract`.

Examples

```r
## following example(factor)
(ff <- factor(substring("statistics", 1:10, 1:10), levels = letters))
ff[, drop = TRUE]
factor(letters[7:10])[2:3, drop = TRUE]
```

Description

Returns the (regular or parallel) maxima and minima of the input values.

`pmax*()` and `pmin*()` take one or more vectors as arguments, recycle them to common length and return a single vector giving the 'parallel' maxima (or minima) of the argument vectors.

Usage

```r
max(..., na.rm = FALSE)
min(..., na.rm = FALSE)
pmax(..., na.rm = FALSE)
pmin(..., na.rm = FALSE)
pmax.int(..., na.rm = FALSE)
pmin.int(..., na.rm = FALSE)
```
Arguments

... numeric or character arguments (see Note).

na.rm a logical indicating whether missing values should be removed.

Details

max and min return the maximum or minimum of all the values present in their arguments, as integer if all are logical or integer, as double if all are numeric, and character otherwise.

If na.rm is FALSE an NA value in any of the arguments will cause a value of NA to be returned, otherwise NA values are ignored.

The minimum and maximum of a numeric empty set are +Inf and -Inf (in this order!) which ensures transitivity, e.g., min(x1, min(x2)) == min(x1, x2). For numeric x max(x) == -Inf and min(x) == +Inf whenever length(x) == 0 (after removing missing values if requested). However, pmax and pmin return NA if all the parallel elements are NA even for na.rm = TRUE.

pmax and pmin take one or more vectors (or matrices) as arguments and return a single vector giving the ‘parallel’ maxima (or minima) of the vectors. The first element of the result is the maximum (minimum) of the first elements of all the arguments, the second element of the result is the maximum (minimum) of the second elements of all the arguments and so on. Shorter inputs (of non-zero length) are recycled if necessary. Attributes (see attributes: such as names or dim) are copied from the first argument (if applicable, e.g., not for an S4 object).

pmax.int and pmin.int are faster internal versions only used when all arguments are atomic vectors and there are no classes: they drop all attributes. (Note that all versions fail for raw and complex vectors since these have no ordering.)

max and min are generic functions: methods can be defined for them individually or via the Summary group generic. For this to work properly, the arguments ... should be unnamed, and dispatch is on the first argument.

By definition the min/max of a numeric vector containing an NaN is NaN, except that the min/max of any vector containing an NA is NA even if it also contains an NaN. Note that max(NA, Inf) == NA even though the maximum would be Inf whatever the missing value actually is.

Character versions are sorted lexicographically, and this depends on the collating sequence of the locale in use: the help for ‘Comparison’ gives details. The max/min of an empty character vector is defined to be character NA. (One could argue that as ”” is the smallest character element, the maximum should be ””, but there is no obvious candidate for the minimum.)

Value

For min or max, a length-one vector. For pmin or pmax, a vector of length the longest of the input vectors, or length zero if one of the inputs had zero length.

The type of the result will be that of the highest of the inputs in the hierarchy integer < double < character.

For min and max if there are only numeric inputs and all are empty (after possible removal of NAs), the result is double (Inf or -Inf).

S4 methods

max and min are part of the S4 Summary group generic. Methods for them must use the signature x, ..., na.rm.
Note

‘Numeric’ arguments are vectors of type integer and numeric, and logical (coerced to integer). For historical reasons, NULL is accepted as equivalent to integer(0).

pmax and pmin will also work on classed S3 or S4 objects with appropriate methods for comparison, i.e. na and rep (if recycling of arguments is needed).

References


See Also

range (both min and max) and which.min (which.max) for the arg min, i.e., the location where an extreme value occurs.

‘plotmath’ for the use of min in plot annotation.

Examples

```r
require(stats); require(graphics)
min(5:1, pi) #-> one number
pmin(5:1, pi) #-> 5 numbers

x <- sort(rnorm(100)); ch <- 1.35
pmin(ch, quantile(x)) # no names
pmin(quantile(x), ch) # has names
plot(x, pmin(ch, pmax(-ch, x)), type = "b", main = "Huber's function")

cut01 <- function(x) pmax(pmin(x, 1), 0)
curve(x^2 - 1/4, -1.4, 1.5, col = 2)
curve(cut01(x^2 - 1/4), col = "blue", add = TRUE, n = 500)
## pmax(), pmin() preserve attributes of *first* argument
D <- diag(x = (3:1)/4) ; n0 <- numeric()
stopifnot(identical(D, cut01(D) ),
   identical(n0, cut01(n0)),
   identical(n0, cut01(NULL)),
   identical(n0, pmax(3:1, n0, 2)),
   identical(n0, pmax(n0, 4)))
```

---

**extSoftVersion**

Report Versions of Third-Party Software

Description

Report versions of (external) third-party software used.

Usage

```r
extSoftVersion()
```
Details

The reports the versions of third-party software libraries in use. These are often external but might have been compiled into R when it was installed.

With dynamic linking, these are the versions of the libraries linked to in this session: with static linking, of those compiled in.

Value

A named character vector, currently with components

<table>
<thead>
<tr>
<th>Component</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>zlib</td>
<td>The version of zlib in use.</td>
</tr>
<tr>
<td>bzlib</td>
<td>The version of bzlib (from bzip2) in use.</td>
</tr>
<tr>
<td>xz</td>
<td>The version of libzma (from xz) in use.</td>
</tr>
<tr>
<td>PCRE</td>
<td>The version of PCRE in use. PCRE1 has versions &lt; 10.00, PCRE2 has versions ( \geq 10.00 ).</td>
</tr>
<tr>
<td>ICU</td>
<td>The version of ICU in use (if any, otherwise &quot;&quot;).</td>
</tr>
<tr>
<td>TRE</td>
<td>The version of libtre in use.</td>
</tr>
<tr>
<td>iconv</td>
<td>The implementation and version of the iconv library in use (if known).</td>
</tr>
<tr>
<td>readline</td>
<td>The version of readline in use (if any, otherwise &quot;). If using the emulation by libedit aka editline this will be &quot;EditLine wrapper&quot; preceded by the readline version it emulates: that is most likely to be seen on macOS.</td>
</tr>
<tr>
<td>BLAS</td>
<td>Name of the binary/executable file with the implementation of BLAS in use (if known, otherwise &quot;).</td>
</tr>
</tbody>
</table>

Note that the values for bzlib and pcre normally contain a date as well as the version number, and that for tre includes several items separated by spaces, the version number being the second.

For iconv this will give the implementation as well as the version, for example "GNU libiconv 1.14", "glibc 2.18" or "win_iconv" (which has no version number).

The name of the binary/executable file for BLAS can be used as an indication of which implementation is in use. Typically, the R version of BLAS will appear as libR.so (libR.dylib), R or libRblas.so (libRblas.dylib), depending on how R was built. Note that libRblas.so (libRblas.dylib) may also be shown for an external BLAS implementation that had been copied, hard-linked or renamed by the system administrator. For an external BLAS, a shared object file will be given and its path/name may indicate the vendor/version. The detection does not work on Windows nor for the Accelerate framework on macOS.

See Also

libcurlVersion for the version of libCurl.
La_version for the version of LAPACK in use.
La_library for binary/executable file with LAPACK in use.
grSoftVersion for third-party graphics software.
tclVersion in package tcltk for the version of Tcl/Tk.
pcre_config for PCRE configuration options.

Examples

```r
extSoftVersion()
# the PCRE version
sub(" .*", "", extSoftVersion()["PCRE"])
```
### Description

The function `factor` is used to encode a vector as a factor (the terms 'category' and 'enumerated type' are also used for factors). If argument `ordered` is `TRUE`, the factor levels are assumed to be ordered. For compatibility with S there is also a function `ordered`. `is.factor`, `is.ordered`, as.factor and as.ordered are the membership and coercion functions for these classes.

### Usage

```r
factor(x = character(), levels, labels = levels,
       exclude = NA, ordered = is.ordered(x), nmax = NA)
```

```r
ordered(x = character(), ...)
```

```r
is.factor(x)
```

```r
is.ordered(x)
```

```r
as.factor(x)
```

```r
as.ordered(x)
```

```r
addNA(x, ifany = FALSE)
```

```r
.valid.factor(object)
```

### Arguments

- **x**: a vector of data, usually taking a small number of distinct values.
- **levels**: an optional vector of the unique values (as character strings) that `x` might have taken. The default is the unique set of values taken by `as.character(x)`, sorted into increasing order of `x`. Note that this set can be specified as smaller than `sort(unique(x))`.
- **labels**: either an optional character vector of labels for the levels (in the same order as `levels` after removing those in `exclude`), or a character string of length 1. Duplicated values in `labels` can be used to map different values of `x` to the same factor level.
- **exclude**: a vector of values to be excluded when forming the set of levels. This may be factor with the same level set as `x` or should be a character.
- **ordered**: logical flag to determine if the levels should be regarded as ordered (in the order given).
- **nmax**: an upper bound on the number of levels; see ‘Details’.
- **...**: (in `ordered(.)`): any of the above, apart from `ordered` itself.
- **ifany**: only add an NA level if it is used, i.e. if `any(is.na(x))`.
- **object**: an R object.
Details

The type of the vector \( x \) is not restricted; it only must have an `as.character` method and be sortable (by `order`).

Ordered factors differ from factors only in their class, but methods and the model-fitting functions treat the two classes quite differently.

The encoding of the vector happens as follows. First all the values in `exclude` are removed from `levels`. If \( x[i] \) equals `levels[j]`, then the \( i \)-th element of the result is \( j \). If no match is found for \( x[i] \) in `levels` (which will happen for excluded values) then the \( i \)-th element of the result is set to `NA`.

Normally the 'levels' used as an attribute of the result are the reduced set of levels after removing those in `exclude`, but this can be altered by supplying `labels`. This should either be a set of new labels for the levels, or a character string, in which case the levels are that character string with a sequence number appended.

`factor(x, exclude = NULL)` applied to a factor without `NA`s is a no-operation unless there are unused levels: in that case, a factor with the reduced level set is returned. If `exclude` is used, since R version 3.4.0, excluding non-existing character levels is equivalent to excluding nothing, and when `exclude` is a `character` vector, that is applied to the levels of \( x \). Alternatively, `exclude` can be a factor with the same level set as \( x \) and will exclude the levels present in `exclude`.

The codes of a factor may contain `NA`. For a numeric \( x \), set `exclude = NULL` to make `NA` an extra level (prints as `<NA>`); by default, this is the last level.

If `NA` is a level, the way to set a code to be missing (as opposed to the code of the missing level) is to use `is.na` on the left-hand-side of an assignment (as in `is.na(f)[i] <- TRUE`; indexing inside `is.na` does not work). Under those circumstances missing values are currently printed as `<NA>`, i.e., identical to entries of level `NA`.

`is.factor` is generic: you can write methods to handle specific classes of objects, see Internal-Methods.

Where `levels` is not supplied, `unique` is called. Since factors typically have quite a small number of levels, for large vectors \( x \) it is helpful to supply `nmax` as an upper bound on the number of unique values.

When using `c` to combine a (possibly ordered) factor with other objects, if all objects are (possibly ordered) factors, the result will be a factor with levels the union of the level sets of the elements, in the order the levels occur in the level sets of the elements (which means that if all the elements have the same level set, that is the level set of the result), equivalent to how `unlist` operates on a list of factor objects.

Value

`factor` returns an object of class "factor" which has a set of integer codes the length of \( x \) with a "levels" attribute of mode `character` and unique (!anyDuplicated(.)) entries. If argument `ordered` is true (or `ordered()` is used) the result has class `c("ordered", "factor")`. Undocumentedly for a long time, `factor(x)` loses all `attributes(x)` but "names", and resets "levels" and "class".

Applying `factor` to an ordered or unordered factor returns a factor (of the same type) with just the levels which occur: see also `[.factor` for a more transparent way to achieve this.

`is.factor` returns TRUE or FALSE depending on whether its argument is of type factor or not. Correspondingly, `is.ordered` returns TRUE when its argument is an ordered factor and FALSE otherwise.

`as.factor` coerces its argument to a factor. It is an abbreviated (sometimes faster) form of `factor`. `as.ordered(x)` returns \( x \) if this is ordered, and `ordered(x)` otherwise.
addNA modifies a factor by turning NA into an extra level (so that NA values are counted in tables, for instance).

.valid.factor(object) checks the validity of a factor, currently only levels(object), and returns TRUE if it is valid, otherwise a string describing the validity problem. This function is used for validObject(<factor>).

Warning

The interpretation of a factor depends on both the codes and the "levels" attribute. Be careful only to compare factors with the same set of levels (in the same order). In particular, as.numeric applied to a factor is meaningless, and may happen by implicit coercion. To transform a factor f to approximately its original numeric values, as.numeric(levels(f))[f] is recommended and slightly more efficient than as.numeric(as.character(f)).

The levels of a factor are by default sorted, but the sort order may well depend on the locale at the time of creation, and should not be assumed to be ASCII.

There are some anomalies associated with factors that have NA as a level. It is suggested to use them sparingly, e.g., only for tabulation purposes.

Comparison operators and group generic methods

There are "factor" and "ordered" methods for the group generic Ops which provide methods for the Comparison operators, and for the min, max, and range generics in Summary of "ordered". (The rest of the groups and the Math group generate an error as they are not meaningful for factors.) Only == and != can be used for factors: a factor can only be compared to another factor with an identical set of levels (not necessarily in the same ordering) or to a character vector. Ordered factors are compared in the same way, but the general dispatch mechanism precludes comparing ordered and unordered factors.

All the comparison operators are available for ordered factors. Collation is done by the levels of the operands: if both operands are ordered factors they must have the same level set.

Note

In earlier versions of R, storing character data as a factor was more space efficient if there is even a small proportion of repeats. However, identical character strings now share storage, so the difference is small in most cases. (Integer values are stored in 4 bytes whereas each reference to a character string needs a pointer of 4 or 8 bytes.)

References


See Also

[.factor for subsetting of factors.

gl for construction of balanced factors and C for factors with specified contrasts. levels and nlevels for accessing the levels, and unclass to get integer codes.

Examples

(ff <- factor(substring("statistics", 1:10, 1:10), levels = letters))
as.integer(ff)  # the internal codes
(f. <- factor(ff)) # drops the levels that do not occur
## Description

Utility function to access information about files on the user’s file systems.

## Usage

```r
file.access(names, mode = 0)
```

## Arguments

- **names**: character vector containing file names. Tilde-expansion will be done: see `path.expand`.
- **mode**: integer specifying access mode required: see ‘Details’.
Details

The mode value can be the exclusive or of the following values

0  test for existence.
1  test for execute permission.
2  test for write permission.
4  test for read permission.

Permission will be computed for real user ID and real group ID (rather than the effective IDs).

Please note that it is not a good idea to use this function to test before trying to open a file. On a multi-tasking system, it is possible that the accessibility of a file will change between the time you call file.access() and the time you try to open the file. It is better to wrap file open attempts in try.

Value

An integer vector with values 0 for success and -1 for failure.

Note

This is intended as a replacement for the S-PLUS function access, a wrapper for the C function of the same name, which explains the return value encoding. Note that the return value is false for success.

See Also

file.info for more details on permissions, Sys.chmod to change permissions, and try for a ‘test it and see’ approach.

file_test for shell-style file tests.

Examples

fa <- file.access(dir("."))
table(fa) # count successes & failures

Description

Choose a file interactively.

Usage

file.choose(new = FALSE)

Arguments

new

Logical: choose the style of dialog box presented to the user: at present only new = FALSE is used.
**file.info**

Value

A character vector of length one giving the file path.

See Also

`list.files` for non-interactive selection.

---

**Extract File Information**

Description

Utility function to extract information about files on the user’s file systems.

Usage

```r
file.info(..., extra_cols = TRUE)
```

```r
file.mode(...)  
file.mtime(...)  
file.size(...)  
```

Arguments

- `...` character vectors containing file paths. Tilde-expansion is done: see `path.expand`
- `extra_cols` Logical: return all cols rather than just the first six.

Details

What constitutes a ‘file’ is OS-dependent but includes directories. (However, directory names must not include a trailing backslash or slash on Windows.) See also the section in the help for `file.exists` on case-insensitive file systems.

The file ‘mode’ follows POSIX conventions, giving three octal digits summarizing the permissions for the file owner, the owner’s group and for anyone respectively. Each digit is the logical or of read (4), write (2) and execute/search (1) permissions.

See `files` for how file paths with marked encodings are interpreted.

**On unix alikes:** On most systems symbolic links are followed, so information is given about the file to which the link points rather than about the link.

**On Windows:** File modes are probably only useful on NTFS file systems, and it seems all three digits refer to the file’s owner. The execute/search bits are set for directories, and for files based on their extensions (e.g., ‘.exe’, ‘.com’, ‘.cmd’ and ‘.bat’ files). `file.access` will give a more reliable view of read/write access availability to the R process.

UTF-8-encoded file names not valid in the current locale can be used.

Junction points and symbolic links are followed, so information is given about the file/directory to which the link points rather than about the link.
Value

For `file.info()`, data frame with row names the file names and columns

- **size**: double: File size in bytes.
- **isdire**: logical: Is the file a directory?
- **mode**: integer of class "octmode". The file permissions, printed in octal, for example 644.
- **mtime, ctime, atime**: object of class "POSIXct": file modification, ‘last status change’ and last access times.

**On unix alikes**: **uid**: integer, the user ID of the file’s owner.

- **gid**: integer, the group ID of the file’s group.
- **uname**: character, `uid` interpreted as a user name.
- **grname**: character, `gid` interpreted as a group name. Unknown user and group names will be NA.

**On Windows only**: **exe**: character indicating the sort of executable. Possible values are "no", "msdos", "win16", "win32", "win64" and "unknown". Note that a file (e.g., a script file) can be executable according to the mode bits but not executable in this sense.

If `extra_cols` is false, only the first six columns are returned: as these can all be found from a single C system call this can be faster. (However, properly configured systems will use a ‘name service cache daemon’ to speed up the name lookups.)

Entries for non-existent or non-readable files will be NA.

The `uid`, `gid`, `uname` and `grname` columns may not be supplied on a non-POSIX Unix-alike system, and will not be on Windows.

What is meant by the three file times depends on the OS and file system. On Windows native file systems `ctime` is the file creation time (something which is not recorded on most Unix-alike file systems). What is meant by ‘file access’ and hence the ‘last access time’ is system-dependent.

The resolution of the file times depends on both the OS and the type of the file system. Modern file systems typically record times to an accuracy of a microsecond or better: notable exceptions are HFS+ on macOS (recorded in seconds) and modification time on older FAT systems (recorded in increments of 2 seconds). Note that "POSIXct" times are by default printed in whole seconds: to change that see `strftime`.

`file.mode()`, `file.mtime()` and `file.size()` are fast convenience wrappers returning just one of the columns.

**Note**

Some (now old) unix alike systems allow files of more than 2Gb to be created but not accessed by the `stat` system call. Such files may show up as non-readable (and very likely not be readable by any of R’s input functions).

**See Also**

`Sys.readlink` to find out about symbolic links, `files`, `file.access`, `list.files`, and `DateTimeClasses` for the date formats.

`Sys.chmod` to change permissions.
Examples

col(finf <- file.info(dir())) # at least six
finf # the whole list
## Those that are more than 100 days old:
finf <- file.info(dir(), extra.cols = FALSE)
finf[difftime(Sys.time(), finf[, "mtime"], units = "days") > 100, 1:4]

file.info("no-such-file-exists")

## E.g., for R-core, in a R-devel version:
if(Sys.info()[["sysname"]][= "Linux"])
  sort(file.mtime(file.path(R.home("bin"),
    c("",
    file.path(c("", "exec"), "R"))
  ))

file.path  

Construct Path to File

Description

Construct the path to a file from components in a platform-independent way.

Usage

file.path(..., fsep = .Platform$file.sep)

Arguments

... character vectors. Long vectors are not supported.

fsep the path separator to use (assumed to be ASCII).

Details

The implementation is designed to be fast (faster than paste) as this function is used extensively in R itself.

It can also be used for environment paths such as PATH and R_LIBS with fsep = .Platform$path.sep.

Trailing path separators are invalid for Windows file paths apart from ‘/’ and ‘d:/’ (although some functions/utilities do accept them), so a trailing / or \ is removed there.

Value

A character vector of the arguments concatenated term-by-term and separated by fsep if all arguments have positive length; otherwise, an empty character vector (unlike paste).

An element of the result will be marked (see Encoding) as UTF-8 if run in a UTF-8 locale (when marked inputs are converted to UTF-8) or if a component of the result is marked as UTF-8, or as Latin-1 in a non-Latin-1 locale.

Note

The components are by default separated by / (not \) on Windows.
file.show

Display One or More Text Files

Description
Display one or more (plain) text files, in a platform specific way, typically via a 'pager'.

Usage
file.show(..., header = rep(“”, nfiles),
  title = “R Information”,
  delete.file = FALSE, pager = getOption(“pager”),
  encoding = “”)

Arguments
... one or more character vectors containing the names of the files to be displayed. Paths with have title expansion.
header character vector (of the same length as the number of files specified in ... ) giving a header for each file being displayed. Defaults to empty strings.
title an overall title for the display. If a single separate window is used for the display, title will be used as the window title. If multiple windows are used, their titles should combine the title and the file-specific header.
delete.file should the files be deleted after display? Used for temporary files.
pager the pager to be used: not used on all platforms
encoding character string giving the encoding to be assumed for the file(s).

Details
This function provides the core of the R help system, but it can be used for other purposes as well, such as page.

How the pager is implemented is highly system-dependent.
The basic Unix version concatenates the files (using the headers) to a temporary file, and displays it in the pager selected by the pager argument, which is a character vector specifying a system command (a full path or a command found on the PATH) to run on the set of files. The ‘factory-fresh’ default is to use ‘R_HOME/bin/pager’, which is a shell script running the command-line specified by the environment variable PAGER whose default is set at configuration, usually to less. On a Unix-alike more is used if pager is empty.
Most GUI systems will use a separate pager window for each file, and let the user leave it up while R continues running. The selection of such pagers could either be done using special pager names being intercepted by lower-level code (such as “internal” and “console” on Windows), or by letting pager be an R function which will be called with arguments (files, header, title, delete.file) corresponding to the first four arguments of file.show and take care of interfacing to the GUI.
The R.app GUI on macOS uses its internal pager irrespective of the setting of pager.
Not all implementations will honour `delete.file`. In particular, using an external pager on Windows does not, as there is no way to know when the external application has finished with the file.

**Author(s)**
Ross Ihaka, Brian Ripley.

**See Also**
`files`, `list.files`, `help`: `RShowDoc` call `file.show()` for `type = "text"`. Consider `getOption("pdfviewer")` and e.g., `system` for displaying pdf files.

`file.edit`.

**Examples**

```r
file.show(file.path(R.home("doc"), "COPYRIGHTS"))
```

---

**Description**

These functions provide a low-level interface to the computer’s file system.

**Usage**

```r
file.create(..., showWarnings = TRUE)
file.exists(...)
file.remove(...)
file.rename(from, to)
file.append(file1, file2)
file.copy(from, to, overwrite = recursive, recursive = FALSE,
          copy.mode = TRUE, copy.date = FALSE)
file.symlink(from, to)
file.link(from, to)
```

**Arguments**

`..., file1, file2`

- character vectors, containing file names or paths.

`from, to`

- character vectors, containing file names or paths. For `file.copy` and `file.symlink` to can alternatively be the path to a single existing directory.

`overwrite`

- logical; should existing destination files be overwritten?

`showWarnings`

- logical; should the warnings on failure be shown?

`recursive`

- logical. If `to` is a directory, should directories in `from` be copied (and their contents)? (Like `cp -R` on POSIX OSES.)

`copy.mode`

- logical: should file permission bits be copied where possible?

`copy.date`

- logical: should file dates be preserved where possible? See `Sys.setFileTime`.

---
Details

The ... arguments are concatenated to form one character string: you can specify the files separately or as one vector. All of these functions expand path names: see `path.expand` (`file.exists` silently reports false for paths that would be too long after expansion: the rest will give a warning.)

`file.create` creates files with the given names if they do not already exist and truncates them if they do. They are created with the maximal read/write permissions allowed by the `umask` setting (where relevant). By default a warning is given (with the reason) if the operation fails.

`file.exists` returns a logical vector indicating whether the files named by its argument exist. (Here ‘exists’ is in the sense of the system’s `stat` call: a file will be reported as existing only if you have the permissions needed by `stat`. Existence can also be checked by `file.access`, which might use different permissions and so obtain a different result. Note that the existence of a file does not imply that it is readable: for that use `file.access`.) What constitutes a ‘file’ is system-dependent, but should include directories. (However, directory names must not include a trailing backslash or slash on Windows.) Note that if the file is a symbolic link on a Unix-alike, the result indicates if the link points to an actual file, not just if the link exists. On Windows, the result is unreliable for a broken symbolic link (junction). Lastly, note the different function `exists` which checks for existence of R objects.

`file.remove` attempts to remove the files named in its argument. On most Unix platforms ‘file’ includes empty directories, symbolic links, fifos and sockets. On Windows, ‘file’ means a regular file and not, say, an empty directory.

`file.rename` attempts to rename files (and `from` and to must be of the same length). Where file permissions allow this will overwrite an existing element of to. This is subject to the limitations of the OS’s corresponding system call (see something like man 2 rename on a Unix-alike): in particular in the interpretation of ‘file’: most platforms will not rename files from one file system to another. **NB:** This means that renaming a file from a temporary directory to the user’s file space or during package installation will often fail. (On Windows, `file.rename` can rename files but not directories across volumes.) On platforms which allow directories to be renamed, typically neither or both of `from` and to must a directory, and if to exists it must be an empty directory.

`file.append` attempts to append the files named by its second argument to those named by its first. The R subscript recycling rule is used to align names given in vectors of different lengths.

`file.copy` works in a similar way to `file.append` but with the arguments in the natural order for copying. Copying to existing destination files is skipped unless `overwrite = TRUE`. The `to` argument can specify a single existing directory. If `copy.mode = TRUE` file read/write/execute permissions are copied where possible, restricted by `umask`. (On Windows this applies only to files.) Other security attributes such as ACLs are not copied. On a POSIX filesystem the targets of symbolic links will be copied rather than the links themselves, and hard links are copied separately. Using `copy.date = TRUE` may or may not copy the timestamp exactly (for example, fractional seconds may be omitted), but is more likely to do so as from R 3.4.0.

`file.symlink` and `file.link` make symbolic and hard links on those file systems which support them. For `file.symlink` the `to` argument can specify a single existing directory. (Unix and macOS native filesystems support both. Windows has hard links to files on NTFS file systems and concepts related to symbolic links on recent versions: see the section below on the Windows version of this help page. What happens on a FAT or SMB-mounted file system is OS-specific.)

File arguments with a marked encoding (see `Encoding` are if possible translated to the native encoding, except on Windows where Unicode file operations are used (so marking as UTF-8 can be used to access file paths not in the native encoding on suitable file systems).
Value

These functions return a logical vector indicating which operation succeeded for each of the files attempted. Using a missing value for a file or path name will always be regarded as a failure.

If showWarnings = TRUE, file.create will give a warning for an unexpected failure.

Case-insensitive file systems

Case-insensitive file systems are the norm on Windows and macOS, but can be found on all OSes (for example a FAT-formatted USB drive is probably case-insensitive).

These functions will most likely match existing files regardless of case on such file systems: however this is an OS function and it is possible that file names might be mapped to upper or lower case.

Warning

Always check the return value of these functions when used in package code. This is especially important for file.rename, which has OS-specific restrictions (and note that the session temporary directory is commonly on a different file system from the working directory): it is only portable to use file.rename to change file name(s) within a single directory.

Author(s)

Ross Ihaka, Brian Ripley

See Also

file.info, file.access, file.path, file.show, list.files, unlink, basename, path.expand.

dir.create.

Sys.glob to expand wildcards in file specifications.

file_test, Sys.readlink (for ‘symlink’s).


Examples

```r
cat("file A\n", file = "A")
cat("file B\n", file = "B")
file.append("A", "B")
file.create("A") # (trashing previous)
file.append("A", rep("B", 10))
if(interactive()) file.show("A") # -> the 10 lines from 'B'
file.copy("A", "C")
dir.create("tmp")
file.copy(c("A", "B"), "tmp")
list.files("tmp") # -> "A" and "B"
setwd("tmp")
file.remove("A") # the tmp/A file
file.symlink(file.path("..", c("A", "B")), ".")
    # |--> (TRUE,FALSE) : ok for A but not B as it exists already
setwd("..")
unlink("tmp", recursive = TRUE)
```
file.remove("A", "B", "C")

**Manipulation of Directories and File Permissions**

**Description**

These functions provide a low-level interface to the computer’s file system.

**Usage**

```r
dir.exists(paths)
dir.create(path, showWarnings = TRUE, recursive = FALSE, mode = "0777")
Sys.chmod(paths, mode = "0777", use_umask = TRUE)
Sys.umask(mode = NA)
```

**Arguments**

- `path` a character vector containing a single path name. Tilde expansion (see `path.expand`) is done.
- `paths` character vectors containing file or directory paths. Tilde expansion (see `path.expand`) is done.
- `showWarnings` logical; should the warnings on failure be shown?
- `recursive` logical. Should elements of the path other than the last be created? If true, like the Unix command `mkdir -p`.
- `mode` the mode to be used on Unix-alikes: it will be coerced by `as.octmode`. For `Sys.chmod` it is recycled along `paths`.
- `use_umask` logical: should the mode be restricted by the `umask` setting?

**Details**

`dir.exists` checks that the paths exist (in the same sense as `file.exists`) and are directories.

`dir.create` creates the last element of the path, unless `recursive = TRUE`. Trailing path separators are discarded. The mode will be modified by the umask setting in the same way as for the system function `mkdir`. What modes can be set is OS-dependent, and it is unsafe to assume that more than three octal digits will be used. For more details see your OS’s documentation on the system call `mkdir`, e.g. `man 2 mkdir` (and not that on the command-line utility of that name).

One of the idiosyncrasies of Windows is that directory creation may report success but create a directory with a different name, for example `dir.create("G.S.")` creates "G.S". This is undocumented, and what are the precise circumstances is unknown (and might depend on the version of Windows). Also avoid directory names with a trailing space.

`Sys.chmod` sets the file permissions of one or more files. It may not be supported on a system (when a warning is issued). See the comments for `dir.create` for how modes are interpreted. Changing mode on a symbolic link is unlikely to work (nor be necessary). For more details see your OS’s documentation on the system call `chmod`, e.g. `man 2 chmod` (and not that on the command-line utility of that name). Whether this changes the permission of a symbolic link or its target is OS-dependent (although to change the target is more common, and POSIX does not support modes for symbolic links: BSD-based Unixes do, though).
Sys.umask sets the umask and returns the previous value: as a special case mode = NA just returns the current value. It may not be supported (when a warning is issued and "0" is returned). For more details see your OS’s documentation on the system call umask, e.g. man 2 umask.

How modes are handled depends on the file system, even on Unix-alikes (although their documentation is often written assuming a POSIX file system). So treat documentation cautiously if you are using, say, a FAT/FAT32 or network-mounted file system.

See files for how file paths with marked encodings are interpreted.

Value

dir.exists returns a logical vector of TRUE or FALSE values (without names).
dir.create and Sys.chmod return invisibly a logical vector indicating if the operation succeeded for each of the files attempted. Using a missing value for a path name will always be regarded as a failure. dir.create indicates failure if the directory already exists. If showWarnings = TRUE, dir.create will give a warning for an unexpected failure (e.g., not for a missing value nor for an already existing component for recursive = TRUE).

Sys.umask returns the previous value of the umask, as a length-one object of class "octmode": the visibility flag is off unless mode is NA.

See also the section in the help for file.exists on case-insensitive file systems for the interpretation of path and paths.

Author(s)

Ross Ihaka, Brian Ripley

See Also

file.info, file.exists, file.path, list.files, unlink, basename, path.expand.

Examples

## Not run:
## Fix up maximal allowed permissions in a file tree
Sys.chmod(list.dirs("."), "777")
f <- list.files(".", all.files = TRUE, full.names = TRUE, recursive = TRUE)
Sys.chmod(f, (file.info(f)$mode | "664"))

## End(Not run)

find.package  

Find Packages

Description

Find the paths to one or more packages.
find.package

Usage

find.package(package, lib.loc = NULL, quiet = FALSE,
verbose = getOption("verbose"))

path.package(package, quiet = FALSE)

packageNotFoundError(package, lib.loc, call = NULL)

Arguments

package character vector: the names of packages.
lib.loc a character vector describing the location of \texttt{R} library trees to search through, or \texttt{NULL}. The default value of \texttt{NULL} corresponds to checking the loaded namespace, then all libraries currently known in \texttt{.libPaths()}.
quiet logical. Should this not give warnings or an error if the package is not found?
verbose a logical. If TRUE, additional diagnostics are printed, notably when a package is found more than once.
call call expression.

Details

\texttt{find.package} returns path to the locations where the given packages are found. If \texttt{lib.loc} is \texttt{NULL}, then loaded namespaces are searched before the libraries. If a package is found more than once, the first match is used. Unless \texttt{quiet} = \texttt{TRUE} a warning will be given about the named packages which are not found, and an error if none are. If \texttt{verbose} is true, warnings about packages found more than once are given. For a package to be returned it must contain a either a ‘\texttt{Meta}’ subdirectory or a ‘\texttt{DESCRIPTION}’ file containing a valid version field, but it need not be installed (it could be a source package if \texttt{lib.loc} was set suitably).

\texttt{find.package} is not usually the right tool to find out if a package is available for use: the only way to do that is to use \texttt{require} to try to load it. It need not be installed for the correct platform, it might have a version requirement not met by the running version of \texttt{R}, there might be dependencies which are not available, ....

\texttt{path.package} returns the paths from which the named packages were loaded, or if none were named, for all currently attached packages. Unless \texttt{quiet} = \texttt{TRUE} it will warn if some of the packages named are not attached, and given an error if none are.

\texttt{packageNotFoundError} creates an error condition object of class \texttt{packageNotFoundError} for signaling errors. The condition object contains the fields \texttt{package} and \texttt{lib.loc}.

Value

A character vector of paths of package directories.

See Also

\texttt{path.expand} and \texttt{normalizePath} for path standardization.

Examples

try(find.package("knitr"))

## will not give an error, maybe a warning about *all* locations it is found:
find.package("kitty", quiet=TRUE, verbose=TRUE)
## Find all .libPaths() entries a package is found:

```r
findPkgAll <- function(pkg)
  unlist(lapply(.libPaths(), function(lib)
    find.package(pkg, lib, quiet=TRUE, verbose=FALSE)))
```

```r
findPkgAll("MASS")
findPkgAll("knitr")
```

---

### Description

Given a vector of non-decreasing breakpoints in `vec`, find the interval containing each element of `x`; i.e., if `i <- findInterval(x, v)`, for each index `j` in `x`, `v_{i_j} ≤ x_j < v_{i_{j+1}}` where `v_0 := -\infty`, `v_{N+1} := +\infty`, and `N <- length(v)`. At the two boundaries, the returned index may differ by 1, depending on the optional arguments `rightmost.closed` and `all.inside`.

### Usage

```r
findInterval(x, vec, rightmost.closed = FALSE, all.inside = FALSE,
              left.open = FALSE)
```

### Arguments

- `x` numeric.
- `vec` numeric, sorted (weakly) increasingly, of length `N`, say.
- `rightmost.closed` logical; if true, the rightmost interval, `vec[N-1] .. vec[N]` is treated as closed, see below.
- `all.inside` logical; if true, the returned indices are coerced into `1, ..., N-1`, i.e., `0` is mapped to `1` and `N` to `N-1`.
- `left.open` logical; if true all the intervals are open at left and closed at right; in the formulas below, `≤` should be swapped with `<` (and `>` with `≥`), and `rightmost.closed` means 'leftmost is closed'. This may be useful, e.g., in survival analysis computations.

### Details

The function `findInterval` finds the index of one vector `x` in another, `vec`, where the latter must be non-decreasing. Where this is trivial, equivalent to `apply( outer(x, vec, "\geq"), 1, sum)`, as a matter of fact, the internal algorithm uses interval search ensuring $O(n \log N)$ complexity where `n <- length(x)` (and `N <- length(vec)`). For (almost) sorted `x`, it will be even faster, basically $O(n)$.

This is the same computation as for the empirical distribution function, and indeed, `findInterval(t, sort(x))` is identical to `nF_n(t; X_1, ..., X_n)` where $F_n$ is the empirical distribution function of $X_1, ..., X_n$.

When `rightmost.closed = TRUE`, the result for `x[j] = vec[N] (= max vec)`, is `N - 1` as for all other values in the last interval.

`left.open = TRUE` is occasionally useful, e.g., for survival data. For (anti-)symmetry reasons, it is equivalent to using "mirrored" data, i.e., the following is always true:
where \( N \leftarrow \text{length}(\text{vec}) \) as above.

**Value**

vector of length \( \text{length}(x) \) with values in \( 0:\text{N} \) (and \( \text{NA} \)) where \( N \leftarrow \text{length}(\text{vec}) \), or values coerced to \( 1:(N-1) \) if and only if \( \text{all.inside} = \text{TRUE} \) (equivalently coercing all \( x \) values inside the intervals). Note that \( \text{NAs} \) are propagated from \( x \), and \( \text{Inf} \) values are allowed in both \( x \) and \( \text{vec} \).

**Author(s)**

Martin Maechler

**See Also**

approx(*, method = "constant") which is a generalization of findInterval(), \( \text{ecdf} \) for computing the empirical distribution function which is (up to a factor of \( n \)) also basically the same as findInterval()().

**Examples**

```r
x <- 2:18
v <- c(5, 10, 15) # create two bins [5,10) and [10,15)
ctb(x, findInterval(x, v))

N <- 100
X <- sort(round(stats::rt(N, df = 2), 2))
tt <- c(-100, seq(-2, 2, length.out = 201), +100)
it <- findInterval(tt, X)
tt[it < 1 | it >= N] # only first and last are outside range(X)
```

## 'left.open = TRUE' means "mirroring":
N <- length(v)
stopifnot(identical(
    findInterval( x, v, left.open=TRUE) ,
    N - findInterval(-x, -v[N:1], left.open=FALSE, ...)
))

---

**Description**

Forces the evaluation of a function argument.

**Usage**

force(x)
Arguments

x a formal argument of the enclosing function.

Details

force forces the evaluation of a formal argument. This can be useful if the argument will be captured in a closure by the lexical scoping rules and will later be altered by an explicit assignment or an implicit assignment in a loop or an apply function.

Note

This is semantic sugar: just evaluating the symbol will do the same thing (see the examples).

force does not force the evaluation of other promises. (It works by forcing the promise that is created when the actual arguments of a call are matched to the formal arguments of a closure, the mechanism which implements lazy evaluation.)

Examples

f <- function(y) function() y
lf <- vector("list", 5)
for (i in seq_along(lf)) lf[[i]] <- f(i)
lf[[1]]() # returns 5

g <- function(y) { force(y); function() y }
lg <- vector("list", 5)
for (i in seq_along(lg)) lg[[i]] <- g(i)
lg[[1]]() # returns 1

## This is identical to
g <- function(y) { y; function() y }

---

forceAndCall Call a function with Some Arguments Forced

Description

Call a function with a specified number of leading arguments forced before the call if the function is a closure.

Usage

forceAndCall(n, FUN, ...)

Arguments

n number of leading arguments to force.
FUN function to call.
... arguments to FUN.
forceAndCall calls the function FUN with arguments specified in .... If the value of FUN is a closure then the first n arguments to the function are evaluated (i.e. their delayed evaluation promises are forced) before executing the function body. If the value of FUN is a primitive then the call FUN(...) is evaluated in the usual way.

forceAndCall is intended to help defining higher order functions like apply to behave more reasonably when the result returned by the function applied is a closure that captured its arguments.

See Also
force, promise, closure.

Foreign Function Interface

Description
Functions to make calls to compiled code that has been loaded into R.

Usage
.C(.NAME, ..., NAOK = FALSE, DUP = TRUE, PACKAGE, ENCODING)
.Fortran(.NAME, ..., NAOK = FALSE, DUP = TRUE, PACKAGE, ENCODING)

Arguments

.NAME a character string giving the name of a C function or Fortran subroutine, or an object of class "NativeSymbolInfo", "RegisteredNativeSymbol" or "NativeSymbol" referring to such a name.

... arguments to be passed to the foreign function. Up to 65.

NAOK if TRUE then any NA or NaN or Inf values in the arguments are passed on to the foreign function. If FALSE, the presence of NA or NaN or Inf values is regarded as an error.

PACKAGE if supplied, confine the search for a character string .NAME to the DLL given by this argument (plus the conventional extension, '.so', '.dll', ...). This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols, and also speeds up the search (see 'Note').

DUP, ENCODING For back-compatibility, accepted but ignored.

Details
These functions can be used to make calls to compiled C and Fortran code. Later interfaces are .Call and .External which are more flexible and have better performance.

These functions are primitive, and .NAME is always matched to the first argument supplied (which should not be named). The other named arguments follow ... and so cannot be abbreviated. For clarity, should avoid using names in the arguments passed to ... that match or partially match .NAME.
Value

A list similar to the ... list of arguments passed in (including any names given to the arguments), but reflecting any changes made by the C or Fortran code.

Argument types

The mapping of the types of \( \mathbb{R} \) arguments to C or Fortran arguments is

\[
\begin{array}{ccc}
\text{R} & \text{C} & \text{Fortran} \\
\text{integer} & \text{int *} & \text{integer} \\
\text{numeric} & \text{double *} & \text{double precision} \\
– \text{or} – & \text{float *} & \text{real} \\
\text{complex} & \text{Rcomplex *} & \text{double complex} \\
\text{logical} & \text{int *} & \text{integer} \\
\text{character} & \text{char **} & \text{[see below]} \\
\text{raw} & \text{unsigned char *} & \text{not allowed} \\
\text{list} & \text{SEXP *} & \text{not allowed} \\
\text{other} & \text{SEXP} & \text{not allowed}
\end{array}
\]

Note: The C types corresponding to integer and logical are \text{int}, not \text{long} as in S. This difference matters on most 64-bit platforms, where \text{int} is 32-bit and \text{long} is 64-bit (but not on 64-bit Windows).

Note: The Fortran type corresponding to logical is integer, not logical: the difference matters on some Fortran compilers.

Numeric vectors in \( \mathbb{R} \) will be passed as type \text{double *} to C (and as double precision to Fortran) unless the argument has attribute \text{Csingle} set to \text{TRUE} (use \text{as.single} or \text{single}). This mechanism is only intended to be used to facilitate the interfacing of existing C and Fortran code.

The C type \text{Rcomplex} is defined in \'Complex.h\' as a typedef struct \{double \text{r}; double \text{i};\}. It may or may not be equivalent to the C99 \text{double complex} type, depending on the compiler used.

Logical values are sent as 0 (FALSE), 1 (TRUE) or \text{INT_MIN} = -2147483648 (NA, but only if \text{NAOK} = \text{TRUE}), and the compiled code should return one of these three values: however non-zero values other than \text{INT_MIN} are mapped to \text{TRUE}.

Missing (NA) string values are passed to \text{.C} as the string "NA". As the \text{C} char type can represent all possible bit patterns there appears to be no way to distinguish missing strings from the string "NA". If this distinction is important use \text{.Call}.

Using a character string with \text{.Fortran} is deprecated and will give a warning. It passes the first (only) character string of a character vector as a \text{C} character array to Fortran: that may be usable as \text{character*255} if its true length is passed separately. Only up to 255 characters of the string are passed back. (How well this works, and even if it works at all, depends on the \text{C} and Fortran compilers and the platform.)

Lists, functions or other \( \mathbb{R} \) objects can (for historical reasons) be passed to \text{.C}, but the \text{.Call} interface is much preferred. All inputs apart from atomic vectors should be regarded as read-only, and all apart from vectors (including lists), functions and environments are now deprecated.

Fortran symbol names

All Fortran compilers known to be usable to compile \( \mathbb{R} \) map symbol names to lower case, and so does \text{.Fortran}. 

Symbol names containing underscores are not valid Fortran 77 (although they are valid in Fortran 9x). Many Fortran 77 compilers will allow them but may translate them in a different way to names not containing underscores. Such names will often work with .Fortran (since how they are translated is detected when R is built and the information used by .Fortran), but portable code should not use Fortran names containing underscores.

Use .Fortran with care for compiled Fortran 9x code: it may not work if the Fortran 9x compiler used differs from the Fortran compiler used when configuring R, especially if the subroutine name is not lower-case or includes an underscore. The most portable way to call Fortran 9x code from R is to use .C and the Fortran 2003 module iso_c_binding to provide a C interface to the Fortran code.

Copying of arguments

Character vectors are copied before calling the compiled code and to collect the results. For other atomic vectors the argument is copied before calling the compiled code if it is otherwise used in the calling code.

Non-atomic-vector objects are read-only to the C code and are never copied.

This behaviour can be changed by setting options(CBoundsCheck = TRUE). In that case raw, logical, integer, double and complex vector arguments are copied both before and after calling the compiled code. The first copy made is extended at each end by guard bytes, and on return it is checked that these are unaltered. For .C, each element of a character vector uses guard bytes.

Note

If one of these functions is to be used frequently, do specify PACKAGE (to confine the search to a single DLL) or pass .NAME as one of the native symbol objects. Searching for symbols can take a long time, especially when many namespaces are loaded.

You may see PACKAGE = "base" for symbols linked into R. Do not use this in your own code: such symbols are not part of the API and may be changed without warning.

References


See Also
dyn.load, .Call.

The 'Writing R Extensions' manual.

formals

Access to and Manipulation of the Formal Arguments

Description

Get or set the formal arguments of a function.

Usage

formals(fun = sys.function(sys.parent()), envir = parent.frame())

formals(fun, envir = environment(fun)) <- value
formals

Arguments

fun       a function, or see ‘Details’.
envir     environment in which the function should be defined (or found via get() in
          the first case and when fun a character string).
value     a list (or pairlist) of R expressions.

Details

For the first form, fun can also be a character string naming the function to be manipulated, which
is searched for in envir, by default from the parent frame. If it is not specified, the function calling
formals is used.

Only closures, i.e., non-primitive functions, have formals, not primitive functions.
Note that formals(args(f)) gives a formal argument list for all functions f, primitive or not.

Value

formals returns the formal argument list of the function specified, as a pairlist, or NULL for a
non-function or primitive.

The replacement form sets the formals of a function to the list/pairlist on the right hand side, and
(potentially) resets the environment of the function, dropping attributes.

See Also

formalArgs (from methods), a shortcut for names(formals(.)). args for a human-readable ver-
in, and as intermediary to get formals of a primitive function.
alist to construct a typical formals value, see the examples.
The three parts of a (non-primitive) function are its formals, body, and environment.

Examples

require(stats)
formals(lm)

## If you just want the names of the arguments, use formalArgs instead.
ames(formals(lm))
methods:: formalArgs(lm)       # same

## formals returns a pairlist. Arguments with no default have type symbol (aka name).
str(formals(lm))

## formals returns NULL for primitive functions. Use it in combination with
## args for this case.
is.primitive('+')
formals('+')
formals(args('+'))

## You can overwrite the formal arguments of a function (though this is
## advanced, dangerous coding).
f <- function(x) a + b
formals(f) <- alist(a = , b = 3)
f    # function(a, b = 3) a + b
f(2) # result = 5
format

Encode in a Common Format

Description

Format an \texttt{R} object for pretty printing.

Usage

\begin{verbatim}
format(x, ...)

## Default S3 method:
format(x, trim = FALSE, digits = NULL, nsmall = 0L,
   justify = c("left", "right", "centre", "none"),
   width = NULL, na.encode = TRUE, scientific = NA,
   big.mark = ",", big.interval = 3L,
   small.mark = "\", small.interval = 5L,
   decimal.mark = getOption("OutDec"),
   zero.print = NULL, drop0trailing = FALSE, ...)

## S3 method for class 'data.frame'
format(x, ..., justify = "none")

## S3 method for class 'factor'
format(x, ...)

## S3 method for class 'AsIs'
format(x, width = 12, ...)
\end{verbatim}

Arguments

- \texttt{x} any \texttt{R} object (conceptually); typically numeric.
- \texttt{trim} logical; if FALSE, logical, numeric and complex values are right-justified to a common width: if TRUE the leading blanks for justification are suppressed.
- \texttt{digits} a positive integer indicating how many significant digits are to be used for numeric and complex \texttt{x}. The default, NULL, uses \texttt{getOption("digits").} This is a suggestion: enough decimal places will be used so that the smallest (in magnitude) number has this many significant digits, and also to satisfy \texttt{nsmall.} (For more, notably the interpretation for complex numbers see \texttt{signif.})
- \texttt{nsmall} the minimum number of digits to the right of the decimal point in formatting real/complex numbers in non-scientific formats. Allowed values are 0 <= \texttt{nsmall} <= 20.
- \texttt{justify} should a \texttt{character} vector be left-justified (the default), right-justified, centred or left alone. Can be abbreviated.
- \texttt{width} default method: the minimum field width or NULL or 0 for no restriction. \texttt{AsIs} method: the maximum field width for non-character objects. NULL corresponds to the default 12.
- \texttt{na.encode} logical: should \texttt{NA} strings be encoded? Note this only applies to elements of character vectors, not to numerical, complex nor logical \texttt{NA}s, which are always encoded as "\texttt{NA}".
Either a logical specifying whether elements of a real or complex vector should be encoded in scientific format, or an integer penalty (see \texttt{options("scipen")}). Missing values correspond to the current default penalty.

Further arguments passed to or from other methods.

\texttt{big.mark, big.interval, small.mark, small.interval, decimal.mark, zero.print, drop0trailing} used for prettilying (longish) numerical and complex sequences. Passed to \texttt{prettyNum}: that help page explains the details.

**Details**

\texttt{format} is a generic function. Apart from the methods described here there are methods for dates (see \texttt{format.Date}), date-times (see \texttt{format.POSIXct}) and for other classes such as \texttt{format.octmode} and \texttt{format.dist}.

\texttt{format.data.frame} formats the data frame column by column, applying the appropriate method of \texttt{format} for each column. Methods for columns are often similar to \texttt{as.character} but offer more control. Matrix and data-frame columns will be converted to separate columns in the result, and character columns (normally all) will be given class "\texttt{AsIs}".

\texttt{format.factor} converts the factor to a character vector and then calls the default method (and so \texttt{justify} applies).

\texttt{format.AsIs} deals with columns of complicated objects that have been extracted from a data frame. Character objects and (atomic) matrices are passed to the default method (and so \texttt{width} does not apply). Otherwise it calls \texttt{toString} to convert the object to character (if a vector or list, element by element) and then right-justifies the result.

Justification for character vectors (and objects converted to character vectors by their methods) is done on display width (see \texttt{nchar}), taking double-width characters and the rendering of special characters (as escape sequences, including escaping backslash but not double quote: see \texttt{print.default}) into account. Thus the width is as displayed by \texttt{print(quote = FALSE)} and not as displayed by \texttt{cat}. Character strings are padded with blanks to the display width of the widest. (If \texttt{na.encode = FALSE} missing character strings are not included in the width computations and are not encoded.)

Numeric vectors are encoded with the minimum number of decimal places needed to display all the elements to at least the \texttt{digits} significant digits. However, if all the elements then have trailing zeroes, the number of decimal places is reduced until at least one element has a non-zero final digit; see also the argument documentation for \texttt{big.*}, \texttt{small.*} etc, above. See the note in \texttt{print.default} about \texttt{digits} \geq 16.

Raw vectors are converted to their 2-digit hexadecimal representation by \texttt{as.character}.

\texttt{format.default(x)} now provides a “minimal” string when \texttt{isS4(x)} is true.

The internal code respects the option \texttt{getOption("OutDec")} for the ‘decimal mark’, so if this is set to something other than "." then it takes precedence over argument \texttt{decimal.mark}.

**Value**

An object of similar structure to \texttt{x} containing character representations of the elements of the first argument \texttt{x} in a common format, and in the current locale’s encoding.

For character, numeric, complex or factor \texttt{x}, \texttt{dims} and \texttt{dimnames} are preserved on matrices/arrays and names on vectors: no other attributes are copied.

If \texttt{x} is a list, the result is a character vector obtained by applying \texttt{format.default(x, \ldots)} to each element of the list (after \texttt{unlisting} elements which are themselves lists), and then collapsing the result for each element with \texttt{paste(collapse = ", ")}. The defaults in this case are \texttt{trim = TRUE, justify = "none" since one does not usually want alignment in the collapsed strings.
References


See Also

`format.info` indicates how an atomic vector would be formatted.

`formatC`, `paste`, `as.character`, `sprintf`, `print`, `prettyNum`, `toString`, `encodeString`.

Examples

```r
format(1:10)
format(1:10, trim = TRUE)

zz <- data.frame("(row names)" = c("aaaaa", "b"), check.names = FALSE)
format(zz)
format(zz, justify = "left")

## use of nsmall
format(13.7)
format(13.7, nsmall = 3)
format(c(6.0, 13.1), digits = 2)
format(c(6.0, 13.1), digits = 2, nsmall = 1)

## use of scientific
format(2^31-1)
format(2^31-1, scientific = TRUE)

## a list
z <- list(a = letters[1:3], b = (-pi+0i)^((-2:2)/2), c = c(1,10,100,1000),
         d = c("a", "longer", "character", "string"),
         q = quote(a + b), e = expression(1+x))

## can you find the "2" small differences?
(f1 <- format(z, digits = 2))
(f2 <- format(z, digits = 2, justify = "left", trim = FALSE))

## A "minimal" format() for S4 objects without their own format() method:
cc <- methods::getClassDef("standardGeneric")
format(cc) ## "<S4 class ......>"
```

format.info

format(.) Information

Description

Information is returned on how `format(x, digits, nsmall)` would be formatted.

Usage

`format.info(x, digits = NULL, nsmall = 0)`
Arguments

x  an atomic vector; a potential argument of \texttt{format(x, ...)}.

digits  how many significant digits are to be used for numeric or complex \(x\). The default, \texttt{NULL}, uses \texttt{getOption("digits")}.

nsmall  (see \texttt{format(..., nsmall)}).

Value

An \textbf{integer vector} of length 1, 3 or 6, say \(r\).

For logical, integer and character vectors a single element, the width which would be used by \texttt{format} if \texttt{width = NULL}.

For numeric vectors:

\(r[1]\)  width (in characters) used by \texttt{format(x)}
\(r[2]\)  number of digits after decimal point.
\(r[3]\)  in 0:2; if \(\geq 1\), exponential representation would be used, with exponent length of \(r[3]+1\).

For a complex vector the first three elements refer to the real parts, and there are three further elements corresponding to the imaginary parts.

See Also

\texttt{format} (notably about \texttt{digits >= 16}), \texttt{formatC}.

Examples

\begin{verbatim}
dd <- options("digits") ; options(digits = 7) #-- for the following
format.info(123)  # 3 0 0
format.info(pi)   # 8 6 0
format.info(1e8)  # 5 0 1 - exponential "1e+08"
format.info(1e222) # 6 0 2 - exponential "1e+222"

x <- pi*10^c(-10,-2,0:2,8,20)
names(x) <- formatC(x, width = 1, digits = 3, format = "g")
cbind(sapply(x, format))
t(sapply(x, format.info))

## using at least 8 digits right of "."
t(sapply(x, format.info, nsmall = 8))

# Reset old options:
options(dd)
\end{verbatim}
format.pval  

Format P Values

Description

format.pval is intended for formatting p-values.

Usage

format.pval(pv, digits = max(1, getOption("digits") - 2),
eps = .Machine$double.eps, na.form = "NA", ...)

Arguments

- pv: a numeric vector.
- digits: how many significant digits are to be used.
- eps: a numerical tolerance: see ‘Details’.
- na.form: character representation of NAs.
- ...: further arguments to be passed to format such as nsmall.

Details

format.pval is mainly an auxiliary function for print.summary.lm etc., and does separate formatting for fixed, floating point and very small values; those less than eps are formatted as "< [eps]" (where '[eps]' stands for format(eps, digits)).

Value

A character vector.

Examples

format.pval(c(stats::runif(5), pi^-100, NA))
format.pval(c(0.1, 0.0001, 1e-27))

formatC  

Formatting Using C-style Formats

Description

formatC() formats numbers individually and flexibly using C style format specifications.
prettyNum() is used for “prettifying” (possibly formatted) numbers, also in format.default.
.format.zeros(x), an auxiliary function of prettyNum(), re-formats the zeros in a vector x of formatted numbers.
formatC

Usage

formatC(x, digits = NULL, width = NULL,
format = NULL, flag = "", mode = NULL,
big.mark = "", big.interval = 3L,
small.mark = "", small.interval = 5L,
decimal.mark = getOption("OutDec"),
preserve.width = "individual",
zero.print = NULL, replace.zero = TRUE,
drop0trailing = FALSE)

prettyNum(x, big.mark = "", big.interval = 3L,
small.mark = "", small.interval = 5L,
decimal.mark = getOption("OutDec"), input.d.mark = decimal.mark,
preserve.width = c("common", "individual", "none"),
zero.print = NULL, replace.zero = FALSE,
drop0trailing = FALSE, is.complex = NA,
...)

.format.zeros(x, zero.print, nx = suppressWarnings(as.numeric(x)),
replace = FALSE, warn.non.fitting = TRUE)

Arguments

x

an atomic numerical or character object, possibly complex only for prettyNum(), typically a vector of real numbers. Any class is discarded, with a warning.

digits

the desired number of digits after the decimal point (format = "f") or significant digits (format = "g", = "e" or = "fg"). Default: 2 for integer, 4 for real numbers. If less than 0, the C default of 6 digits is used. If specified as more than 50, 50 will be used with a warning unless format = "f" where it is limited to typically 324. (Not more than 15–21 digits need be accurate, depending on the OS and compiler used. This limit is just a precaution against segfaults in the underlying C runtime.)

width

the total field width; if both digits and width are unspecified, width defaults to 1, otherwise to digits + 1. width = 0 will use width = digits, width < 0 means left justify the number in this field (equivalent to flag = "-"). If necessary, the result will have more characters than width. For character data this is interpreted in characters (not bytes nor display width).

format

equal to "d" (for integers), "f", "e", "E", "g", "G", "fg" (for reals), or "s" (for strings). Default is "d" for integers, "g" for reals. "f" gives numbers in the usual xxx.xxx format; "e" and "E" give n.ddde+nn or n.dddE+nn (scientific format); "g" and "G" put x[i] into scientific format only if it saves space to do so and drop trailing zeros and decimal point - unless flag contains "#" which keeps trailing zeros for the "g", "G" formats.

"fg" (our own hybrid format) uses fixed format as "f", but digits as the minimum number of significant digits. This can lead to quite long result strings, see examples below. Note that unlike signif this prints large numbers with more significant digits than digits. Trailing zeros are dropped in this format, unless flag contains ".#".

flag

for formatC, a character string giving a format modifier as in Kernighan and Ritchie (1988, page 243) or the C+99 standard.
"0" pads leading zeros;
"-" does left adjustment,
"+" ensures a sign in all cases, i.e., "+" for positive numbers,
" " if the first character is not a sign, the space character " " will be used instead.
"#" specifies "an alternative output form", specifically depending on format.
"\"" on some platform–locale combination, activates "thousands' grouping" for
decimal conversion,
"I" in some versions of `glibc` allow for integer conversion to use the locale's
alternative output digits, if any.

There can be more than one of these flags, in any order. Other characters used
to have no effect for character formatting, but signal an error since R 3.4.0.

**mode**

"double" (or "real"), "integer" or "character". Default: Determined from
the storage mode of x.

**big.mark**

character; if not empty used as mark between every big.interval decimals
before (hence big) the decimal point.

**big.interval**

see big.mark above; defaults to 3.

**small.mark**

character; if not empty used as mark between every small.interval decimals
after (hence small) the decimal point.

**small.interval**

see small.mark above; defaults to 5.

**decimal.mark**

the character to be used to indicate the numeric decimal point.

**input.d.mark**

if x is character, the character known to have been used as the numeric decimal
point in x.

**preserve.width**

string specifying if the string widths should be preserved where possible in those
cases where marks (big.mark or small.mark) are added. "common", the de-
fault, corresponds to format-like behavior whereas "individual" is the default
in formatC(). Value can be abbreviated.

**zero.print**

logical, character string or NULL specifying if and how zeros should be formatted
specially. Useful for pretty printing 'sparse' objects.

**replace.zero, replace**

logical; if zero.print is a character string, indicates if the exact zero entries
in x should be simply replaced by zero.print. Otherwise, depending on the
widths of the respective strings, the (formatted) zeroes are partly replaced by
zero.print and then padded with " " to the right were applicable. In that case
(false replace[.zero]), if the zero.print string does not fit, a warning is
produced (if warn.non.fitting is true).

This works via prettyNum(), which calls .format.zeros(*,
replace=replace.zero) three times in this case, see the 'Details'.

**warn.non.fitting**

logical; if it is true, replace[.zero] is false and the zero.print string does
not fit, a warning is signalled.

**drop0trailing**

logical, indicating if trailing zeros, i.e., "0" after the decimal mark, should be
removed; also drops "e+00" in exponential formats. This is simply passed to
prettyNum(), see the 'Details'.

**is.complex**

optional logical, to be used when x is "character" to indicate if it stems from
complex vector or not. By default (NA), x is checked to 'look like' complex.

... arguments passed to format.

**nx**

numeric vector of the same length as x, typically the numbers of which the
character vector x is the pre-format.
Details

For numbers, formatC() calls prettyNum() when needed which itself calls .format.zeros(*, replace=replace.zero). ("when needed": when zero.print is not NULL, drop0trailing is true, or one of big.mark, small.mark, or decimal.mark is not at default.)

If you set format it overrides the setting of mode, so formatC(123.45, mode = "double", format = "d") gives 123.

The rendering of scientific format is platform-dependent: some systems use n.ddde+nnn or n.dddenn rather than n.ddde+nn.

formatC does not necessarily align the numbers on the decimal point, so formatC(c(6.11, 13.1), digits = 2, format = "fg") gives c("6.1", "13"). If you want common formatting for several numbers, use format.

prettyNum is the utility function for prettifying x. x can be complex (or format(<complex>), here.
If x is not a character, format(x[i], ...) is applied to each element, and then it is left unchanged if all the other arguments are at their defaults. Use the input.d.mark argument for prettyNum(x) when x is a character vector not resulting from something like format(<number>) with a period as decimal mark.

Because gsub is used to insert the big.mark and small.mark, special characters need escaping. In particular, to insert a single backslash, use "\\".

The C doubles used for R numerical vectors have signed zeros, which formatC may output as -0, -0.000 ....

There is a warning if big.mark and decimal.mark are the same: that would be confusing to those reading the output.

Value

A character object of same size and attributes as x (after discarding any class), in the current locale’s encoding.

Unlike format, each number is formatted individually. Looping over each element of x, the C function sprintf(....) is called for numeric inputs (inside the C function str_signif).

formatC: for character x, do simple (left or right) padding with white space.

Note

The default for decimal.mark in formatC() was changed in R 3.2.0: for use within print methods in packages which might be used with earlier versions: use decimal.mark = getOption("OutDec") explicitly.

Author(s)

formatC was originally written by Bill Dunlap for S-PLUS, later much improved by Martin Maechler.

It was first adapted for R by Friedrich Leisch and since much improved by the R Core team.

References

See Also

format. sprintf for more general C-like formatting.

Examples

xx <- pi * 10^(-5:4)
cbind(format(xx, digits = 4), formatC(xx))
cbind(format(xx, width = 9, flag = "-"))
cbind(format(xx, digits = 5, width = 8, format = "f", flag = "0"))
cbind(format(xx, digits = 4), formatC(xx, digits = 4, format = "fg"))

f <- (-2:4); f <- f*16^f
# Default ("g") format:
formatC(pi*f)
# Fixed ("f") format, more than one flag ("width" partly "enlarged"):
cbind(formatC(pi*f, digits = 3, width=9, format = "f", flag = "0+"))

formatC( c("a", "Abc", "no way"), width = -7)  # ==> flag = "-"
cbind(formatC(c((-1:1)/0,c(1,100)*pi), width = 8, digits = 1))

## note that some of the results here depend on the implementation
## of long-double arithmetic, which is platform-specific.
xx <- c(1e-12,-3.98765e-10,1.45645e-69,1e-70,pi*1e37,3.44e4)
## 1 2 3 4 5 6
formatC(xx)
formatC(xx, format = "fg")  # special "fixed" format.
formatC(xx[1:4], format = "f", digits = 75)  #>> even longer strings

formatC(c(3.24, 2.3e-6), format = "f", digits = 11)
formatC(c(3.24, 2.3e-6), format = "f", digits = 11, drop0trailing = TRUE)
r <- c("76491283764.97430", "29.12345678901", "-7.1234", "-100.1","1123")
## American:
prettyNum(r, big.mark = ",")
## Some Europeans:
prettyNum(r, big.mark = ",", decimal.mark = ",")

(dd <- sapply(1:10, function(i) paste((9:0)[1:i], collapse = ""))
prettyNum(dd, big.mark = ",")

## examples of 'small.mark'
pN <- stats::qnorm(1:7, lower.tail = FALSE)
cbind(format (pN, small.mark = " ", digits = 15))
cbind(formatC(pN, small.mark = " ", digits = 17, format = "f"))
cbind(ff <- format(1.2345 + 10^(0:5), width = 11, big.mark = " "))

## all with same width (one more than the specified minimum)

## individual formatting to common width:
fc <- formatC(1.234 + 10^(0:8), format = "fg", width = 11, big.mark = " ")
cbind(fc)

## Powers of two, stored exactly, formatted individually:
pow.2 <- formatC(2^(-1:32), digits = 24, width = 1, format = "fg")

## nicely printed (the last line showing 5^32 exactly):
noquote(cbind(pow.2))
formatDL

## complex numbers:
r <- 10.0000001; rv <- (r/10)^(1:10)
\[(zv <- (rv + 1i*rv))\]

op <- options(digits = 7) ## (system default)
\[(pnv <- prettyNum(zv))\]
stopifnot(pnv == "1+1i", pnv == format(zv),
  pnv == prettyNum(zv, drop0trailing = TRUE))

## more digits change the picture:
options(digits = 8)
\[(pnv <- prettyNum(zv, 3))\]

## The ’ flag :
doLC <- FALSE # <= R warns, so change to TRUE manually if you want see the effect
if(doLC) {
oldLC <- Sys.getlocale("LC_NUMERIC")
  Sys.setlocale("LC_NUMERIC", "de.CH.UTF-8")
}

formatC(1.234 + 10^(0:4), format = "fg", width = 11, flag = "\"")

## --> ..... " 1'001" " 1'001" on supported platforms
if(doLC) ## revert, typically to "C" :
  Sys.setlocale("LC_NUMERIC", oldLC)

---

formatDL

Format Description Lists

Description

Format vectors of items and their descriptions as 2-column tables or LaTeX-style description lists.

Usage

formatDL(x, y, style = c("table", "list"),
  width = 0.9 * getOption("width"), indent = NULL)

Arguments

- **x**
a vector giving the items to be described, or a list of length 2 or a matrix with 2 columns giving both items and descriptions.

- **y**
a vector of the same length as x with the corresponding descriptions. Only used if x does not already give the descriptions.

- **style**
a character string specifying the rendering style of the description information. Can be abbreviated. If "table", a two-column table with items and descriptions as columns is produced (similar to Texinfo's @table environment). If "list", a LaTeX-style tagged description list is obtained.

- **width**
a positive integer giving the target column for wrapping lines in the output.

- **indent**
a positive integer specifying the indentation of the second column in table style, and the indentation of continuation lines in list style. Must not be greater than width/2, and defaults to width/3 for table style and width/9 for list style.
Details

After extracting the vectors of items and corresponding descriptions from the arguments, both are coerced to character vectors.

In table style, items with more than indent - 3 characters are displayed on a line of their own.

Value

A character vector with the formatted entries.

Examples

```r
## Provide a nice summary of the numerical characteristics of the machine R is running on:
writeLines(formatDL(unlist(.Machine)))
## Inspect Sys.getenv() results in "list" style (by default, these are printed in "table" style):
writeLines(formatDL(Sys.getenv(), style = "list"))
```

<table>
<thead>
<tr>
<th>function</th>
<th>Function Definition</th>
</tr>
</thead>
</table>

Description

These functions provide the base mechanisms for defining new functions in the R language.

Usage

```r
function( arglist ) expr
\( arglist ) expr
return(value)
```

Arguments

- arglist: Empty or one or more name or name=expression terms.
- expr: An expression.
- value: An expression.

Details

The names in an argument list can be back-quoted non-standard names (see `backquote`).

If value is missing, NULL is returned. If it is a single expression, the value of the evaluated expression is returned. (The expression is evaluated as soon as return is called, in the evaluation frame of the function and before any on.exit expression is evaluated.)

If the end of a function is reached without calling return, the value of the last evaluated expression is returned.

The shorthand form \(x + 1\) is parsed as `function(x) x + 1`. It may be helpful in making code containing simple function expressions more readable.
funprog

Technical details

This type of function is not the only type in R: they are called closures (a name with origins in LISP) to distinguish them from primitive functions.

A closure has three components, its `formals` (its argument list), its `body` (expr in the ‘Usage’ section) and its `environment` which provides the enclosure of the evaluation frame when the closure is used.

There is an optional further component if the closure has been byte-compiled. This is not normally user-visible, but is indicated when functions are printed.

References


See Also

`args`, `formals`, `body` and `environment` for accessing the component parts of a function. `debug` for debugging; using `invisible` inside `return(.)` for returning invisibly.

Examples

```r
norm <- function(x) sqrt(x%*%x)
norm(1:4)
## An anonymous function:
(function(x, y){ z <- x^2 + y^2; x+y+z })(0:7, 1)
```

funprog Common Higher-Order Functions in Functional Programming Languages

Description

Reduce uses a binary function to successively combine the elements of a given vector and a possibly given initial value. Filter extracts the elements of a vector for which a predicate (logical) function gives true. Find and Position give the first or last such element and its position in the vector, respectively. Map applies a function to the corresponding elements of given vectors. Negate creates the negation of a given function.

Usage

```r
Reduce(f, x, init, right = FALSE, accumulate = FALSE)
Filter(f, x)
Find(f, x, right = FALSE, nomatch = NULL)
Map(f, ...)
Negate(f)
Position(f, x, right = FALSE, nomatch = NA_integer_)
```
funprog

Arguments

- **f**: a function of the appropriate arity (binary for Reduce, unary for Filter, Find and Position, k-ary for Map if this is called with k arguments). An arbitrary predicate function for Negate.
- **x**: a vector.
- **init**: an R object of the same kind as the elements of x.
- **right**: a logical indicating whether to proceed from left to right (default) or from right to left.
- **accumulate**: a logical indicating whether the successive reduce combinations should be accumulated. By default, only the final combination is used.
- **nomatch**: the value to be returned in the case when “no match” (no element satisfying the predicate) is found.
- **...**: vectors.

Details

If init is given, Reduce logically adds it to the start (when proceeding left to right) or the end of x, respectively. If this possibly augmented vector v has \( n > 1 \) elements, Reduce successively applies f to the elements of v from left to right or right to left, respectively. I.e., a left reduce computes \( l_1 = f(v_1, v_2), l_2 = f(l_1, v_3), \ldots \), and returns \( l_{n-1} = f(l_{n-2}, v_n) \), and a right reduce does \( r_{n-1} = f(v_{n-1}, v_n), r_{n-2} = f(v_{n-2}, r_{n-1}) \) and returns \( r_1 = f(v_1, r_2) \). (E.g., if v is the sequence (2, 3, 4) and f is division, left and right reduce give \( (2/3)/4 = 1/6 \) and \( 2/(3/4) = 8/3 \), respectively.) If v has only a single element, this is returned; if there are no elements, NULL is returned. Thus, it is ensured that f is always called with 2 arguments.

The current implementation is non-recursive to ensure stability and scalability.

Reduce is patterned after Common Lisp’s reduce. A reduce is also known as a fold (e.g., in Haskell) or an accumulate (e.g., in the C++ Standard Template Library). The accumulative version corresponds to Haskell’s scan functions.

Filter applies the unary predicate function f to each element of x, coercing to logical if necessary, and returns the subset of x for which this gives true. Note that possible NA values are currently always taken as false; control over NA handling may be added in the future. Filter corresponds to filter in Haskell or remove-if-not in Common Lisp.

Find and Position are patterned after Common Lisp’s find-if and position-if, respectively. If there is an element for which the predicate function gives true, then the first or last such element or its position is returned depending on whether right is false (default) or true, respectively. If there is no such element, the value specified by nomatch is returned. The current implementation is not optimized for performance.

Map is a simple wrapper to mapply which does not attempt to simplify the result, similar to Common Lisp’s mapcar (with arguments being recycled, however). Future versions may allow some control of the result type.

Negate corresponds to Common Lisp’s complement. Given a (predicate) function f, it creates a function which returns the logical negation of what f returns.

See Also

Function clusterMap and mcmapply (not Windows) in package parallel provide parallel versions of Map.
Examples

## A general-purpose adder:
add <- function(x) Reduce(`+`, x)
add(list(1, 2, 3))
## Like sum(), but can also be used for adding matrices etc., as it will
## use the appropriate '+' method in each reduction step.
## More generally, many generics meant to work on arbitrarily many
## arguments can be defined via reduction:
FOO <- function(...) Reduce(FOO2, list(...))
FOO2 <- function(x, y) UseMethod("FOO2")
## FOO() methods can then be provided via FOO2() methods.

## A general-purpose cumulative adder:
cadd <- function(x) Reduce(`+`, x, accumulate = TRUE)
cadd(seq_len(7))

## A simple function to compute continued fractions:
cfrac <- function(x) Reduce(function(u, v) u + 1 / v, x, right = TRUE)
## Continued fraction approximation for pi:
cfrac(c(3, 7, 15, 1, 292))
## Continued fraction approximation for Euler's number (e):
cfrac(c(2, 1, 2, 1, 4, 1, 1, 6, 1, 1, 8))

## Map() now recycles similar to basic Ops:
Map(`+`, 1, 1 : 3) ; 1 + 1:3
Map(`+`, numeric(), 1 : 3) ; numeric() + 1:3

## Iterative function application:
Funcall <- function(f, ...) f(...)
## Compute log(exp(acos(cos(0))))
Reduce(Funcall, list(log, exp, acos, cos), 0, right = TRUE)
## n-fold iterate of a function, functional style:
Iterate <- function(f, n = 1)
  function(x) Reduce(Funcall, rep.int(list(f), n), x, right = TRUE)
## Continued fraction approximation to the golden ratio:
Iterate(function(x) 1 + 1 / x, 30)(1)
## which is the same as
cfrac(rep.int(1, 31))

## Computing square root approximations for x as fixed points of the
## function t |-> (t + x / t) / 2, as a function of the initial value:
asqrt <- function(x, n) Iterate(function(t) (t + x / t) / 2, n)
asqrt(2, 30)(10) # Starting from a positive value => +sqrt(2)
asqrt(2, 30)(-1) # Starting from a negative value => -sqrt(2)

## A list of all functions in the base environment:
funs <- Filter(is.function, sapply(ls(baseenv()), get, baseenv()))
## Functions in base with more than 10 arguments:
names(Filter(function(f) length(formals(f)) > 10, funs))
## Number of functions in base with a '...' argument:
length(Filter(function(f)
  any(names(formals(f)) %in% "..."),
  funs))

## Find all objects in the base environment which are *not* functions:
Filter(Negate(is.function), sapply(ls(baseenv()), get, baseenv()))
Description

A call of gc causes a garbage collection to take place. gcinfo sets a flag so that automatic collection is either silent (verbose = FALSE) or prints memory usage statistics (verbose = TRUE).

Usage

gc((verbose = getOption("verbose"), reset = FALSE, full = TRUE)
gcinfo(verbose)

Arguments

verbose logical; if TRUE, the garbage collection prints statistics about cons cells and the space allocated for vectors.
reset logical; if TRUE the values for maximum space used are reset to the current values.
full logical; if TRUE a full collection is performed; otherwise only more recently allocated objects may be collected.

Details

A call of gc causes a garbage collection to take place. This will also take place automatically without user intervention, and the primary purpose of calling gc is for the report on memory usage. For an accurate report full = TRUE should be used.

It can be useful to call gc after a large object has been removed, as this may prompt R to return memory to the operating system.

R allocates space for vectors in multiples of 8 bytes: hence the report of "Vcells", a relic of an earlier allocator (that used a vector heap).

When gcinfo(TRUE) is in force, messages are sent to the message connection at each garbage collection of the form

Garbage collection 12 = 10+0+2 (level 0) ...
6.4 Mbytes of cons cells used (58%)
2.0 Mbytes of vectors used (32%)

Here the last two lines give the current memory usage rounded up to the next 0.1Mb and as a percentage of the current trigger value. The first line gives a breakdown of the number of garbage collections at various levels (for an explanation see the ‘R Internals’ manual).

Value

gc returns a matrix with rows "Ncells" (cons cells), usually 28 bytes each on 32-bit systems and 56 bytes on 64-bit systems, and "Vcells" (vector cells, 8 bytes each), and columns "used" and "gc trigger", each also interpreted in megabytes (rounded up to the next 0.1Mb).

If maxima have been set for either "Ncells" or "Vcells", a fifth column is printed giving the current limits in Mb (with NA denoting no limit).
The final two columns show the maximum space used since the last call to `gc(reset = TRUE)` (or since R started).

gcinfo returns the previous value of the flag.

**See Also**

The ‘R Internals’ manual.

*Memory* on R’s memory management, and *gctorture* if you are an R developer.

*gc.time* reports time used for garbage collection.

*reg.finalizer* for actions to happen at garbage collection.

**Examples**

```r
gc()  #-- do it now
gcinfo(TRUE)  #-- in the future, show when R does it
## vvvvv use larger to *show* something
x <- integer(100000); for(i in 1:18) x <- c(x, i)
gcinfo(VERBOSE = FALSE)  #-- don’t show it anymore

gc(TRUE)
gc(reset = TRUE)
```

---

**gc.time**

*Report Time Spent in Garbage Collection*

**Description**

This function reports the time spent in garbage collection so far in the R session while GC timing was enabled.

**Usage**

```r
gc.time(on = TRUE)
```

**Arguments**

- **on**
  
  logical; if TRUE, GC timing is enabled.

**Details**

Due to timer resolution this may be under-estimate.

This is a primitive.

**Value**

A numerical vector of length 5 giving the user CPU time, the system CPU time, the elapsed time and children’s user and system CPU times (normally both zero), of time spent doing garbage collection whilst GC timing was enabled.

Times of child processes are not available on Windows and will always be given as NA.
See Also

gc, proc.time for the timings for the session.

Examples

gc.time()

Description

Provokes garbage collection on (nearly) every memory allocation. Intended to ferret out memory
protection bugs. Also makes R run very slowly, unfortunately.

Usage

gctorture(on = TRUE)
gctorture2(step, wait = step, inhibit_release = FALSE)

Arguments

on logical; turning it on/off.
step integer; run GC every step allocations; step = 0 turns the GC torture off.
wait integer; number of allocations to wait before starting GC torture.
inhibit_release logical; do not release free objects for re-use: use with caution.

Details

Calling gctorture(TRUE) instructs the memory manager to force a full GC on every allocation. gctorture2 provides a more refined interface that allows the start of the GC torture to be deferred and also gives the option of running a GC only every step allocations.

The third argument to gctorture2 is only used if R has been configured with a strict write barrier enabled. When this is the case all garbage collections are full collections, and the memory manager marks free nodes and enables checks in many situations that signal an error when a free node is used. This can help greatly in isolating unprotected values in C code. It does not detect the case where a node becomes free and is reallocated. The inhibit_release argument can be used to prevent such reallocation. This will cause memory to grow and should be used with caution and in conjunction with operating system facilities to monitor and limit process memory use.

gctorture2 can also be invoked via environment variables at the start of the R session. R_GCTORTURE corresponds to the step argument, R_GCTORTURE_WAIT to wait, and R_GCTORTURE_INHIBIT_RELEASE to inhibit_release.

Value

Previous value of first argument.

Author(s)

Peter Dalgaard and Luke Tierney
Return the Value of a Named Object

**Description**

Search by name for an object (`get`) or zero or more objects (`mget`).

**Usage**

```r
get(x, pos = -1, envir = as.environment(pos), mode = "any", inherits = TRUE)

mget(x, envir = as.environment(-1), mode = "any", ifnotfound, inherits = FALSE)

dynGet(x, ifnotfound = , minframe = 1L, inherits = FALSE)
```

**Arguments**

- `x` For `get`, an object name (given as a character string or a symbol). For `mget`, a character vector of object names.
- `pos, envir` where to look for the object (see ‘Details’); if omitted search as if the name of the object appeared unquoted in an expression.
- `mode` the mode or type of object sought: see the ‘Details’ section.
- `inherits` should the enclosing frames of the environment be searched?
- `ifnotfound` For `mget`, a list of values to be used if the item is not found: it will be coerced to a list if necessary. For `dynGet` any R object, e.g., a call to `stop()`.
- `minframe` integer specifying the minimal frame number to look into.

**Details**

The `pos` argument can specify the environment in which to look for the object in any of several ways: as a positive integer (the position in the search list); as the character string name of an element in the search list; or as an `environment` (including using `sys.frame` to access the currently active function calls). The default of `-1` indicates the current environment of the call to `get`. The `envir` argument is an alternative way to specify an environment.

These functions look to see if each of the name(s) `x` have a value bound to it in the specified environment. If `inherits` is `TRUE` and a value is not found for `x` in the specified environment, the enclosing frames of the environment are searched until the name `x` is encountered. See `environment` and the ‘R Language Definition’ manual for details about the structure of environments and their enclosures.

If `mode` is specified then only objects of that type are sought. `mode` here is a mixture of the meanings of `typeof` and `mode`: "function" covers primitive functions and operators, "numeric", "integer" and "double" all refer to any numeric type, "symbol" and "name" are equivalent but "language" must be used (and not "call" or "").

For `get`, the values of `mode` and `ifnotfound` can be either the same length as `x` or of length 1. The argument `ifnotfound` must be a list containing either the value to use if the requested item is not found or a function of one argument which will be called if the item is not found, with argument the name of the item being requested.
getDLLRegisteredRoutines

Reflectance Information for C/Fortran routines in a DLL

dynGet() is somewhat experimental and to be used inside another function. It looks for an object in the callers, i.e., the sys.frame()s of the function. Use with caution.

Value

For get, the object found. If no object is found an error results.
For mget, a named list of objects (found or specified via ifnotfound).

Note

The reverse (or “inverse”) of a <- get(nam) is assign(nam, a), assigning a to name nam.
inherits = TRUE is the default for get in R but not for S where it had a different meaning.

References


See Also

exists for checking whether an object exists; get0 for an efficient way of both checking existence and getting an object.
assign, the inverse of get(), see above.
Use getAnywhere for searching for an object anywhere, including in other namespaces, and
getFromNamespace to find an object in a specific namespace.

Examples

get("%o%")

## test mget
e1 <- new.env()
mget(letters, e1, ifnotfound = as.list(LETTERS))

getDLLRegisteredRoutines
dll, addNames = TRUE)
Arguments

dll
  a character string or DLLInfo object. The character string specifies the file name of the DLL of interest, and is given without the file name extension (e.g., the '.dll' or '.so') and with no directory/path information. So a file ‘MyPackage/libMyPackage.so’ would be specified as ‘MyPackage’.

The DLLInfo objects can be obtained directly in calls to dyn.load and library.dynam, or can be found after the DLL has been loaded using getLoadedDLLs, which returns a list of DLLInfo objects (index-able by DLL file name).

The DLLInfo approach avoids any ambiguities related to two DLLs having the same name but corresponding to files in different directories.

addNames
  a logical value. If this is TRUE, the elements of the returned lists are named using the names of the routines (as seen by R via registration or raw name). If FALSE, these names are not computed and assigned to the lists. As a result, the call should be quicker. The name information is also available in the NativeSymbolInfo objects in the lists.

Details

This takes the registration information after it has been registered and processed by the R internals. In other words, it uses the extended information.

There is print methods for the class, which prints only the types which have registered routines.

Value

A list of class "DLLRegisteredRoutines" with four elements corresponding to the routines registered for the .C, .Call, .Fortran and .External interfaces. Each is a list (of class "NativeRoutineList") with as many elements as there were routines registered for that interface.

Each element identifies a routine and is an object of class "NativeSymbolInfo". An object of this class has the following fields:

name
  the registered name of the routine (not necessarily the name in the C code).

address
  the memory address of the routine as resolved in the loaded DLL. This may be NULL if the symbol has not yet been resolved.

dll
  an object of class DLLInfo describing the DLL. This is same for all elements returned.

numParameters
  the number of arguments the native routine is to be called with.

Author(s)

Duncan Temple Lang <duncan@wald.ucdavis.edu>

References

‘Writing R Extensions’ manual for symbol registration.


See Also

getLoadedDLLs, getNativeSymbolInfo for information on the entry points listed.
Examples

dlls <- getLoadedDLLs()
getDLLRegisteredRoutines(dlls[["base"]])
getDLLRegisteredRoutines("stats")

Description

This function provides a way to get a list of all the DLLs (see \texttt{dyn.load}) that are currently loaded in the \texttt{R} session.

Usage

\texttt{getLoadedDLLs()}

Details

This queries the internal table that manages the DLLs.

Value

An object of class "DLLInfoList" which is a \texttt{list} with an element corresponding to each DLL that is currently loaded in the session. Each element is an object of class "DLLInfo" which has the following entries.

- \texttt{name}: the abbreviated name.
- \texttt{path}: the fully qualified name of the loaded DLL.
- \texttt{dynamicLookup}: a logical value indicating whether \texttt{R} uses only the registration information to resolve symbols or whether it searches the entire symbol table of the DLL.
- \texttt{handle}: a reference to the C-level data structure that provides access to the contents of the DLL. This is an object of class "DLLHandle".

Note that the class DLLInfo has a method for \texttt{\$} which can be used to resolve native symbols within that DLL. Therefore, one must access the R-level elements described above using [[, e.g. \texttt{x["name"]} or \texttt{x[["handle"]]}.

Note

We are starting to use the handle elements in the DLL object to resolve symbols more directly in \texttt{R}.

Author(s)

Duncan Temple Lang <duncan@wald.ucdavis.edu>.

See Also

\texttt{getDLLRegisteredRoutines, getNativeSymbolInfo}
getNativeSymbolInfo

Examples

getLoadedDLLs()

utils::tail(getLoadedDLLs(), 2) # the last 2 loaded ones, still a DLLInfoList

getNativeSymbolInfo Obtain a Description of one or more Native (C/Fortran) Symbols

Description

This finds and returns a description of one or more dynamically loaded or ‘exported’ built-in native symbols. For each name, it returns information about the name of the symbol, the library in which it is located and, if available, the number of arguments it expects and by which interface it should be called (i.e. .Call, .C, .Fortran, or .External). Additionally, it returns the address of the symbol and this can be passed to other C routines. Specifically, this provides a way to explicitly share symbols between different dynamically loaded package libraries. Also, it provides a way to query where symbols were resolved, and aids diagnosing strange behavior associated with dynamic resolution.

Usage

getNativeSymbolInfo(name, PACKAGE, unlist = TRUE,
  withRegistrationInfo = FALSE)

Arguments

name the name(s) of the native symbol(s).

PACKAGE an optional argument that specifies to which DLL to restrict the search for this symbol. If this is “base”, we search in the R executable itself.

unlist a logical value which controls how the result is returned if the function is called with the name of a single symbol. If unlist is TRUE and the number of symbol names in name is one, then the NativeSymbolInfo object is returned. If it is FALSE, then a list of NativeSymbolInfo objects is returned. This is ignored if the number of symbols passed in name is more than one. To be compatible with earlier versions of this function, this defaults to TRUE.

withRegistrationInfo a logical value indicating whether, if TRUE, to return information that was registered with R about the symbol and its parameter types if such information is available, or if FALSE to return just the address of the symbol.

Details

This uses the same mechanism for resolving symbols as is used in all the native interfaces (.Call, etc.). If the symbol has been explicitly registered by the DLL in which it is contained, information about the number of arguments and the interface by which it should be called will be returned. Otherwise, a generic native symbol object is returned.
getNativeSymbolInfo

Value

Generally, a list of NativeSymbolInfo elements whose elements can be indexed by the elements of name in the call. Each NativeSymbolInfo object is a list containing the following elements:

- **name**: the name of the symbol, as given by the name argument.
- **address**: if withRegistrationInfo is FALSE, this is the native memory address of the symbol which can be used to invoke the routine, and also to compare with other symbol addresses. This is an external pointer object and of class NativeSymbol. If withRegistrationInfo is TRUE and registration information is available for the symbol, then this is an object of class RegisteredNativeSymbol and is a reference to an internal data type that has access to the routine pointer and registration information. This too can be used in calls to `.Call`, `.C`, `.Fortran` and `.External`.
- **dll**: a list containing 3 elements:
  - **name**: the short form of the library name which can be used as the value of the PACKAGE argument in the different native interface functions.
  - **path**: the fully qualified name of the DLL.
  - **dynamicLookup**: a logical value indicating whether dynamic resolution is used when looking for symbols in this library, or only registered routines can be located.

If the routine was explicitly registered by the dynamically loaded library, the list contains a fourth field:

- **numParameters**: the number of arguments that should be passed in a call to this routine.

Additionally, the list will have an additional class, being CRoutine, CallRoutine, FortranRoutine or ExternalRoutine corresponding to the R interface by which it should be invoked.

If any of the symbols is not found, an error is raised.

If name contains only one symbol name and unlist is TRUE, then the single NativeSymbolInfo is returned rather than the list containing that one element.

Note

The third element of the NativeSymbolInfo objects was renamed from package to dll in R version 3.6.0, for consistency with the names of the NativeSymbolInfo objects returned by `getDLLRegisteredRoutines()`.

Note

One motivation for accessing this reflectance information is to be able to pass native routines to C routines as function pointers in C. This allows us to treat native routines and R functions in a similar manner, such as when passing an R function to C code that makes callbacks to that function at different points in its computation (e.g., `nls`). Additionally, we can resolve the symbol just once and avoid resolving it repeatedly or using the internal cache.

Author(s)

Duncan Temple Lang
gettext

Translate Text Messages

Description

Translation of text messages typically from calls to stop(), warning(), or message() happens when Native Language Support (NLS) was enabled in this build of R as it is almost always, see also the bindtextdomain() example.

The functions documented here are the low level building blocks used explicitly or implicitly in almost all such message producing calls and they attempt to translate character vectors or set where the translations are to be found.

Usage

ggettext(..., domain = NULL, trim = TRUE)
ngettext(n, msg1, msg2, domain = NULL)
bindtextdomain(domain, dirname = NULL)
Sys.setLanguage(lang, unset = "en")

Arguments

... One or more character vectors.
trim logical indicating if the white space trimming in gettext() should happen. trim = FALSE may be needed for compiled code (C / C++) messages which often end with \n.
domain the `domain’ for the translation, a character string, or NULL; see ‘Details’.
n a non-negative integer.
msg1 the message to be used in English for \n = 1.
msg2 the message to be used in English for \n = 0, 2, 3, 

dirname The directory in which to find translated message catalogs for the domain.
lang a character string specifying a language for which translations should be sought.
unset a string, specifying the default language assumed to be current in the case Sys.getenv(“LANGUAGE”) is unset or empty.

References


See Also

Details

If domain is NULL (the default) in gettext or ngettext, the domain is inferred. If gettext or ngettext is called from a function in the namespace of package pkg including called via \texttt{stop()}, warning(), or message() from the function, or, say, evaluated as if called from that namespace, see the \texttt{evalq()} example, the domain is set to "R-pkg". Otherwise there is no default domain and messages are not translated.

Setting domain = NA in gettext or ngettext suppresses any translation.

"" does not match any domain. In gettext or ngettext, domain = "" is effectively the same as domain = NA.

If the domain is found, each character string is offered for translation, and replaced by its translation into the current language if one is found.

The \textit{language} to be used for message translation is determined by your OS default and/or the locale setting at R's startup, see \texttt{Sys.getlocale()}, and notably the LANGUAGE environment variable, and also \texttt{Sys.setLanguage()} here.

Conventionally the domain for \texttt{R} warning/error messages in package pkg is "R-pkg", and that for C-level messages is "pkg".

For gettext, when trim is true as by default, leading and trailing whitespace is ignored ("trimmed") when looking for the translation.

ngettext is used where the message needs to vary by a single integer. Translating such messages is subject to very specific rules for different languages: see the GNU Gettext Manual. The string will often contain a single instance of \texttt{%d} to be used in \texttt{sprintf}. If English is used, \texttt{msg1} is returned if \texttt{n == 1} and \texttt{msg2} in all other cases.

\texttt{bindtextdomain} is typically wrapper for the C function of the same name: your system may have a \textit{man} page for it. With a non-NULL dirname it specifies where to look for message catalogues: with dirname = NULL it returns the current location. If NLS is not enabled, bindtextdomain(*,* returns NULL.

The special case bindtextdomain(NULL) calls C level textdomain(textdomain(NULL)) for the purpose of flushing (i.e., emptying) the cache of already translated strings; it returns TRUE when NLS is enabled.

The utility \texttt{Sys.setlanguage(lang)} combines setting the LANGUAGE environment variable with flushing the translation cache by bindtextdomain(NULL).

Value

For gettext, a character vector, one element per string in .... If translation is not enabled or no domain is found or no translation is found in that domain, the original strings are returned.

For ngettext, a character string.

For bindtextdomain, a character string giving the current base directory, or NULL if setting it failed.

For \texttt{Sys.setLanguage()}, the previous LANGUAGE setting with attribute \texttt{attr(*, "ok")}, a \texttt{logical} indicating success. Note that currently, using a non-existing language lang is still set and no translation will happen, without any message.

See Also

\texttt{stop} and \texttt{warning} make use of gettext to translate messages.

\texttt{xgettext} (package \texttt{tools}) for extracting translatable strings from R source files.
Examples

bindtextdomain("R")  # non-null if and only if NLS is enabled

for(n in 0:3)
  print(sprintf(ngettext(n, "%d variable has missing values", "%d variables have missing values"), n))

## Not run:
## for translation, those strings should appear in R-pkg.pot as
msgid "%d variable has missing values"
msgid_plural "%d variables have missing values"
msgstr[0] ""
msgstr[1] ""
## End(Not run)

miss <- "One only" # this line, or the next for the ngettext() below
miss <- c("one", "or", "another")
cat(ngettext(length(miss), "variable", "variables"),
    paste(sQuote(miss), collapse = " ", " "),
    ngettext(length(miss), "contains", "contain"), "missing values
")

## better for translators would be to use
cat(sprintf(ngettext(length(miss),
    "variable %s contains missing values
", "variables %s contain missing values
"),
    paste(sQuote(miss), collapse = " ", " "))) thisLang <- Sys.getenv("LANGUAGE", unset = NA) # so we can reset it
if(is.na(thisLang) || !nzchar(thisLang)) thisLang <- "en" # "factory" default
enT <- "empty model supplied"
Sys.setenv(LANGUAGE = "de") # may not always 'work'
gettext(enT, domain="R-stats")# "leeres Modell angegeben" (if translation works)
tget <- function() gettext(enT)
tget() # not translated as fn tget() is not from "stats" pkg/namespace
evalq(function() gettext(enT), asNamespace("stats"))() # *is* translated

## Sys.setLanguage() -- typical usage --
Sys.setLanguage("en") -> oldSet # does set LANGUAGE env.var
errMsg <- function(expr) tryCatch(expr, error=conditionMessage)
  (errMsg(1 + "2") -> err)
Sys.setLanguage("fr")
errMsg(1 + "2")
Sys.setLanguage("de")
errMsg(1 + "2")
## Usually, you would reset the language to "previous" via
Sys.setLanguage(oldSet)

## A show off of translations -- platform (font etc) dependent:
## The translation languages available for "base" R in this version of R:
## IGNORE_RDIFF_BEGIN
if(capabilities("NLS")) withAutoprint(
  langs <- list.files(bindtextdomain("R"),
    pattern = "^[a-z](\[a-zA-Z]@quot)?")
  langs
  langs
getwd

Get or Set Working Directory

Description

getwd returns an absolute filepath representing the current working directory of the R process; setwd(dir) is used to set the working directory to dir.

Usage

getwd()
setwd(dir)

Arguments

dir A character string: tilde expansion will be done.

Details

See files for how file paths with marked encodings are interpreted.

Value

getwd returns a character string or NULL if the working directory is not available. On Windows the path returned will use / as the path separator and be encoded in UTF-8. The path will not have a trailing / unless it is the root directory (of a drive or share on Windows).

setwd returns the current directory before the change, invisibly and with the same conventions as getwd. It will give an error if it does not succeed (including if it is not implemented).

Note

Note that the return value is said to be an absolute filepath: there can be more than one representation of the path to a directory and on some OSes the value returned can differ after changing directories and changing back to the same directory (for example if symbolic links have been traversed).
See Also

list.files for the contents of a directory.
normalizePath for a ‘canonical’ path name.

Examples

(WD <- getwd())
if (!is.null(WD)) setwd(WD)

Description

Generate factors by specifying the pattern of their levels.

Usage

gl(n, k, length = n*k, labels = seq_len(n), ordered = FALSE)

Arguments

n an integer giving the number of levels.
k an integer giving the number of replications.
length an integer giving the length of the result.
labels an optional vector of labels for the resulting factor levels.
ordered a logical indicating whether the result should be ordered or not.

Value

The result has levels from 1 to n with each value replicated in groups of length k out to a total length of length.

gl is modelled on the GLIM function of the same name.

See Also

The underlying factor().

Examples

## First control, then treatment:
gl(2, 8, labels = c("Control", "Treat"))
## 20 alternating 1s and 2s
gl(2, 1, 20)
## alternating pairs of 1s and 2s
gl(2, 2, 20)
grep, grepl, regexpr, gregexpr, regexec and gregexec search for matches to argument pattern within each element of a character vector: they differ in the format of and amount of detail in the results.

sub and gsub perform replacement of the first and all matches respectively.

Usage

grep(pattern, x, ignore.case = FALSE, perl = FALSE, value = FALSE, fixed = FALSE, useBytes = FALSE, invert = FALSE)

grepl(pattern, x, ignore.case = FALSE, perl = FALSE, fixed = FALSE, useBytes = FALSE)

sub(pattern, replacement, x, ignore.case = FALSE, perl = FALSE, fixed = FALSE, useBytes = FALSE)

gsub(pattern, replacement, x, ignore.case = FALSE, perl = FALSE, fixed = FALSE, useBytes = FALSE)

regexpr(pattern, text, ignore.case = FALSE, perl = FALSE, fixed = FALSE, useBytes = FALSE)

gregexpr(pattern, text, ignore.case = FALSE, perl = FALSE, fixed = FALSE, useBytes = FALSE)

regexec(pattern, text, ignore.case = FALSE, perl = FALSE, fixed = FALSE, useBytes = FALSE)

gregexec(pattern, text, ignore.case = FALSE, perl = FALSE, fixed = FALSE, useBytes = FALSE)

Arguments

pattern character string containing a regular expression (or character string for fixed = TRUE) to be matched in the given character vector. Coerced by as.character to a character string if possible. If a character vector of length 2 or more is supplied, the first element is used with a warning. Missing values are allowed except for regexpr, gregexpr and regexec.

x, text a character vector where matches are sought, or an object which can be coerced by as.character to a character vector. Long vectors are supported.

ignore.case if FALSE, the pattern matching is case sensitive and if TRUE, case is ignored during matching.

perl logical. Should Perl-compatible regexps be used?
grep

value
if FALSE, a vector containing the (integer) indices of the matches determined by grep is returned, and if TRUE, a vector containing the matching elements themselves is returned.

fixed
logical. If TRUE, pattern is a string to be matched as is. Overrides all conflicting arguments.

useBytes
logical. If TRUE the matching is done byte-by-byte rather than character-by-character. See 'Details'.

invert
logical. If TRUE return indices or values for elements that do not match.

replacement
a replacement for matched pattern in sub and gsub. Coerced to character if possible. For fixed = FALSE this can include backreferences "\1" to "\9" to parenthesized subexpressions of pattern. For perl = TRUE only, it can also contain "\U" or "\L" to convert the rest of the replacement to upper or lower case and "\E" to end case conversion. If a character vector of length 2 or more is supplied, the first element is used with a warning. If NA, all elements in the result corresponding to matches will be set to NA.

Details

Arguments which should be character strings or character vectors are coerced to character if possible.

Each of these functions operates in one of three modes:

1. fixed = TRUE: use exact matching.
2. perl = TRUE: use Perl-style regular expressions.
3. fixed = FALSE, perl = FALSE: use POSIX 1003.2 extended regular expressions (the default).

See the help pages on regular expression for details of the different types of regular expressions.

The two *sub functions differ only in that sub replaces only the first occurrence of a pattern whereas gsub replaces all occurrences. If replacement contains backreferences which are not defined in pattern the result is undefined (but most often the backreference is taken to be "")..

For regexpr, gregexpr, regexec and gregexec it is an error for pattern to be NA, otherwise NA is permitted and gives an NA match.

Both grep and grepl take missing values in x as not matching a non-missing pattern.

The main effect of useBytes = TRUE is to avoid errors/warnings about invalid inputs and spurious matches in multibyte locales, but for regexpr it changes the interpretation of the output. It inhibits the conversion of inputs with marked encodings, and is forced if any input is found which is marked as "bytes" (see Encoding).

Caseless matching does not make much sense for bytes in a multibyte locale, and you should expect it only to work for ASCII characters if useBytes = TRUE.

regexpr and gregexpr with perl = TRUE allow Python-style named captures, but not for long vector inputs.

Invalid inputs in the current locale are warned about up to 5 times.

Caseless matching with perl = TRUE for non-ASCII characters depends on the PCRE library being compiled with ‘Unicode property support’, which PCRE2 is by default.
Value

grep(value = FALSE) returns a vector of the indices of the elements of x that yielded a match (or not, for invert = TRUE). This will be an integer vector unless the input is a long vector, when it will be a double vector.

grep(value = TRUE) returns a character vector containing the selected elements of x (after coercion, preserving names but no other attributes).

grepl returns a logical vector (match or not for each element of x).

sub and gsub return a character vector of the same length and with the same attributes as x (after possible coercion to character). Elements of character vectors x which are not substituted will be returned unchanged (including any declared encoding if useBytes = FALSE). If useBytes = FALSE a non-ASCII substituted result will often be in UTF-8 with a marked encoding (e.g., if there is a UTF-8 input, and in a multibyte locale unless fixed = TRUE). Such strings can be re-encoded by enc2native. If any of the inputs is marked as "bytes", elements of character vectors x which are substituted will be returned marked as "bytes", but the encoding flag on elements not substituted is unspecified (it may be the original or "bytes"). If none of the inputs is marked as "bytes", but useBytes = TRUE is given explicitly, the encoding flag is unspecified even on the substituted elements (it may be "bytes" or "unknown", possibly invalid in the current encoding). Mixed use of "bytes" and other marked encodings is discouraged, but if still desired one may use iconv to re-encode the result e.g. to UTF-8 with suitably substituted invalid bytes.

regexpr returns an integer vector of the same length as text giving the starting position of the first match or −1 if there is none, with attribute "match.length", an integer vector giving the length of the matched text (or −1 for no match). The match positions and lengths are in characters unless useBytes = TRUE is used, when they are in bytes (as they are for ASCII-only matching: in either case an attribute useBytes with value TRUE is set on the result). If named capture is used there are further attributes "capture.start", "capture.length" and "capture.names".

gregexpr returns a list of the same length as text each element of which is of the same form as the return value for regexpr, except that the starting positions of every (disjoint) match are given.

regexec returns a list of the same length as text each element of which is either −1 if there is no match, or a sequence of integers with the starting positions of the match and all substrings corresponding to parenthesized subexpressions of pattern, with attribute "match.length" a vector giving the lengths of the matches (or −1 for no match). The interpretation of positions and length and the attributes follows regexpr.

gregexec returns the same as regexec, except that to accommodate multiple matches per element of text, the integer sequences for each match are made into columns of a matrix, with one matrix per element of text with matches.

Where matching failed because of resource limits (especially for perl = TRUE) this is regarded as a non-match, usually with a warning.

Warning

The POSIX 1003.2 mode of gsub and gregexprr does not work correctly with repeated word-boundaries (e.g., pattern = "\b"). Use perl = TRUE for such matches (but that may not work as expected with non-ASCII inputs, as the meaning of ‘word’ is system-dependent).

Performance considerations

If you are doing a lot of regular expression matching, including on very long strings, you will want to consider the options used. Generally perl = TRUE will be faster than the default regular expression engine, and fixed = TRUE faster still (especially when each pattern is matched only a few times).
If you are working with texts with non-ASCII characters, which can be easily turned into ASCII (e.g. by substituting fancy quotes), doing so is likely to improve performance.

If you are working in a single-byte locale (though not common since R 4.2) and have marked UTF-8 strings that are representable in that locale, convert them first as just one UTF-8 string will force all the matching to be done in Unicode, which attracts a penalty of around $3 \times$ for the default POSIX 1003.2 mode.

While useBytes = TRUE will improve performance further, because the strings will not be checked before matching and the actual matching will be faster, it can produce unexpected results so is best avoided. With fixed = TRUE and useBytes = FALSE, optimizations are in place that take advantage of byte-based matching working for such patterns in UTF-8. With useBytes = TRUE, character ranges, wildcards, and other regular expression patterns may produce unexpected results.

PCRE-based matching by default used to put additional effort into ‘studying’ the compiled pattern when x/text has length 10 or more. That study may use the PCRE JIT compiler on platforms where it is available (see pcre_config). As from PCRE2 (PCRE version >= 10.00 as reported by extSoftVersion), there is no study phase, but the patterns are optimized automatically when possible, and PCRE JIT is used when enabled. The details are controlled by options PCRE_study and PCRE_use_JIT. (Some timing comparisons can be seen by running file ‘tests/PCRE.R’ in the R sources (and perhaps installed).) People working with PCRE and very long strings can adjust the maximum size of the JIT stack by setting environment variable R_PCRE_JIT_STACK_MAXSIZE before JIT is used to a value between 1 and 1000 in MB: the default is 64. When JIT is not used with PCRE version < 10.30 (that is with PCRE1 and old versions of PCRE2), it might also be wise to set the option PCRE_limit_recursion.

Note

Aspects will be platform-dependent as well as locale-dependent: for example the implementation of character classes (except [:digit:] and [:xdigit:]). One can expect results to be consistent for ASCII inputs and when working in UTF-8 mode (when most platforms will use Unicode character tables, although those are updated frequently and subject to some degree of interpretation – is a circled capital letter alphabetic or a symbol?). However, results in 8-bit encodings can differ considerably between platforms, modes and from the UTF-8 versions.

Source

The C code for POSIX-style regular expression matching has changed over the years. As from R 2.10.0 (Oct 2009) the TRE library of Ville Laurikari (https://github.com/laurikari/tre) is used. The POSIX standard does give some room for interpretation, especially in the handling of invalid regular expressions and the collation of character ranges, so the results will have changed slightly over the years.

For Perl-style matching PCRE2 or PCRE (https://www.pcre.org) is used: again the results may depend (slightly) on the version of PCRE in use.

References


See Also

regular expression (aka regexp) for the details of the pattern specification.

regmatches for extracting matched substrings based on the results of regexpr, gregexpr and regexec.
glob2rx to turn wildcard matches into regular expressions.
agrep for approximate matching.
charmatch, pmatch for partial matching, match for matching to whole strings, startsWith for matching of initial parts of strings.
tolower, toupper and chartr for character translations.
apropos uses regexps and has more examples.
grepRaw for matching raw vectors.

Options PCRE_limit_recursion, PCRE_study and PCRE_use_JIT.
extSoftVersion for the versions of regex and PCRE libraries in use, pcre_config for more details for PCRE.

Examples

grep("[a-z]", letters)

txt <- c("arm","foot","lefroo", "bafoobar")
if(length(i <- grep("foo", txt)))
  cat("'foo' appears at least once in\n\t", txt, "\n")
i # 2 and 4
txt[i]

## Double all 'a' or 'b's; "\" must be escaped, i.e., 'doubled'
gsub("([ab])", "\1_\1\_", "abc and ABC")

txt <- c("The", "licenses", "for", "most", "software", "are", "designed", "to", "take", "away", "your", "freedom", "to", "share", "and", "change", "it.", "", "By", "contrast.", "the", "GNU", "General", "Public", "License", "is", "intended", "to", "guarantee", "your", "freedom", "to", "share", "and", "change", "free", "software", "--", "to", "make", "sure", "the", "software", "is", "free", "for", "all", "its", "users")
( i <- grep("[gu]", txt) ) # indices
stopifnot( txt[i] == grep("[gu]", txt, value = TRUE) )

## Note that for some implementations character ranges are
## locale-dependent (but not currently). Then [b-e] in locales such as
## en_US may include B as the collation order is aAbBcCdDe ...
(ot <- sub("[b-e]","\.", txt))# gsub does "global" substitution

## In caseless matching, ranges include both cases:
a <- grep("[b-e]", txt, value = TRUE)
b <- grep("[b-e]", txt, ignore.case = TRUE, value = TRUE)
setdiff(b, a)

txt[gsub("g","\#", txt) !=
  gsub("g","\#", txt, ignore.case = TRUE)] # the "G" words

regexp("en", txt)

gregexpr("e", txt)

## Using grepl() for filtering
## Find functions with argument names matching "warn":

grep
findArgs <- function(env, pattern) {
  nms <- ls(envir = as.environment(env))
  nms <- nms[is.na(match(nms, c("F","T")))] # work around "checking hack"
  aa <- sapply(nms, function(.) { o <- get(.)
    if(is.function(o) names(formals(o)) })
  iw <- sapply(aa, function(a) any(grepl(pattern, a, ignore.case=TRUE))
  aa[iw]
}
findArgs("package:base", "warn")

## trim trailing white space
str <- "Now is the time 
sub(" +\$", ", str) ## spaces only
## what is considered 'white space' depends on the locale.
sub("\[[:space:]]+$", ", str, perl = TRUE) ## POSIX-style white space
## what PCRE considered white space changed in version 8.34: see ?regex
sub("\s+$", ", str, perl = TRUE) ## PCRE-style white space

## capitalizing
txt <- "a test of capitalizing"
gsub("\\w\\(\\w*\\)\\”， "\\\\L\\2", txt, perl=TRUE)
gsub("\\b\\w\\”， "\\\\L", txt, perl=TRUE)

txt2 <- "useRs may fly into JFK or laGuardia"
gsub("\\w\\(\\w*)\\(\\w*\)\\”， "\\\\L\\2\\L\\3", txt2, perl=TRUE)
gsub("\\w\\(\\w*)\\(\\w*)\\”， "\\\\L\\2\\L\\3", txt2, perl=TRUE)

## named capture
notables <- c(" Ben Franklin and Jefferson Davis",
"Millard Fillmore")
# name groups 'first' and 'last'
name.rex <- "(?<first>[:upper:][:lower:]+) (?<last>[:upper:][:lower:]+)"
(parsed <- regexpr(name.rex, notables, perl = TRUE))
greexpr(name.rex, notables, perl = TRUE)[2]

parse.one <- function(res, result) {
  m <- do.call(rbind, sapply(seq_along(res), function(i) {
    if(result[i] == -1) return(""
    st <- attr(result, "capture.start")[i, ]
    substring(res[i], st, st + attr(result, "capture.length")[i, ] - 1)
  }))
  colnames(m) <- attr(result, "capture.names")
  m
}
parse.one(notables, parsed)

## Decompose a URL into its components.
## Example by LT (http://www.cs.uiowa.edu/~luke/R/regexp.html).
x <- "http://stat.umn.edu:80/xyz"
m <- regexec("([[:^:]+]:/\?/:([0-9]+))?, x, m
regmatches(x, m)
## Element 3 is the protocol, 4 is the host, 6 is the port, and 7
## is the path. We can use this to make a function for extracting the
## parts of a URL:
URL_parts <- function(x) {
  m <- regexec("([^[:^:]+]:/\?/:([0-9]+))?, x, m
  parts <- do.call(rbind,
grepRaw

Pattern Matching for Raw Vectors

description

grepRaw() searches for substring pattern matches within a raw vector x.

Usage

grepRaw(pattern, x, offset = 1L, ignore.case = FALSE, value = FALSE, fixed = FALSE, all = FALSE, invert = FALSE)

Arguments

- pattern: raw vector containing a regular expression (or fixed pattern for fixed = TRUE) to be matched in the given raw vector. Coerced by charToRaw to a character string if possible.
- x: a raw vector where matches are sought, or an object which can be coerced by charToRaw to a raw vector. Long vectors are not supported.
- ignore.case: if FALSE, the pattern matching is case sensitive and if TRUE, case is ignored during matching.
- offset: An integer specifying the offset from which the search should start. Must be positive. The beginning of line is defined to be at that offset so "^" will match there.
- value: logical. Determines the return value: see 'Value'.
- fixed: logical. If TRUE, pattern is a pattern to be matched as is.
- all: logical. If TRUE all matches are returned, otherwise just the first one.
- invert: logical. If TRUE return indices or values for elements that do not match. Ignored (with a warning) unless value = TRUE.
Details

Unlike grep, seeks matching patterns within the raw vector x. This has implications especially in the all = TRUE case, e.g., patterns matching empty strings are inherently infinite and thus may lead to unexpected results.

The argument invert is interpreted as asking to return the complement of the match, which is only meaningful for value = TRUE. Argument offset determines the start of the search, not of the complement. Note that invert = TRUE with all = TRUE will split x into pieces delimited by the pattern including leading and trailing empty strings (consequently the use of regular expressions with "^" or "$" in that case may lead to less intuitive results).

Some combinations of arguments such as fixed = TRUE with value = TRUE are supported but are less meaningful.

Value

grepRaw(value = FALSE) returns an integer vector of the offsets at which matches have occurred. If all = FALSE then it will be either of length zero (no match) or length one (first matching position).

grepRaw(value = TRUE, all = FALSE) returns a raw vector which is either empty (no match) or the matched part of x.

grepRaw(value = TRUE, all = TRUE) returns a (potentially empty) list of raw vectors corresponding to the matched parts.

Source

The TRE library of Ville Laurikari (https://github.com/laurikari/tre/) is used except for fixed = TRUE.

See Also

regular expression (aka regexp) for the details of the pattern specification.

grep for matching character vectors.

Examples

grepRaw("no match", "textText")  # integer(0): no match
grepRaw("adf", "adadfadfadayf")  # 3 - the first match
grepRaw("adf", "adadfadfadayf", all=TRUE, fixed=TRUE)
## [1] 3 6 13 -- three matches

Description

Group generic methods can be defined for the following pre-specified groups of functions, Math, Ops, matrixOps, Summary and Complex. (There are no objects of these names in base R, but there are in the methods package, not yet for matrixOps.)

A method defined for an individual member of the group takes precedence over a method defined for the group as a whole.
Usage

## S3 methods for group generics have prototypes:
Math(x, ...)
Ops(e1, e2)
Complex(z)
Summary(..., na.rm = FALSE)
matrixOps(x, y)

Arguments

x, y, z, e1, e2  objects.
...
...  further arguments passed to methods.
na.rm  logical: should missing values be removed?

Details

There are five groups for which S3 methods can be written, namely the "Math", "Ops", "Summary", "matrixOps", and "Complex" groups. These are not R objects in base R, but methods can be supplied for them and base R contains factor, data.frame and difftime methods for the first three groups. (There is also a ordered method for Ops, POSIXt and Date methods for Math and Ops, package_version methods for Ops and Summary, as well as a ts method for Ops in package stats.)

1. Group "Math":
   - abs, sign, sqrt,
   - floor, ceiling, trunc,
   - round, signif
   - exp, log, expm1, log1p,
   - cos, sin, tan,
   - cospi, sinpi, tanpi,
   - acos, asin, atan
   - cosh, sinh, tanh,
   - acosh, asinh, atanh
   - lgamma, gamma, digamma, trigamma
   - cumsum, cumprod, cummax, cummin

Members of this group dispatch on x. Most members accept only one argument, but members log, round and signif accept one or two arguments, and trunc accepts one or more.

2. Group "Ops":
   - "+", "-", "*", "/", "+%", "+%-%", "+%/%
   - "+&", "+|", "+!"
   - "==", "!=", "\<\", "\<\="

This group contains both binary and unary operators (+, - and !): when a unary operator is encountered the Ops method is called with one argument and e2 is missing.

The classes of both arguments are considered in dispatching any member of this group. For each argument its vector of classes is examined to see if there is a matching specific (preferred) or Ops method. If a method is found for just one argument or the same method is found for both, it is used. If different methods are found, then the generic chooseOpsMethod() is called to pick the appropriate method. (See chooseOpsMethod for details). If chooseOpsMethod() does not resolve the method, then there is a warning about ‘incompatible methods’: in that case or if no method is found for either argument the internal method is used.
Note that the `data.frame` methods for the comparison ("Compare": ==, <, ...) and logic ("Logic": & | and !) operators return a logical `matrix` instead of a `data.frame`, for convenience and back compatibility.

If the members of this group are called as functions, any argument names are removed to ensure that positional matching is always used.

3. Group "matrixOps":
   • `%*%`
   This group currently contains the matrix multiply `%*%` binary operator only, where at least `crossprod()` and `tcrossprod()` are meant to follow. Members of the group have the same dispatch semantics (using both arguments) as the `Ops` group.

4. Group "Summary":
   • all, any
   • sum, prod
   • min, max
   • range
   Members of this group dispatch on the first argument supplied.

   Note that the `data.frame` methods for the "Summary" and "Math" groups require "numeric-alike" columns \( x \), i.e., fulfilling

   \[ \text{is.numeric}(x) \text{ || is.logical}(x) \text{ || is.complex}(x) \]

5. Group "Complex":
   • Arg, Conj, Im, Mod, Re
   Members of this group dispatch on \( z \).

   Note that a method will be used for one of these groups or one of its members only if it corresponds to a "class" attribute, as the internal code dispatches on `oldClass` and not on `class`. This is for efficiency: having to dispatch on, say, `Ops.integer` would be too slow.

   The number of arguments supplied for primitive members of the "Math" group generic methods is not checked prior to dispatch.

   There is no lazy evaluation of arguments for group-generic functions.

**Technical Details**

These functions are all primitive and internal generic.

The details of method dispatch and variables such as `.Generic` are discussed in the help for `UseMethod`. There are a few small differences:

- For the operators of group `Ops`, the object `.Method` is a length-two character vector with elements the methods selected for the left and right arguments respectively. (If no method was selected, the corresponding element is "").
- Object `.Group` records the group used for dispatch (if a specific method is used this is ")").

**Note**

Package `methods` does contain objects with these names, which it has re-used in confusing similar (but different) ways. See the help for that package.

**References**

Appendix A, *Classes and Methods* of
See Also

methods for methods of non-internal generic functions.
S4groupGeneric for group generics for S4 methods.

Examples

require(utils)
d.fr <- data.frame(x = 1:9, y = stats::rnorm(9))
class(1 + d.fr) == "data.frame" #-- add to d.f. ...

methods("Math")
methods("Ops")
methods("Summary")
methods("Complex")  # none in base R

<table>
<thead>
<tr>
<th>grouping</th>
<th>Grouping Permutation</th>
</tr>
</thead>
</table>

Description

grouping returns a permutation which rearranges its first argument such that identical values are adjacent to each other. Also returned as attributes are the group-wise partitioning and the maximum group size.

Usage

grouping(...)

Arguments

...  a sequence of numeric, character or logical vectors, all of the same length, or a classed R object.

Details

The function partially sorts the elements so that identical values are adjacent. NA values come last. This is guaranteed to be stable, so ties are preserved, and if the data are already grouped/sorted, the grouping is unchanged. This is useful for aggregation and is particularly fast for character vectors.

Under the covers, the "radix" method of order is used, and the same caveats apply, including restrictions on character encodings and lack of support for long vectors (those with $2^{31}$ or more elements). Real-valued numbers are slightly rounded to account for numerical imprecision.

Like order, for a classed R object the grouping is based on the result of xtfrm.

Value

An object of class "grouping", the representation of which should be considered experimental and subject to change. It is an integer vector with two attributes:

ends  subscripts in the result corresponding to the last member of each group
maxgrpn  the maximum group size
gzcon

See Also

order, xtfrm.

Examples

(ii <- grouping(x <- c(1, 1, 3:1, 1:4, 3), y <- c(9, 9:1), z <- c(2, 1:9)))
## 6 5 2 1 7 4 10 8 3 9
rbind(x, y, z)[, ii]

Description

gzcon provides a modified connection that wraps an existing connection, and decompresses reads or compresses writes through that connection. Standard gzip headers are assumed.

Usage

gzcon(con, level = 6, allowNonCompressed = TRUE, text = FALSE)

Arguments

con a connection.
level integer between 0 and 9, the compression level when writing.
allowNonCompressed logical. When reading, should non-compressed input be allowed?
text logical. Should the connection be text-oriented? This is distinct from the mode of the connection (must always be binary). If TRUE, pushBack works on the connection, otherwise readBin and friends apply.

Details

If con is open then the modified connection is opened. Closing the wrapper connection will also close the underlying connection.

Reading from a connection which does not supply a gzip magic header is equivalent to reading from the original connection if allowNonCompressed is true, otherwise an error.

Compressed output will contain embedded NUL bytes, and so con is not permitted to be a textConnection opened with open = "w". Use a writable rawConnection to compress data into a variable.

The original connection becomes unusable: any object pointing to it will now refer to the modified connection. For this reason, the new connection needs to be closed explicitly.

Value

An object inheriting from class "connection". This is the same connection number as supplied, but with a modified internal structure. It has binary mode.

See Also

gzfile
Examples

```r
## Uncompress a data file from a URL
z <- gzcon(url("https://www.stats.ox.ac.uk/pub/datasets/csb/ch12.dat.gz"))
# read.table can only read from a text-mode connection.
raw <- textConnection(readLines(z))
close(z)
dat <- read.table(raw)
close(raw)
dat[1:4, ]
```

```r
## gzfile and gzcon can inter-work.
## Of course here one would use gzfile, but file() can be replaced by
## any other connection generator.
zzfil <- tempfile(fileext = ".gz")
zz <- gzfile(zzfil, "w")
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzcon(file(zzfil, "rb")))
close(zz)
unlink(zzfil)

zzfil2 <- tempfile(fileext = ".gz")
zz <- gzcon(file(zzfil2, "wb"))
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzfile(zzfil2))
close(zz)
unlink(zzfil2)
```

---

### Integer Numbers Displayed in Hexadecimal

**Description**

Integers which are displayed in hexadecimal (short ‘hex’) format, with as many digits as are needed to display the largest, using leading zeroes as necessary.

Arithmetic works as for integers, and non-integer valued mathematical functions typically work by truncating the result to integer.

**Usage**

```r
as.hexmode(x)
```

```r
## S3 method for class 'hexmode'
as.character(x, keepStr = FALSE, ...)
```

```r
## S3 method for class 'hexmode'
format(x, width = NULL, upper.case = FALSE, ...)
```

```r
## S3 method for class 'hexmode'
print(x, ...)
```
hexmode

Arguments

- **x** an object, for the methods inheriting from class "hexmode".
- **keepStr** a logical indicating that names and dimensions should be kept; set TRUE for back compatibility, if needed.
- **width** NULL or a positive integer specifying the minimum field width to be used, with padding by leading zeroes.
- **upper.case** a logical indicating whether to use upper-case letters or lower-case letters (default).
- ... further arguments passed to or from other methods.

Details

Class "hexmode" consists of integer vectors with that class attribute, used primarily to ensure that they are printed in hex. Subsetting ([) works too, as do arithmetic or other mathematical operations, albeit truncated to integer.

`as.character(x)` drops all attributes (unless when keepStr=TRUE where it keeps, dim, dimnames and names for back compatibility) and converts each entry individually, hence with no leading zeroes, whereas in `format()`, when width = NULL (the default), the output is padded with leading zeroes to the smallest width needed for all the non-missing elements.

`as.hexmode` can convert integers (of type "integer" or "double") and character vectors whose elements contain only 0-9, a-f, A-F (or are NA) to class "hexmode".

There is a ! method and methods for | and &:
these recycle their arguments to the length of the longer and then apply the operators bitwise to each element.

See Also

`octmode`, `sprintf` for other options in converting integers to hex, `strtoi` to convert hex strings to integers.

Examples

```r
i <- as.hexmode("7fffffff")
i; class(i)
identical(as.integer(i), .Machine$integer.max)

hm <- as.hexmode(c(NA, 1)); hm
as.integer(hm)

Xm <- as.hexmode(1:16)
Xm # print()s via format()
stopifnot(nchar(format(Xm)) == 2)
Xm[-16] # *no* leading zeroes!
stopifnot(format(Xm[-16]) == c(1:9, letters[1:6]))

## Integer arithmetic (remaining "hexmode"):
16*Xm
Xm^2
-Xm
(fac <- factorial(Xm[1:12])) # !1, !2, !3, !4 .. in hexadecimals
as.integer(fac) # indeed the same as factorial(1:12)
```
Description

These functions give the obvious hyperbolic functions. They respectively compute the hyperbolic cosine, sine, tangent, and their inverses, arc-cosine, arc-sine, arc-tangent (or ‘area cosine’, etc).

Usage

cosh(x)  
sinh(x)  
tanh(x)  
acosh(x) 
asinh(x)  
atanh(x)

Arguments

x         a numeric or complex vector

Details

These are internal generic primitive functions: methods can be defined for them individually or via the Math group generic.

Branch cuts are consistent with the inverse trigonometric functions as in et seq, and agree with those defined in Abramowitz and Stegun, figure 4.7, page 86. The behaviour actually on the cuts follows the C99 standard which requires continuity coming round the endpoint in a counter-clockwise direction.

S4 methods

All are S4 generic functions: methods can be defined for them individually or via the Math group generic.

References


See Also

The trigonometric functions, cos, sin, tan, and their inverses acos, asin, atan.

The logistic distribution function plogis is a shifted version of tanh() for numeric x.
iconv

iconv

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Convert Character Vector between Encodings

Description
This uses system facilities to convert a character vector between encodings: the ‘i’ stands for ‘internationalization’.
Usage
iconv(x, from = "", to = "", sub = NA, mark = TRUE, toRaw = FALSE)
iconvlist()
Arguments
x

a character vector, or an object to be converted to a character vector
by as.character, or a list with NULL and raw elements as returned by
iconv(toRaw = TRUE).

from

a character string describing the current encoding.

to

a character string describing the target encoding.

sub

character string. If not NA it is used to replace any non-convertible bytes in the input. (This would normally be a single character, but can be more.) If "byte", the
indication is "<xx>" with the hex code of the byte. If "Unicode" and converting
from UTF-8, the Unicode point in the form "<U+xxxx>", or if c99, a C99-style
escape "\uxxxx". (For points in a ‘supplementary plane’, "<U+xxxxxxxx>" or
"\Uxxxxxxxx" is used.)

mark

logical, for expert use. Should encodings be marked?

toRaw

logical. Should a list of raw vectors be returned rather than a character vector?

Details
The names of encodings and which ones are available are platform-dependent. All R platforms
support "" (for the encoding of the current locale), "latin1" and "UTF-8". Generally case is
ignored when specifying an encoding.
On most platforms iconvlist provides an alphabetical list of the supported encodings. On others,
the information is on the man page for iconv(5) or elsewhere in the man pages (but beware that
the system command iconv may not support the same set of encodings as the C functions R calls).
Unfortunately, the names are rarely supported across all platforms.
Elements of x which cannot be converted (perhaps because they are invalid or because they cannot
be represented in the target encoding) will be returned as NA (or NULL for toRaw = TRUE) unless sub
is specified.
Most versions of iconv will allow transliteration by appending ‘//TRANSLIT’ to the to encoding:
see the examples.
Encoding "ASCII" is accepted, and on most systems "C" and "POSIX" are synonyms for ASCII.
Where "ASCII/TRANSLIT" is unsupported by the OS, "ASCII" is used with sub = "c99" if from
UTF-8, else sub = "?". (However, musl’s version of "ASCII" substitutes *.)


Elements of `x` with a declared encoding (UTF-8 or latin1, see Encoding) are converted from that encoding if `from` = "", otherwise they are taken as being in the encoding specified by `from`.

Note that implementations of `iconv` typically do not do much validity checking and will often mis-convert inputs which are invalid in encoding `from`.

If `sub = "Unicode"` or `sub = "c99"` is used for a non-UTF-8 input it is the same as `sub = "byte"`.

**Value**

If `toRaw = FALSE` (the default), the value is a character vector of the same length and the same attributes as `x` (after conversion to a character vector). If conversion fails for an element that element of the result is set to `NA_character_` (NB: whether conversion fails is implementation-specific.) `NA_character_` inputs give `NA_character_` outputs.

If `mark = TRUE` (the default) the elements of the result have a declared encoding if `to` is "latin1" or "UTF-8", or if `to = ""` and the current locale’s encoding is detected as Latin-1 (or its superset CP1252 on Windows) or UTF-8.

If `toRaw = TRUE`, the value is a list of the same length and the same attributes as `x` whose elements are either `NULL` (if conversion fails or the input was `NA_character_`) or a raw vector.

For `iconvlist()`, a character vector (typically of a few hundred elements) of known encoding names.

**Implementation Details**

There are three main implementations of `iconv` in use. Linux’s most common C runtime, ‘glibc’, contains one. Several platforms supply versions or emulations of GNU ‘libiconv’, including previous versions of macOS and FreeBSD, in some cases with additional encodings. On Windows we use a version of Yukihiro Nakadaira’s ‘win_iconv’, which is based on Windows’ codepages. (We have added many encoding names for compatibility with other systems.) All three have `iconvlist`, ignore case in encoding names and support ‘//TRANSLIT’ (but with different results, and for ‘win_iconv’ currently a ‘best fit’ strategy is used except for `to = "ASCII"`).

The macOS 14 implementation is attributed to the ‘Citrus Project’: the Apple headers declare it as ‘compatible’ with GNU ‘libiconv’ 1.11 from 2006. However, it differs in significant ways including using transliteration for conversions which cannot be represented exactly in the target encoding. (It seems this implementation is also used in recent versions of FreeBSD. Earlier versions of macOS used GNU ‘libiconv’ 1.11 and some CRAN builds still do.) For a failing conversion macOS 14 generally translated character(s) to ? but 14.1 gives an error (so an NA result in R).

Most commercial Unixes contain an implementation of `iconv` but none we have encountered have supported the encoding names we need: the ‘R Installation and Administration’ manual recommended installing GNU ‘libiconv’ on Solaris and AIX.

Some Linux distributions use ‘musl’ as their C runtime. This is less comprehensive than ‘glibc’: it does not support ‘//TRANSLIT’ but does inexact conversions (currently using ‘*’). There are other implementations, e.g. NetBSD has used one from the Citrus project (which does not support ‘//TRANSLIT’) and there is an older FreeBSD port.

Note that you cannot rely on invalid inputs being detected, especially for `to = "ASCII"` where some implementations allow 8-bit characters and pass them through unchanged or with transliteration or substitution.

Some of the implementations have interesting extra encodings: for example GNU ‘libiconv’ and macOS 14 allow `to = "C99"` to use ‘\uxxxx’ escapes (or if needed ‘\uxxxxxxxxx’ for non-ASCII characters.)
**Byte Order Marks**

most commonly known as ‘BOMs’.

Encodings using character units which are more than one byte in size can be written on a file in either big-endian or little-endian order: this applies most commonly to UCS-2, UTF-16 and UTF-32/UCS-4 encodings. Some systems will write the Unicode character U+FEFF at the beginning of a file in these encodings and perhaps also in UTF-8. In that usage the character is known as a BOM, and should be handled during input (see the ‘Encodings’ section under connection: re-encoded connections have some special handling of BOMs). The rest of this section applies when this has not been done so x starts with a BOM.

Implementations will generally interpret a BOM for from given as one of “UCS-2”, “UTF-16” and “UTF-32”. Implementations differ in how they treat BOMs in x in other from encodings: they may be discarded, returned as character U+FEFF or regarded as invalid.

**Note**

The most portable name for the ISO 8859-15 encoding, commonly known as ‘Latin 9’, is “iso885915”: most platforms support both “latin-9” and “latin9” but GNU ‘libiconv’ does not support the latter. ‘musl’ (as used by Alpine Linux) supports neither.

Encoding names "utf8", "mac" and "macroman" are not portable. "utf8" is converted to “UTF-8” for from and to by iconv, but not for e.g. fileEncoding arguments. "macintosh" is the official (and most widely supported) name for ‘Mac Roman’ ([https://en.wikipedia.org/wiki/Mac_OS_Roman](https://en.wikipedia.org/wiki/Mac_OS_Roman)).

Using sub substitutes each non-convertible byte in the input, so when converting from UTF-8 a non-convertible character may be replaced by two or more bytes. Using sub = "c99" or sub = "Unicode" will be clearer.

**See Also**

localeToCharset, file.

**Examples**

```r
## In principle, as not all systems have iconvlist
try(utils::head(iconvlist(), n = 50))

## Not run:
## convert from Latin-2 to UTF-8: two of the glibc iconv variants.
iconv(x, "ISO_8859-2", "UTF-8")
iconv(x, "LATIN2", "UTF-8")

## End(Not run)

## Both x below are in latin1 and will only display correctly in a
## locale that can represent and display latin1.
x <- "fran\x7ais"
Encoding(x) <- "latin1"
x
charToRaw(xx <- iconv(x, "latin1", "UTF-8"))
xx

## The results in the comments are those from glibc and GNU libiconv
iconv(x, "latin1", "ASCII") # NA
iconv(x, "latin1", "ASCII", "?") # "fran?ais"
```
icuSetCollate

Description

Controls the way collation is done by ICU (an optional part of the R build).

Usage

icuSetCollate(...)

icuGetCollate(type = c("actual", "valid"))

Arguments

... Named arguments, see ‘Details’.

type character string: can be abbreviated. Either the actual locale in use for collation or the most specific locale which would be valid.

Details

Optionally, R can be built to collate character strings by ICU (https://icu.unicode.org/). For such systems, icuSetCollate can be used to tune the way collation is done. On other builds calling this function does nothing, with a warning.

Possible arguments are

locale: A character string such as “da DK” giving the language and country whose collation rules are to be used. If present, this should be the first argument.

case_first: "upper", "lower" or "default", asking for upper- or lower-case characters to be sorted first. The default is usually lower-case first, but not in all languages (not under the default settings for Danish, for example).

alternate_handling: Controls the handling of ‘variable’ characters (mainly punctuation and symbols). Possible values are "non_ignorable" (primary strength) and "shifted" (quaternary strength).
strength: Which components should be used? Possible values "primary", "secondary", "tertiary" (default), "quaternary" and "identical".

french_collation: In a French locale the way accents affect collation is from right to left, whereas in most other locales it is from left to right. Possible values "on", "off" and "default".

normalization: Should strings be normalized? Possible values are "on" and "off" (default). This affects the collation of composite characters.

case_level: An additional level between secondary and tertiary, used to distinguish large and small Japanese Kana characters. Possible values "on" and "off" (default).

hiragana_quaternary: Possible values "on" (sort Hiragana first at quaternary level) and "off".

Only the first three are likely to be of interest except to those with a detailed understanding of collation and specialized requirements.

Some special values are accepted for locale:

"none": ICU is not used for collation: the OS’s collation services are used instead.

"ASCII": ICU is not used for collation: the C function strcmp is used instead, which should sort byte-by-byte in (unsigned) numerical order.

"default": obtains the locale from the OS as is done at the start of the session (except on Windows). If environment variable R_ICU_LOCALE is set to a non-empty value, its value is used rather than consulting the OS, unless environment variable LC_ALL is set to 'C' (or unset but LC_COLLATE is set to 'C').

"", "root": the ‘root’ collation: see https://www.unicode.org/reports/tr35/tr35-collation.html#Root_Collation.

For the specifications of ‘real’ ICU locales, see https://unicode-org.github.io/icu/userguide/locale/. Note that ICU does not report that a locale is not supported, but falls back to its idea of ‘best fit’ (which could be rather different and is reported by icuGetCollate("actual"), often "root"). Most English locales fall back to "root" as although e.g. "en_GB" is a valid locale (at least on some platforms), it contains no special rules for collation. Note that "C" is not a supported ICU locale and hence R_ICU_LOCALE should never be set to "C".

Some examples are case_level = "on", strength = "primary" to ignore accent differences and alternate_handling = "shifted" to ignore space and punctuation characters.

Initially ICU will not be used for collation if the OS is set to use the C locale for collation and R_ICU_LOCALE is not set. Once this function is called with a value for locale, ICU will be used until it is called again with locale = "none". ICU will not be used once Sys.setlocale is called with a "C" value for LC_ALL or LC_COLLATE, even if R_ICU_LOCALE is set. ICU will be used again honoring R_ICU_LOCALE once Sys.setlocale is called to set a different collation order. Environment variables LC_ALL (or LC_COLLATE) take precedence over R_ICU_LOCALE if and only if they are set to 'C'. Due to the interaction with other ways of setting the collation order, R_ICU_LOCALE should be used with care and only when needed.

All customizations are reset to the default for the locale if locale is specified: the collation engine is reset if the OS collation locate category is changed by Sys.setlocale.

Value

For icuGetCollate, a character string describing the ICU locale in use (which may be reported as "ICU not in use"). The ‘actual’ locale may be simpler than the requested locale: for example “da” rather than "da_DK": English locales are likely to report "root".
Note

Except on Windows, ICU is used by default wherever it is available. As it works internally in UTF-8, it will be most efficient in UTF-8 locales.

On Windows, R is normally built including ICU, but it will only be used if environment variable R_ICU_LOCALE had been set when R is started or after icuSetCollate is called to select the locale (as ICU and Windows differ in their idea of locale names). Note that icuSetCollate(locale = "default") should work reasonably well, but finds the system default ignoring environment variables such as LC_COLLATE.

See Also

Comparison, sort.

capabilities for whether ICU is available; extSoftVersion for its version.

The ICU user guide chapter on collation (https://unicode-org.github.io/icu/userguide/collation/).

Examples

## These examples depend on having ICU available, and on the locale.
## As we don’t know the current settings, we can only reset to the default.
if(capabilities("ICU")) withAutoprint({
  icuGetCollate()
  icuGetCollate("valid")
  x <- c("Aarhus", "aarhus", "safe", "test", "Zoo")
  sort(x)
  icuSetCollate(case_first = "upper"); sort(x)
  icuSetCollate(case_first = "lower"); sort(x)

  ## Danish collates upper-case-first and with 'aa' as a single letter
  icuSetCollate(locale = "da_DK", case_first = "default"); sort(x)
  ## Estonian collates Z between S and T
  icuSetCollate(locale = "et_EE"); sort(x)
  icuSetCollate(locale = "default"); icuGetCollate("valid")
})

identical  Test Objects for Exact Equality

Description

The safe and reliable way to test two objects for being exactly equal. It returns TRUE in this case, FALSE in every other case.

Usage

`identical(x, y, num.eq = TRUE, single.NA = TRUE, attrib.as.set = TRUE,
        ignore.bytecode = TRUE, ignore.environment = FALSE,
        ignore.srcref = TRUE, extptr.as.ref = FALSE)`
**Arguments**

- **x, y**: any R objects.
- **num.eq**: logical indicating if (double and complex non-NA) numbers should be compared using `==` ('equal'), or by bitwise comparison. The latter (non-default) differentiates between -0 and +0.
- **single.NA**: logical indicating if there is conceptually just one numeric NA and one NaN; `single.NA = FALSE` differentiates bit patterns.
- **attrib.as.set**: logical indicating if attributes of x and y should be treated as unordered tagged pairlists ("sets"); this currently also applies to slots of S4 objects. It may well be too strict to set `attrib.as.set = FALSE`.
- **ignore.bytecode**: logical indicating if byte code should be ignored when comparing closures.
- **ignore.environment**: logical indicating if their environments should be ignored when comparing closures.
- **ignore.srcref**: logical indicating if their "srcref" attributes should be ignored when comparing closures.
- **extptr.as.ref**: logical indicating whether external pointer objects should be compared as reference objects and considered identical only if they are the same object in memory. By default, external pointers are considered identical if the addresses they contain are identical.

**Details**

A call to `identical` is the way to test exact equality in `if` and `while` statements, as well as in logical expressions that use `&&` or `||`. In all these applications you need to be assured of getting a single logical value.

Users often use the comparison operators, such as `==` or `!=`, in these situations. It looks natural, but it is not what these operators are designed to do in R. They return an object like the arguments. If you expected x and y to be of length 1, but it happened that one of them was not, you will not get a single `FALSE`. Similarly, if one of the arguments is NA, the result is also NA. In either case, the expression `if(x == y)....` won’t work as expected.

The function `all.equal` is also sometimes used to test equality this way, but was intended for something different: it allows for small differences in numeric results. The computations in `identical` are also reliable and usually fast. There should never be an error. The only known way to kill `identical` is by having an invalid pointer at the C level, generating a memory fault. It will usually find inequality quickly. Checking equality for two large, complicated objects can take longer if the objects are identical or nearly so, but represent completely independent copies. For most applications, however, the computational cost should be negligible.

If `single.NA` is true, as by default, `identical` sees NaN as different from `NA_real_`, but all NaNs are equal (and all NA of the same type are equal).

Character strings (except those in marked encoding "bytes") are regarded as identical even if they are in different marked encodings but would agree when translated to UTF-8. A character string in marked encoding "bytes" is only regarded as identical to a character string in the same encoding and with the same content.

If `attrib.as.set` is true, as by default, comparison of attributes view them as a set (and not a vector, so order is not tested).
If `ignore.bytecode` is true (the default), the compiled bytecode of a function (see `cmpfun`) will be ignored in the comparison. If it is false, functions will compare equal only if they are copies of the same compiled object (or both are uncompiled). To check whether two different compiles are equal, you should compare the results of `disassemble()`.

You almost never want to use `identical` on datetimes of class "POSIXlt": not only can different times in the different time zones represent the same time and time zones have multiple names, but several of the components are optional.

Note that the strictest test for equality is

```r
identical(x, y,
num.eq = FALSE, single.NA = FALSE, attrib.as.set = FALSE,
ignore.bytecode = FALSE, ignore.environment = FALSE,
ignore.srcref = FALSE, extptr.as.ref = TRUE)
```

**Value**

A single logical value, TRUE or FALSE, never NA and never anything other than a single value.

**Author(s)**

John Chambers and R Core

**References**


**See Also**

`all.equal` for descriptions of how two objects differ; `Comparison` and `Logic` for elementwise comparisons.

**Examples**

```r
identical(1, NULL)  ## FALSE -- don't try this with ==
identical(1, 1.)     ## TRUE in R (both are stored as doubles)
identical(1, as.integer(1))  ## FALSE, stored as different types

x <- 1.0; y <- 0.99999999999
## how to test for object equality allowing for numeric fuzz :
(E <- all.equal(x, y))
identical(TRUE, E)
isTRUE(E) # alternative test
## If all.equal thinks the objects are different, it returns a
## character string, and the above expression evaluates to FALSE

## even for unusual R objects :
identical(.GlobalEnv, environment())

### ------- Pickyness Flags : -----------------------------

## the infamous example:
identical(0., -0.)  # TRUE, i.e. not differentiated
identical(0., -0., num.eq = FALSE)
## similar:
identical(NaN, -NaN) # TRUE
```
identical(NaN, -NaN, single.NA = FALSE) # differ on bit-level

### For functions ("closure"s): ----------------------------------------------
### ~~~~~~~~~
f <- function(x) x
g <- compiler::cmpfun(f)
identical(f, g) # TRUE, as bytecode is ignored by default
identical(f, g, ignore.bytecode=FALSE) # FALSE: bytecode differs

## GLM families contain several functions, some of which share an environment:
p1 <- poisson(); p2 <- poisson()
identical(p1, p2) # FALSE
identical(p1, p2, ignore.environment=TRUE) # TRUE

## in interactive use, the 'keep.source' option is typically true:
op <- options(keep.source = TRUE) # and so, these have differing "srcref":
f1 <- function() {}
f2 <- function() {}
identical(f1,f2)# ignore.srcref= TRUE : TRUE
identical(f1,f2, ignore.srcref=FALSE)# FALSE
options(op) # revert to previous state

---

### identity

Identity Function

**Description**

A trivial identity function returning its argument.

**Usage**

`identity(x)`

**Arguments**

- `x` an R object.

**See Also**

`diag` creates diagonal matrices, including identity ones.
ifelse  

Conditional Element Selection

Description

ifelse returns a value with the same shape as test which is filled with elements selected from either yes or no depending on whether the element of test is TRUE or FALSE.

Usage

ifelse(test, yes, no)

Arguments

test  
an object which can be coerced to logical mode.

yes  
return values for true elements of test.

no  
return values for false elements of test.

Details

If yes or no are too short, their elements are recycled. yes will be evaluated if and only if any element of test is true, and analogously for no.

Missing values in test give missing values in the result.

Value

A vector of the same length and attributes (including dimensions and "class") as test and data values from the values of yes or no. The mode of the answer will be coerced from logical to accommodate first any values taken from yes and then any values taken from no.

Warning

The mode of the result may depend on the value of test (see the examples), and the class attribute (see oldClass) of the result is taken from test and may be inappropriate for the values selected from yes and no.

Sometimes it is better to use a construction such as

(tmp <- yes; tmp[!test] <- no[!test]; tmp)

, possibly extended to handle missing values in test.

Further note that if(test) yes else no is much more efficient and often much preferable to ifelse(test, yes, no) whenever test is a simple true/false result, i.e., when length(test) == 1.

The srcref attribute of functions is handled specially: if test is a simple true result and yes evaluates to a function with srcref attribute, ifelse returns yes including its attribute (the same applies to a false test and no argument). This functionality is only for backwards compatibility, the form if(test) yes else no should be used whenever yes and no are functions.
integer

References


See Also

if.

Examples

```r
x <- c(6:-4)
sqrt(x) # gives warning
sqrt(ifelse(x >= 0, x, NA)) # no warning

## Note: the following also gives the warning!
ifelse(x >= 0, sqrt(x), NA)

## ifelse() strips attributes
## This is important when working with Dates and factors
x <- seq(as.Date("2000-02-29"), as.Date("2004-10-04"), by = "1 month")
## has many "yyyy-mm-29", but a few "yyyy-03-01" in the non-leap years
y <- ifelse(as.POSIXlt(x)$mday == 29, x, NA)
head(y) # not what you expected ... ==> need restore the class attribute:
class(y) <- class(x)
y
## This is a (not atypical) case where it is better *not* to use ifelse(),
## but rather the more efficient and still clear:

y2 <- x
y2[as.POSIXlt(x)$mday != 29] <- NA
## which gives the same as ifelse()+class() hack:
stopifnot(identical(y2, y))

## example of different return modes (and 'test' alone determining length):
yes <- 1:3
no <- pi^c(1:4)
utils::str( ifelse(NA, yes, no) ) # logical, length 1
utils::str( ifelse(TRUE, yes, no) ) # integer, length 1
utils::str( ifelse(FALSE, yes, no) ) # double, length 1
```

---

### integer

**Integer Vectors**

**Description**

Creates or tests for objects of type "integer".

**Usage**

```r
integer(length = 0)
as.integer(x, ...)
is.integer(x)
```
Arguments

- **length**: A non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
- **x**: object to be coerced or tested.
- **...**: further arguments passed to or from other methods.

Details

Integer vectors exist so that data can be passed to C or Fortran code which expects them, and so that (small) integer data can be represented exactly and compactly.

Note that current implementations of R use 32-bit integers for integer vectors, so the range of representable integers is restricted to about $\pm 2 \times 10^9$: doubles can hold much larger integers exactly.

Value

- `integer` creates a integer vector of the specified length. Each element of the vector is equal to 0.
- `as.integer` attempts to coerce its argument to be of integer type. The answer will be `NA` unless the coercion succeeds. Real values larger in modulus than the largest integer are coerced to `NA` (unlike S which gives the most extreme integer of the same sign). Non-integral numeric values are truncated towards zero (i.e., `as.integer(x)` equals `trunc(x)` there), and imaginary parts of complex numbers are discarded (with a warning). Character strings containing optional whitespace followed by either a decimal representation or a hexadecimal representation (starting with `0x` or `0X`) can be converted, as well as any allowed by the platform for real numbers. Like `as.vector` it strips attributes including names. (To ensure that an object `x` is of integer type without stripping attributes, use `storage.mode(x) <- "integer"`.)
- `is.integer` returns `TRUE` or `FALSE` depending on whether its argument is of integer type or not, unless it is a factor when it returns `FALSE`.

Note

- `is.integer(x)` does **not** test if `x` contains integer numbers! For that, use `round`, as in the function `is.wholenumber(x)` in the examples.

References


See Also

- `numeric`, `storage.mode`.
- `round` (and ceiling and floor on that help page) to convert to integral values.

Examples

```r
## as.integer() truncates:
x <- pi * c(-1:1, 10)
as.integer(x)

is.integer(1) # is FALSE !
```
interaction <-
  function(x, tol = .Machine$double.eps^0.5) abs(x - round(x)) < tol
is.wholenumber(1) # is TRUE
(x <- seq(1, 5, by = 0.5))
is.wholenumber(x) #---> TRUE FALSE TRUE ...

---

<table>
<thead>
<tr>
<th>interaction</th>
<th>Compute Factor Interactions</th>
</tr>
</thead>
</table>

**Description**

interaction computes a factor which represents the interaction of the given factors. The result of interaction is always unordered.

**Usage**

interaction(..., drop = FALSE, sep = ".", lex.order = FALSE)

**Arguments**

- **...** the factors for which interaction is to be computed, or a single list giving those factors.
- **drop** if drop is TRUE, unused factor levels are dropped from the result. The default is to retain all factor levels.
- **sep** string to construct the new level labels by joining the constituent ones.
- **lex.order** logical indicating if the order of factor concatenation should be lexically ordered.

**Value**

A factor which represents the interaction of the given factors. The levels are labelled as the levels of the individual factors joined by sep which is . by default.

By default, when lex.order = FALSE, the levels are ordered so the level of the first factor varies fastest, then the second and so on. This is the reverse of lexicographic ordering (which you can get by lex.order = TRUE), and differs from ::. (It is done this way for compatibility with S.)

**References**


**See Also**

factor; :: where f:g is similar to interaction(f, g, sep = ":\)
where f and g are factors.
Examples

```r
a <- gl(2, 4, 8)
b <- gl(2, 2, 8, labels = c("ctrl", "treat"))
s <- gl(2, 1, 8, labels = c("M", "F"))
interaction(a, b)
interaction(a, b, s, sep = ":")
stopifnot(identical(a:s, interaction(a, s, sep = ":", lex.order = TRUE)),
          identical(a:s:b, interaction(a, s, b, sep = ":", lex.order = TRUE)))
```
Description

.Internal performs a call to an internal code which is built in to the R interpreter.
Only true R wizards should even consider using this function, and only R developers can add to the list of internal functions.

Usage

.Internal(call)

Arguments

call a call expression

See Also

.Primitive, .External (the nearest equivalent available to users).

InternalMethods

Internal Generic Functions

Description

Many R-internal functions are generic and allow methods to be written for.

Details

The following primitive and internal functions are generic, i.e., you can write methods for them:

[.
\[.\]
$.
[<-.
\[[<-.
\[[<-.
$<-.
length.
length<-.
lengths,
In addition, \texttt{is.name} is a synonym for \texttt{is.symbol} and dispatches methods for the latter. Similarly, \texttt{as.numeric} is a synonym for \texttt{as.double} and dispatches methods for the latter, i.e., S3 methods are for \texttt{as.double}, whereas S4 methods are to be written for \texttt{as.numeric}.

Note that all of the \texttt{group generic} functions are also internal/primitive and allow methods to be written for them.
invisible

.S3PrimitiveGenerics is a character vector listing the primitives which are internal generic and not group generic. Currently \texttt{as.vector, cbind, rbind} and \texttt{unlist} are the internal non-primitive functions which are internally generic.

For efficiency, internal dispatch only occurs on objects, that is those for which \texttt{is.object} returns true.

See Also

\texttt{methods} for the methods which are available.

---

\textbf{invisible} \hspace{1cm} \textit{Change the Print Mode to Invisible}

\textbf{Description}

Return a (temporarily) invisible copy of an object.

\textbf{Usage}

\[ \text{invisible}(x = \text{NULL}) \]

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} an arbitrary \texttt{R} object, by default \texttt{NULL}.
\end{itemize}

\textbf{Details}

This function can be useful when it is desired to have functions return values which can be assigned, but which do not print when they are not assigned.

This is a \texttt{primitive} function.

\textbf{References}


\textbf{See Also}

\texttt{withVisible, return, function}.

\textbf{Examples}

\begin{verbatim}
# These functions both return their argument
f1 <- function(x) x
f2 <- function(x) invisible(x)
f1(1) # prints
f2(1) # does not
\end{verbatim}
is.finite and is.infinite return a vector of the same length as x, indicating which elements are finite (not infinite and not missing) or infinite.

Inf and -Inf are positive and negative infinity whereas NaN means ‘Not a Number’. (These apply to numeric values and real and imaginary parts of complex values but not to values of integer vectors.) Inf and NaN are reserved words in the R language.

is.finite(x)

Arguments

x

R object to be tested: the default methods handle atomic vectors.

Details

is.finite returns a vector of the same length as x the jth element of which is TRUE if x[j] is finite (i.e., it is not one of the values NA, NaN, Inf or -Inf) and FALSE otherwise. Complex numbers are finite if both the real and imaginary parts are.

is.infinite returns a vector of the same length as x the jth element of which is TRUE if x[j] is infinite (i.e., equal to one of Inf or -Inf) and FALSE otherwise. This will be false unless x is numeric or complex. Complex numbers are infinite if either the real or the imaginary part is.

is.nan tests if a numeric value is NaN. Do not test equality to NaN, or even use identical, since systems typically have many different NaN values. One of these is used for the numeric missing value NA, and is.nan is false for that value. A complex number is regarded as NaN if either the real or imaginary part is NaN but not NA. All elements of logical, integer and raw vectors are considered not to be NaN.

All three functions accept NULL as input and return a length zero result. The default methods accept character and raw vectors, and return FALSE for all entries. Prior to R version 2.14.0 they accepted all input, returning FALSE for most non-numeric values; cases which are not atomic vectors are now signalled as errors.

All three functions are generic: you can write methods to handle specific classes of objects, see InternalMethods.

Value

A logical vector of the same length as x: dim, dimnames and names attributes are preserved.
Note

In R, basically all mathematical functions (including basic Arithmetic), are supposed to work properly with +/- Inf and NaN as input or output.
The basic rule should be that calls and relations with Ins really are statements with a proper mathematical limit.
Computations involving NaN will return NaN or perhaps NA: which of those two is not guaranteed and may depend on the R platform (since compilers may re-order computations).

References

The IEC 60559 standard, also known as the ANSI/IEEE 754 Floating-Point Standard.
https://en.wikipedia.org/wiki/NaN.

Also available at https://docs.oracle.com/cd/E19957-01/806-3568/ncg_goldberg.html.
The C99 function isfinite is used for is.finite.

See Also

NA, ‘Not Available’ which is not a number as well, however usually used for missing values and applies to many modes, not just numeric and complex.
Arithmetic, double.

Examples

pi / 0 ## = Inf a non-zero number divided by zero creates infinity
0 / 0 ## = NaN

1/0 + 1/0 # Inf
1/0 - 1/0 # NaN

stopifnot(
   1/0 == Inf,
   1/Inf == 0
)
sin(Inf)
cos(Inf)
tan(Inf)

is.function(x) is a (primitive) function.

Usage

is.function(x)
is.primitive(x)
Arguments

x an R object.

Details

is.primitive(x) tests if x is a primitive function, i.e., if typeof(x) is either "builtin" or "special".

Value

TRUE if x is a (primitive) function, and FALSE otherwise.

Examples

is.function(1) # FALSE
is.function(is.primitive) # TRUE: it is a function, but ..
is.primitive(is.primitive) # FALSE: it's not a primitive one, whereas
is.primitive(is.function) # TRUE: that one *is*

is.language                         Is an Object a Language Object?

Description

is.language returns TRUE if x is a variable name, a call, or an expression.

Usage

is.language(x)

Arguments

x object to be tested.

Note

A name is also known as 'symbol', from its type (typeof), see is.symbol.
If typeof(x) == "language", then is.language(x) is always true, but the reverse does not hold as expressions or names y also fulfill is.language(y), see the examples.
This is a primitive function.

References


Examples

ll <- list(a = expression(x^2 - 2*x + 1), b = as.name("Jim"),
c = as.expression(exp(1)), d = call("sin", pi))
sapply(ll, typeof)
sapply(ll, mode)
stopifnot(sapply(ll, is.language))
is.object

Is an Object ‘internally classed’?

Description

A function mostly for internal use. It returns TRUE if the object x has the R internal OBJECT bit set, and FALSE otherwise. The OBJECT bit is set when a "class" attribute is added and removed when that attribute is removed, so this is a very efficient way to check if an object has a class attribute. (S4 objects always should.)

Note that typical basic (‘atomic’, see is.atomic) R vectors and arrays x are not objects in the above sense as attributes(x) does not contain “class”.

Usage

is.object(x)

Arguments

x object to be tested.

Note

This is a primitive function.

See Also

class, and methods.
isS4.

Examples

is.object(1) # FALSE
is.object(as.factor(1:3)) # TRUE

is.R

Are we using R, rather than S?

Description

Test if running under R.

Usage

is.R()
Details

The function has been written such as to correctly run in all versions of R, S and S-PLUS. In order for code to be runnable in both R and S dialects previous to S-PLUS 8.0, your code must either define `is.R` or use it as

```r
if (exists("is.R") && is.function(is.R) && is.R()) {
  ## R-specific code
} else {
  ## S-version of code
}
```

Value

`is.R` returns `TRUE` if we are using R and `FALSE` otherwise.

See Also

`R.version`, `system`.

Examples

```r
x <- stats::runif(20); small <- x < 0.4
## In the early years of R, 'which()' only existed in R:
if(is.R()) which(small) else seq(along = small)[small]
```

---

**is.recursive**

Is an Object Atomic or Recursive?

Description

`is.atomic` returns `TRUE` if `x` is of an atomic type (or NULL) and `FALSE` otherwise.
`is.recursive` returns `TRUE` if `x` has a recursive (list-like) structure and `FALSE` otherwise.

Usage

```r
is.atomic(x)

is.recursive(x)
```

Arguments

`x` object to be tested.

Details

`is.atomic` is true for the atomic types ("logical", "integer", "numeric", "complex", "character" and "raw") and NULL.

Most types of objects are regarded as recursive. Exceptions are the atomic types, NULL, symbols (as given by `as.name`), S4 objects with slots, external pointers, and—rarely visible from R—weak references and byte code, see `typeof`.

It is common to call the atomic types ‘atomic vectors’, but note that `is.vector` imposes further restrictions: an object can be atomic but not a vector (in that sense).

These are primitive functions.
is.single

References


See Also

`is.list`, `is.language`, etc, and the `demo("is.things")`.

Examples

```r
require(stats)

is.a.r <- function(x) c(is.atomic(x), is.recursive(x))

is.a.r(c(a = 1, b = 3)) # TRUE FALSE
is.a.r(list()) # FALSE TRUE - a list is a list
is.a.r(list(2)) # FALSE TRUE
is.a.r(lm) # FALSE TRUE
is.a.r(y ~ x) # FALSE TRUE
is.a.r(expression(x+1)) # FALSE TRUE
is.a.r(quote(exp)) # FALSE FALSE
```

---

is.single  

Is an Object of Single Precision Type?

Description

is.single reports an error. There are no single precision values in R.

Usage

`is.single(x)`

Arguments

x  

object to be tested.

References

is.unsorted

Description
Test if an object is not sorted (in increasing order), without the cost of sorting it.

Usage

\[
\text{is.unsorted}(x, \text{na.rm} = \text{FALSE}, \text{strictly} = \text{FALSE})
\]

Arguments

- \text{x} an \text{R} object with a class or a numeric, complex, character, logical or raw vector.
- \text{na.rm} logical. Should missing values be removed before checking?
- \text{strictly} logical indicating if the check should be for \text{strictly} increasing values.

Details

\text{is.unsorted} is generic: you can write methods to handle specific classes of objects, see \text{Internal-Methods}.

Value

A length-one logical value. All objects of length 0 or 1 are sorted. Otherwise, the result will be \text{NA} except for atomic vectors and objects with an S3 class (where the \text{\ge} or \text{\textgreater} method is used to compare \text{x[i]} with \text{x[i-1]} for \text{i} in 2:length(\text{x})) or with an S4 class where you have to provide a method for \text{is.unsorted}().

Note

This function is designed for objects with one-dimensional indices, as described above. Data frames, matrices and other arrays may give surprising results.

See Also

\text{sort}, \text{order}.

ISOdatetime

Date-time Conversion Functions from Numeric Representations

Description

Convenience wrappers to create date-times from numeric representations.

Usage

\[
\text{ISOdatetime}(\text{year}, \text{month}, \text{day}, \text{hour}, \text{min}, \text{sec}, \text{tz} = \text{""})
\]

\[
\text{ISOdate}(\text{year}, \text{month}, \text{day}, \text{hour} = 12, \text{min} = 0, \text{sec} = 0, \text{tz} = \text{"GMT"})
\]
Arguments

- year, month, day: numerical values to specify a day.
- hour, min, sec: numerical values for a time within a day. Fractional seconds are allowed.
- tz: A time zone specification to be used for the conversion. "" is the current time zone and "GMT" is UTC. Invalid values are most commonly treated as UTC, on some platforms with a warning.

Details

ISOdatetime and ISOdate are convenience wrappers for strptime that differ only in their defaults and that ISOdate sets UTC as the time zone. For dates without times it would normally be better to use the "Date" class.

The main arguments will be recycled using the usual recycling rules.

Because these make use of strptime, only years in the range 0:9999 are accepted.

Value

An object of class "POSIXct".

See Also

DateTimeClasses for details of the date-time classes; strptime for conversions from character strings.

---

isS4

Test for an S4 object

Description

Tests whether the object is an instance of an S4 class.

Usage

isS4(object)

asS4(object, flag = TRUE, complete = TRUE)

asS3(object, flag = TRUE, complete = TRUE)

Arguments

- object: Any R object.
- flag: Optional, logical: indicate direction of conversion.
- complete: Optional, logical: whether conversion to S3 is completed. Not usually needed, but see the details section.
Details
Note that isS4 does not rely on the methods package, so in particular it can be used to detect the need to require that package.

asS3 uses the value of complete to control whether an attempt is made to transform object into a valid object of the implied S3 class. If complete is TRUE, then an object from an S4 class extending an S3 class will be transformed into an S3 object with the corresponding S3 class (see S3Part). This includes classes extending the pseudo-classes array and matrix: such objects will have their class attribute set to NULL.
isS4 is primitive.

Value
isS4 always returns TRUE or FALSE according to whether the internal flag marking an S4 object has been turned on for this object.

asS4 and asS3 will turn this flag on or off, and asS3 will set the class from the objects .S3Class slot if one exists. Note that asS3 will not turn the object into an S3 object unless there is a valid conversion; that is, an object of type other than "S4" for which the S4 object is an extension, unless argument complete is FALSE.

See Also
is.object for a more general test; Introduction for general information on S4; Classes_Details for more on S4 class definitions.

Examples
isS4(pi) # FALSE
isS4(getClass("MethodDefinition")) # TRUE

isSymmetric
Test if a Matrix or other Object is Symmetric (Hermitian)

Description
Generic function to test if object is symmetric or not. Currently only a matrix method is implemented, where a complex matrix Z must be “Hermitian” for isSymmetric(Z) to be true.

Usage
isSymmetric(object, ...)  # S3 method for class 'matrix'

isSymmetric(object, tol = 100 * .Machine$double.eps, toll = 8 * tol, ...)

isSymmetric

Arguments

object any R object; a matrix for the matrix method.
tol numeric scalar >= 0. Smaller differences are not considered, see all.equal.numeric.
tol1 numeric scalar >= 0. isSymmetric.matrix() ‘pre-tests’ the first and last few rows for fast detection of ‘obviously’ asymmetric cases with this tolerance. Setting it to length zero will skip the pre-tests.

Details

The matrix method is used inside eigen by default to test symmetry of matrices up to rounding error, using all.equal. It might not be appropriate in all situations.

Note that a matrix m is only symmetric if its rownames and colnames are identical. Consider using unname(m).

Value

logical indicating if object is symmetric or not.

See Also

eigen which calls isSymmetric when its symmetric argument is missing.

Examples

isSymmetric(D3 <- diag(3)) # -> TRUE

D3[2, 1] <- 1e-100
D3
isSymmetric(D3) # TRUE
isSymmetric(D3, tol = 0) # FALSE for zero-tolerance

## Complex Matrices - Hermitian or not
Z <- sqrt(matrix(-1:2 + 0i, 2)); Z <- t(Conj(Z)) %*% Z
Z
isSymmetric(Z) # TRUE
isSymmetric(Z + 1) # TRUE
isSymmetric(Z + 1i) # FALSE -- a Hermitian matrix has a *real* diagonal

colnames(D3) <- c("X", "Y", "Z")

isSymmetric(D3) # FALSE (as row and column names differ)
isSymmetric(D3, check.attributes=FALSE) # TRUE (as names are not checked)
jitter

‘Jitter’ (Add Noise) to Numbers

Description

Add a small amount of noise to a numeric vector.

Usage

jitter(x, factor = 1, amount = NULL)

Arguments

x numeric vector to which jitter should be added.
factor numeric.
amount numeric; if positive, used as amount (see below), otherwise, if = 0 the default is factor * z/50. Default (NULL): factor * d/5 where d is about the smallest difference between x values.

Details

The result, say r, is r <- x + runif(n, -a, a) where n <- length(x) and a is the amount argument (if specified).

Let z <- max(x) - min(x) (assuming the usual case). The amount a to be added is either provided as positive argument amount or otherwise computed from z, as follows:

If amount == 0, we set a <- factor * z/50 (same as S).

If amount is NULL (default), we set a <- factor * d/5 where d is the smallest difference between adjacent unique (apart from fuzz) x values.

Value

jitter(x, ...) returns a numeric of the same length as x, but with an amount of noise added in order to break ties.

Author(s)

Werner Stahel and Martin Maechler, ETH Zurich

References


See Also

rug which you may want to combine with jitter.
Examples

```r
round(jitter(c(rep(1, 3), rep(1.2, 4), rep(3, 3))), 3)
## These two 'fail' with S-plus 3.x:
jitter(rep(0, 7))
jitter(rep(10000, 5))
```

---

### kappa

**Compute or Estimate the Condition Number of a Matrix**

**Description**

The condition number of a regular (square) matrix is the product of the norm of the matrix and the norm of its inverse (or pseudo-inverse), and hence depends on the kind of matrix-norm.

kappa() computes by default (an estimate of) the 2-norm condition number of a matrix or of the \( R \) matrix of a \( QR \) decomposition, perhaps of a linear fit. The 2-norm condition number can be shown to be the ratio of the largest to the smallest non-zero singular value of the matrix.

rcond() computes an approximation of the reciprocal condition number, see the details.

**Usage**

```r
kappa(z, ...)
```

```r
## Default S3 method:
kappa(z, exact = FALSE,
       norm = NULL, method = c("qr", "direct"), ...)
## S3 method for class 'lm'
kappa(z, ...)
## S3 method for class 'qr'
kappa(z, ...)
```

```r
.kappa_tri(z, exact = FALSE, LINPACK = TRUE, norm = NULL, ...)
```

```r
rcond(x, norm = c("O","I","1"), triangular = FALSE, ...)
```

**Arguments**

- `z, x` A matrix or a the result of `qr` or a fit from a class inheriting from "lm".
- `exact` logical. Should the result be exact?
- `norm` character string, specifying the matrix norm with respect to which the condition number is to be computed, see also norm. For rcond, the default is "0", meaning the One- or 1-norm. The (currently only) other possible value is "i" for the infinity norm.
- `method` a partially matched character string specifying the method to be used; "qr" is the default for back-compatibility, mainly.
- `triangular` logical. If true, the matrix used is just the lower triangular part of `z`.
- `LINPACK` logical. If true and `z` is not complex, the LINPACK routine `dtrco()` is called; otherwise the relevant LAPACK routine is.
- `...` further arguments passed to or from other methods; for `kappa.*()`, notably LINPACK when `norm` is not "2".
For **kappa()**, if **exact = FALSE** (the default) the 2-norm condition number is estimated by a cheap approximation. However, the exact calculation (via **svd**)) is also likely to be quick enough.

Note that the 1- and Inf-norm condition numbers are much faster to calculate, and **rcond()** computes these **reciprocal** condition numbers, also for complex matrices, using standard LAPACK routines.

**kappa** and **rcond** are different interfaces to partly identical functionality.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

**Value**

The condition number, **kappa**, or an approximation if **exact = FALSE**.

**Author(s)**

The design was inspired by (but differs considerably from) the S function of the same name described in Chambers (1992).

**Source**

The LAPACK routines **DTRCON** and **ZTRCON** and the LINPACK routine **DTRCO**.

LAPACK and LINPACK are from [https://netlib.org/lapack/](https://netlib.org/lapack/) and [https://netlib.org/linpack/](https://netlib.org/linpack/) and their guides are listed in the references.

**References**


**See Also**

**norm; svd** for the singular value decomposition and **qr** for the **QR** one.

**Examples**

```r
kappa(x1 <- cbind(1, 1:10)) # 15.71
kappa(x1, exact = TRUE)     # 13.68
kappa(x2 <- cbind(x1, 2:11)) # high! [x2 is singular!]

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
sv9 <- svd(h9 <- hilbert(9))$ d
kappa(h9)     # pretty high!
kappa(h9, exact = TRUE) == max(sv9) / min(sv9)
kappa(h9, exact = TRUE) / kappa(h9) # 0.677 (i.e., rel.error = 32%)
```
kronecker

Kronecker Products on Arrays

Description

Computes the generalised kronecker product of two arrays, X and Y.

Usage

kronecker(X, Y, FUN = "*", make.dimnames = FALSE, ...)
X %x% Y

Arguments

X       A vector or array.
Y       A vector or array.
FUN     a function; it may be a quoted string.
make.dimnames Provide dimnames that are the product of the dimnames of X and Y.
...     optional arguments to be passed to FUN.

Details

If X and Y do not have the same number of dimensions, the smaller array is padded with dimensions of size one. The returned array comprises submatrices constructed by taking X one term at a time and expanding that term as FUN(x, Y, ...).

%x% is an alias for kronecker (where FUN is hardwired to "*").

Value

An array A with dimensions dim(X) * dim(Y).

Author(s)

Jonathan Rougier

References


See Also

outer, on which kronecker is built and %*% for usual matrix multiplication.
Examples

# simple scalar multiplication
( M <- matrix(1:6, ncol = 2) )
kroncker(4, M)

# Block diagonal matrix:
kroncker(diag(1, 3), M)

# ask for dimnames

fred <- matrix(1:12, 3, 4, dimnames = list(LETTERS[1:3], LETTERS[4:7]))
 bill <- c("happy" = 100, "sad" = 1000)
kroncker(fred, bill, make.dimnames = TRUE)

bill <- outer(bill, c("cat" = 3, "dog" = 4))
kroncker(fred, bill, make.dimnames = TRUE)

---

110n_info

Localization Information

Description

Report on localization information.

Usage

110n_info()

Details

‘A Latin-1 locale’ includes supersets (for printable characters) such as Windows codepage 1252 but not Latin-9 (ISO 8859-15).

On Windows (where the resulting list contains codepage and system.codepage components additionally), common codepages are 1252 (Western European), 1250 (Central European), 1251 (Cyrillic), 1253 (Greek), 1254 (Turkish), 1255 (Hebrew), 1256 (Arabic), 1257 (Baltic), 1258 (Vietnamese), 874 (Thai), 932 (Japanese), 936 (Simplified Chinese), 949 (Korean) and 950 (Traditional Chinese). Codepage 28605 is Latin-9 and 65001 is UTF-8 (where supported). R does not allow the C locale, and uses 1252 as the default codepage.

Value

A list with three logical elements and further OS-specific elements:

MBCS If a multi-byte character set in use?
UTF-8 Is this known to be a UTF-8 locale?
Latin-1 Is this known to be a Latin-1 locale?

Not on Windows:

codeset character. The encoding name as reported by the OS, possibly "". (Added in R 4.1.0. Encoding names are OS-specific.)

Only on Windows:
labels

codepage
integer: the Windows codepage corresponding to the locale \( \mathbf{R} \) is using (and not necessarily that Windows is using).

system.codepage
integer: the Windows system/ANSI codepage (the codepage Windows is using). Added in \( \mathbf{R} \) 4.1.0.

See Also

Sys.getlocale, localeconv

Examples

l10n_info()

---

labels

Find Labels from Object

Description

Find a suitable set of labels from an object for use in printing or plotting, for example. A generic function.

Usage

labels(object, ...)

Arguments

object
Any \( \mathbf{R} \) object: the function is generic.

...
further arguments passed to or from other methods.

Value

A character vector or list of such vectors. For a vector the results is the names or seq_along(x) and for a data frame or array it is the dimnames (with NULL expanded to seq_len(d[i])).

References

lapply

Apply a Function over a List or Vector

Description

lapply returns a list of the same length as X, each element of which is the result of applying FUN to the corresponding element of X.
sapply is a user-friendly version and wrapper of lapply by default returning a vector, matrix or, if simplify = "array", an array if appropriate, by applying simplify2array(). sapply(x, f, simplify = FALSE, USE.NAMES = FALSE) is the same as lapply(x, f).
vapply is similar to sapply, but has a pre-specified type of return value, so it can be safer (and sometimes faster) to use.
replicate is a wrapper for the common use of sapply for repeated evaluation of an expression (which will usually involve random number generation).
simplify2array() is the utility called from sapply() when simplify is not false and is similarly called from mapply().

Usage

lapply(X, FUN, ...)
sapply(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE)
vapply(X, FUN, FUN.VALUE, ..., USE.NAMES = TRUE)
replicate(n, expr, simplify = "array")
simplify2array(x, higher = TRUE, except = c(0L, 1L))

Arguments

X a vector (atomic or list) or an expression object. Other objects (including classed objects) will be coerced by base::as.list.
FUN the function to be applied to each element of X; see ‘Details’. In the case of functions like +, %*%, the function name must be backquoted or quoted.
... optional arguments to FUN.
simplify logical or character string; should the result be simplified to a vector, matrix or higher dimensional array if possible? For sapply it must be named and not abbreviated. The default value, TRUE, returns a vector or matrix if appropriate, whereas if simplify = "array" the result may be an array of “rank” (=length(dim(.))) one higher than the result of FUN(X[[i]]).
USE.NAMES logical; if TRUE and if X is character, use X as names for the result unless it had names already. Since this argument follows ... its name cannot be abbreviated.
FUN.VALUE a (generalized) vector; a template for the return value from FUN. See ‘Details’.
n integer: the number of replications.
expr the expression (a language object, usually a call) to evaluate repeatedly.
x a list, typically returned from lapply().
lapply

higher logical; if true, simplify2array() will produce a (“higher rank”) array when appropriate, whereas higher = FALSE would return a matrix (or vector) only. These two cases correspond to sapply(*, simplify = “array”) or simplify = TRUE, respectively.

except integer vector or NULL; the default c(0L, 1L) corresponds to the exceptions used by sapply: a list with elements of common length 0 or 1 is not simplified to an array but is returned, respectively, as is or unlisted. These exceptions can be disabled by specifying only a subset of 0:1, or NULL to always simplify to an array (if possible).

Details

FUN is found by a call to match.fun and typically is specified as a function or a symbol (e.g., a backquoted name) or a character string specifying a function to be searched for from the environment of the call to lapply.

Function FUN must be able to accept as input any of the elements of X. If the latter is an atomic vector, FUN will always be passed a length-one vector of the same type as X.

Arguments in ... cannot have the same name as any of the other arguments, and care may be needed to avoid partial matching to FUN. In general-purpose code it is good practice to name the first two arguments X and FUN if ... is passed through: this both avoids partial matching to FUN and ensures that a sensible error message is given if arguments named X or FUN are passed through ....

Simplification in sapply is only attempted if X has length greater than zero and if the return values from all elements of X are all of the same (positive) length. If the common length is one the result is a vector, and if greater than one is a matrix with a column corresponding to each element of X.

Simplification is always done in vapply. This function checks that all values of FUN are compatible with the FUN.VALUE, in that they must have the same length and type. (Types may be promoted to a higher type within the ordering logical < integer < double < complex, but not demoted.)

Users of S4 classes should pass a list to lapply and vapply: the internal coercion is done by the as.list in the base namespace and not one defined by a user (e.g., by setting S4 methods on the base function).

Value

For lapply, sapply(simplify = FALSE) and replicate(simplify = FALSE), a list.

For sapply(simplify = TRUE) and replicate(simplify = TRUE): if X has length zero or n = 0, an empty list. Otherwise an atomic vector or matrix or list of the same length as X (of length n for replicate). If simplification occurs, the output type is determined from the highest type of the return values in the hierarchy NULL < raw < logical < integer < double < complex < character < list < expression, after coercion of pairlists to lists.

vapply returns a vector or array of type matching the FUN.VALUE. If length(FUN.VALUE) == 1 a vector of the same length as X is returned, otherwise an array. If FUN.VALUE is not an array, the result is a matrix with length(FUN.VALUE) rows and length(X) columns, otherwise an array a with dim(a) == c(dim(FUN.VALUE), length(X)).

The (Dim)names of the array value are taken from the FUN.VALUE if it is named, otherwise from the result of the first function call. Column names of the matrix or more generally the names of the last dimension of the array value or names of the vector value are set from X as in sapply.

Note

sapply(*, simplify = FALSE, USE.NAMES = FALSE) is equivalent to lapply(*).
For historical reasons, the calls created by `lapply` are unevaluated, and code has been written (e.g., `bquote`) that relies on this. This means that the recorded call is always of the form \texttt{FUN(X[[i]], \ldots)}, with \texttt{i} replaced by the current (integer or double) index. This is not normally a problem, but it can be if \texttt{FUN} uses \texttt{sys.call} or \texttt{match.call} or if it is a primitive function that makes use of the call. This means that it is often safer to call primitive functions with a wrapper, so that e.g. \texttt{lapply(1:11, function(x) is.numeric(x))} is required to ensure that method dispatch for \texttt{is.numeric} occurs correctly.

If \texttt{expr} is a function call, be aware of assumptions about where it is evaluated, and in particular what \ldots{} might refer to. You can pass additional named arguments to a function call as additional named arguments to \texttt{replicate}: see ‘Examples’.

References


See Also

\texttt{apply}, \texttt{tapply}, \texttt{mapply} for applying a function to multiple arguments, and \texttt{rapply} for a recursive version of \texttt{lapply()}, \texttt{eapply} for applying a function to each entry in an \texttt{environment}.

Examples

```r
require(stats); require(graphics)
x <- list(a = 1:10, beta = exp(-3:3), logic = c(TRUE,FALSE,FALSE,TRUE))
# compute the list mean for each list element
lapply(x, mean)
# median and quartiles for each list element
lapply(x, quantile, probs = 1:3/4)
sapply(x, quantile)
i39 <- sapply(3:9, seq) # list of vectors
sapply(i39, fivenum)
vapply(i39, fivenum, c(Min. = 0, "1st Qu." = 0, Median = 0, "3rd Qu." = 0, Max. = 0))
## sapply(*, "array") -- artificial example
(v <- structure(10*(5:8), names = LETTERS[1:4]))
f2 <- function(x, y) outer(rep(x, length.out = 3), y)
(a2 <- sapply(v, f2, y = 2*(1:5), simplify = "array"))
a.2 <- vapply(v, f2, outer(1:3, 1:5), y = 2*(1:5))
stopifnot(dim(a2) == c(3,5,4), all.equal(a2, a.2),
       identical(dimnames(a2), list(NULL,NULL,LETTERS[1:4])))

hist(replicate(100, mean(rexp(10))))
## use of replicate() with parameters:
foo <- function(x = 1, y = 2) c(x, y)
# does not work: bar <- function(n, ...) replicate(n, foo(...))
bar <- function(n, x) replicate(n, foo(x = x))
bar(5, x = 3)
```
Description

The value of the internal evaluation of a top-level R expression is always assigned to `.Last.value` (in package:base) before further processing (e.g., printing).

Usage

`.Last.value`

Details

The value of a top-level assignment is put in `.Last.value`, unlike S.

Do not assign to `.Last.value` in the workspace, because this will always mask the object of the same name in package:base.

See Also

eval

Examples

```r
## These will not work correctly from example(),
## but they will in make check or if pasted in,
## as example() does not run them at the top level
gamma(1:15)  # think of some intensive calculation...
fac14 <- .Last.value # keep them

library("splines") # returns invisibly
.Last.value  # shows what library(.) above returned
```

---

Description

Report the name of the shared object file with LAPACK implementation in use.

Usage

`La_library()`
La_version

Value
A character vector of length one ("" when the name is not known). The value can be used as an indication of which LAPACK implementation is in use. Typically, the R version of LAPACK will appear as libRlapack.so (libRlapack.dylib), depending on how R was built. Note that libRlapack.so (libRlapack.dylib) may also be shown for an external LAPACK implementation that had been copied, hard-linked or renamed by the system administrator. Otherwise, the shared object file will be given and its path/name may indicate the vendor/version.

The detection does not work on Windows, nor for the Accelerate framework on macOS, nor in the rare (and unsupported) case of a static external library.

It is possible to build R against an enhanced BLAS which contains some but not all LAPACK routines, in which case this function reports the library containing routine ILAVER.

See Also
- extSoftVersion for versions of other third-party software including BLAS.
- La_version for the version of LAPACK in use.

Examples
La_version()

<table>
<thead>
<tr>
<th>La_version</th>
<th>LAPACK Version</th>
</tr>
</thead>
</table>

Description
Report the version of LAPACK in use.

Usage
La_version()

Value
A character vector of length one.

Note that this is the version as reported by the library at runtime. It may differ from the reference ('netlib') implementation, for example by having some optimized or patched routines. For the version included with R, the older (not Fortran 90) versions of

DLARTG DLASSQ ZLARTG ZLASSQ

are used.

See Also
- extSoftVersion for versions of other third-party software.
- La_library for binary/executable file with LAPACK in use.

Examples
La_version()
Description
Get or set the length of vectors (including lists) and factors, and of any other R object for which a method has been defined.

Usage
length(x)
length(x) <- value

Arguments
x an R object. For replacement, a vector or factor.
value a non-negative integer or double (which will be rounded down).

Details
Both functions are generic: you can write methods to handle specific classes of objects, see InternalMethods. length<- has a "factor" method.

The replacement form can be used to reset the length of a vector. If a vector is shortened, extra values are discarded and when a vector is lengthened, it is padded out to its new length with NAs (nul for raw vectors).

Both are primitive functions.

Value
The default method for length currently returns a non-negative integer of length 1, except for vectors of more than $2^{31} - 1$ elements, when it returns a double.

For vectors (including lists) and factors the length is the number of elements. For an environment it is the number of objects in the environment, and NULL has length 0. For expressions and pairlists (including language objects and dotlists) it is the length of the pairlist chain. All other objects (including functions) have length one: note that for functions this differs from S.

The replacement form removes all the attributes of x except its names, which are adjusted (and if necessary extended by "").

Warning
Package authors have written methods that return a result of length other than one (Formula) and that return a vector of type double (Matrix), even with non-integer values (earlier versions of sets). Where a single double value is returned that can be represented as an integer it is returned as a length-one integer vector.

References
See Also

nchar for counting the number of characters in character vectors, lengths for getting the length of every element in a list.

Examples

length(diag(4)) # = 16 (4 x 4)
length(options()) # 12 or more
length(y ~ x1 + x2 + x3) # 3
length(expression(x, {y <- x^2; y+2}, x^y)) # 3

## from example(warpbreaks)
require(stats)
fm1 <- lm(breaks ~ wool * tension, data = warpbreaks)
length(fm1$call) # 3, lm() and two arguments.
length(formula(fm1)) # 3, ~ lhs rhs

lengths Lengths of List or Vector Elements

Description

Get the length of each element of a list or atomic vector (is.atomic) as an integer or numeric vector.

Usage

lengths(x, use.names = TRUE)

Arguments

x a list, list-like such as an expression or an atomic vector (for which the result is trivial).
use.names logical indicating if the result should inherit the names from x.

Details

This function loops over x and returns a compatible vector containing the length of each element in x. Effectively, length(x[[i]]) is called for all i, so any methods on length are considered.

lengths is generic: you can write methods to handle specific classes of objects, see InternalMethods.

Value

A non-negative integer of length length(x), except when any element has a length of more than $2^{31} - 1$ elements, when it returns a double vector. When use.names is true, the names are taken from the names on x, if any.
Note

One raison d'être of `lengths(x)` is its use as a more efficient version of `sapply(x, length)` and similar `*apply` calls to `length`. This is the reason why `x` may be an atomic vector, even though `lengths(x)` is trivial in that case.

See Also

`length` for getting the length of any R object.

Examples

```r
require(stats)
## summarize by month
l <- split(airquality$Ozone, airquality$Month)
avgOz <- lapply(l, mean, na.rm=TRUE)
## merge result
airquality$avgOz <- rep(unlist(avgOz, use.names=FALSE), lengths(l))
## but this is safer and cleaner, but can be slower
airquality$avgOz <- unsplit(avgOz, airquality$Month)

## should always be true, except when a length does not fit in 32 bits
stopifnot(identical(lengths(l), vapply(l, length, integer(1L))))

## empty lists are not a problem
x <- list()
stopifnot(identical(lengths(x), integer()))

## nor are "list-like" expressions:
lengths(expression(u, v, 1+ 0:9))

## and we should dispatch to length methods
f <- c(rep(1, 3), rep(2, 6), 3)
dates <- split(as.POSIXlt(Sys.time() + 1:10), f)
stopifnot(identical(lengths(dates), vapply(dates, length, integer(1L))))
```

levels

Levels Attributes

Description

`levels` provides access to the levels attribute of a variable. The first form returns the value of the levels of its argument and the second sets the attribute.

Usage

```r
levels(x)
levels(x) <- value
```

Arguments

- `x`: an object, for example a factor.
- `value`: A valid value for `levels(x)`. For the default method, `NULL` or a character vector. For the `factor` method, a vector of character strings with length at least the number of levels of `x`, or a named list specifying how to rename the levels.
Details

Both the extractor and replacement forms are generic and new methods can be written for them. The most important method for the replacement function is that for factors.

For the factor replacement method, a NA in value causes that level to be removed from the levels and the elements formerly with that level to be replaced by NA.

Note that for a factor, replacing the levels via levels(x) <- value is not the same as (and is preferred to) attr(x, "levels") <- value.

The replacement function is primitive.

References


See Also

nlevels, relevel, reorder.

Examples

## assign individual levels
x <- gl(2, 4, 8)
levels(x)[1] <- "low"
levels(x)[2] <- "high"
x

## or as a group
y <- gl(2, 4, 8)
levels(y) <- c("low", "high")
y

## combine some levels
z <- gl(3, 2, 12, labels = c("apple", "salad", "orange"))
z
levels(z) <- c("fruit", "veg", "fruit")
z

## same, using a named list
z <- gl(3, 2, 12, labels = c("apple", "salad", "orange"))
z
levels(z) <- list("fruit" = c("apple", "orange"),
                 "veg" = "salad")
z

## we can add levels this way:
f <- factor(c("a","b"))
levels(f) <- c("c", "a", "b")
f

f <- factor(c("a","b"))
levels(f) <- list(C = "c", A = "a", B = "b")
f
libcurlVersion

Report Version of libcurl

Description

Report version of libcurl in use.

Usage

libcurlVersion()

Value

A character string, with value the libcurl version in use or "" if none is. If libcurl is available, has attributes

- `ssl_version`: A character string naming the SSL/TLS implementation and version, possibly "none". It is intended for the version of OpenSSL used, but not all implementations of libcurl use OpenSSL — for example macOS reports "SecureTransport", its wrapper for SSL/TLS.

- `libssh_version`: A character string naming the libssh version, which may or may not be available (it is used for e.g. scp and sftp protocols). Where present, something like "libssh2/1.5.0".

- `protocols`: A character vector of the names of supported protocols, also known as 'schemes' when part of a URL.

Warning

In late 2017 a libcurl installation was seen divided into two libraries, libcurl and libcurl-feature, and the first had been updated but not the second. As the compiled function recording the version was in the latter, the version reported by libcurlVersion was misleading.

See Also

extSoftVersion for versions of other third-party software.
curlGetHeaders, download.file and url for functions which (optionally) use libcurl.
https://curl.se/docs/sslcerts.html and https://curl.se/docs/ssl-compared.html for more details on SSL versions (the current standard being known as TLS). Normally libcurl used with R uses SecureTransport on macOS, OpenSSL on Windows and GnuTLS, NSS or OpenSSL on Unix-alikes. (At the time of writing Debian-based Linux use GnuTLS and RedHat-based ones use OpenSSL, having previously used NSS.)

Examples

libcurlVersion()
libPaths

Search Paths for Packages

Description

.libPaths gets/sets the library trees within which packages are looked for.

Usage

.libPaths(new, include.site = TRUE)

.Arguments

new a character vector with the locations of R library trees. Tilde expansion (path.expand) is done, and if any element contains one of *?[], globbing is done where supported by the platform: see Sys.glob.

include.site a logical value indicating whether the value of .Library.site should be included in the new set of library tree locations. Defaulting to TRUE, it is ignored when .libPaths is called without the new argument.

Details

.Library is a character string giving the location of the default library, the ‘library’ subdirectory of R_HOME.

.Library.site is a (possibly empty) character vector giving the locations of the site libraries.

.libPaths is used for getting or setting the library trees that R knows about and hence uses when looking for packages (the library search path). If called with argument new, by default, the library search path is set to the existing directories in unique(c(new, .Library.site, .Library)) and this is returned. If include.site is FALSE when the new argument is set, .Library.site is not added to the new library search path. If called without the new argument, a character vector with the currently active library trees is returned.

How paths in new with a trailing slash are treated is OS-dependent. On a POSIX filesystem existing directories can usually be specified with a trailing slash. On Windows filepaths with a trailing slash (or backslash) are invalid and existing directories specified with a trailing slash may not be added to the library search path.

At startup, the library search path is initialized from the environment variables R_LIBS, R_LIBS_USER and R_LIBS_SITE, which if set should give lists of directories where R library trees are rooted, colon-separated on Unix-alike systems and semicolon-separated on Windows. For the latter two, a value of NULL indicates an empty list of directories. (Note that as from R 4.2.0, both are set by R start-up code if not already set or empty so can be interrogated from an R session to find their defaults: in earlier versions this was true only for R_LIBS_USER.)

First, .Library.site is initialized from R_LIBS_SITE. If this is unset or empty, the ‘site-library’ subdirectory of R_HOME is used. Only directories which exist at the time of initialization are retained. Then, .libPaths() is called with the combination of the directories given by R_LIBS and R_LIBS_USER. By default R_LIBS is unset, and if R_LIBS_USER is unset or empty, it is set to directory ‘R/R.version$platform-library/x.y’ of the home directory on Unix-alike systems.
(or 'Library/R/m/x.y/library' for CRAN macOS builds, with m Sys.info()['machine']) and 'R/win-library/x.y' subdirectory of LOCALAPPDATA on Windows, for \texttt{R} x.y.z.

Both \texttt{R_LIBS_USER} and \texttt{R_LIBS_SITE} feature possible expansion of specifiers for \texttt{R}-version-specific information as part of the startup process. The possible conversion specifiers all start with a '%' and are followed by a single letter (use '%%' to obtain '%'), with currently available conversion specifications as follows:

- '%V' \texttt{R} version number including the patchlevel (e.g., '2.5.0').
- '%v' \texttt{R} version number excluding the patchlevel (e.g., '2.5').
- '%p' the platform for which \texttt{R} was built, the value of \texttt{R.version}$\texttt{platform}$.
- '%o' the underlying operating system, the value of \texttt{R.version}$\texttt{os}$. 
- '%a' the architecture (CPU) \texttt{R} was built on/for, the value of \texttt{R.version}$\texttt{arch}$. 

(See \texttt{version} for details on \texttt{R} version information.) In addition, '%U' and '%S' expand to the \texttt{R} defaults for, respectively, \texttt{R_LIBS_USER} and \texttt{R_LIBS_SITE}.

Function \texttt{.libPaths} always uses the values of \texttt{.Library} and \texttt{.Library.site} in the base namespace. \texttt{.Library.site} can be set by the site in \texttt{'Rprofile.site'}, which should be followed by a call to \texttt{.libPaths(.libPaths())} to make use of the updated value.

For consistency, the paths are always normalized by \texttt{normalizePath(winslash = "/")}. 

LOCALAPPDATA (usually C:\Users\username\AppData\Local) on Windows is a hidden directory and may not be viewed by some software. It may be opened by \texttt{shell.exec(Sys.getenv("LOCALAPPDATA"))}.

### Value

A character vector of file paths.

### References


### See Also

\texttt{library}

### Examples

\texttt{.libPaths()}  \hfill \# all library trees \texttt{R} knows about

---

\texttt{library} \hfill \textit{Loading/Attaching and Listing of Packages}

### Description

\texttt{library} and \texttt{require} load and attach add-on packages.
library

Usage

library(package, help, pos = 2, lib.loc = NULL,
character.only = FALSE, logical.return = FALSE,
warn.conflicts, quietly = FALSE,
verbose = getOption("verbose"),
mask.ok, exclude, include.only,
attach.required = missing(include.only))

require(package, lib.loc = NULL, quietly = FALSE,
warn.conflicts,
character.only = FALSE,
mask.ok, exclude, include.only,
attach.required = missing(include.only))

conflictRules(pkg, mask.ok = NULL, exclude = NULL)

Arguments

package, help the name of a package, given as a name or literal character string, or a character string, depending on whether character.only is FALSE (default) or TRUE.
pos the position on the search list at which to attach the loaded namespace. Can also be the name of a position on the current search list as given by search().
lib.loc a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known to.libPaths(). Non-existent library trees are silently ignored.
character.only a logical indicating whether package or help can be assumed to be character strings.
logical.return logical. If it is TRUE, FALSE or TRUE is returned to indicate success.
warn.conflicts logical. If TRUE, warnings are printed about conflicts from attaching the new package. A conflict is a function masking a function, or a non-function masking a non-function. The default is TRUE unless specified as FALSE in the conflicts.policy option.
verbose a logical. If TRUE, additional diagnostics are printed.
quietly a logical. If TRUE, no message confirming package attaching is printed, and most often, no errors/warnings are printed if package attaching fails.
pkg character string naming a package.
mask.ok character vector of names of objects that can mask objects on the search path without signaling an error when strict conflict checking is enabled
exclude,include.only character vector of names of objects to exclude or include in the attached frame. Only one of these arguments may be used in a call to library or require.
attach.required logical specifying whether required packages listed in the Depends clause of the DESCRIPTION file should be attached automatically.

Details

library(package) and require(package) both load the namespace of the package with name package and attach it on the search list. require is designed for use inside other functions; it returns
FALSE and gives a warning (rather than an error as library() does by default) if the package does not exist. Both functions check and update the list of currently attached packages and do not reload a namespace which is already loaded. (If you want to reload such a package, call detach(unload = TRUE) or unloadNamespace first.) If you want to load a package without attaching it on the search list, see requireNamespace.

To suppress messages during the loading of packages use suppressPackageStartupMessages: this will suppress all messages from R itself but not necessarily all those from package authors.

If library is called with no package or help argument, it lists all available packages in the libraries specified by lib.loc, and returns the corresponding information in an object of class "libraryIQR". (The structure of this class may change in future versions.) Use .packages(all = TRUE) to obtain just the names of all available packages, and installed.packages() for even more information.

library(help = somename) computes basic information about the package somename, and returns this in an object of class "packageInfo". (The structure of this class may change in future versions.) When used with the default value (NULL) for lib.loc, the attached packages are searched before the libraries.

Value

Normally library returns (invisibly) the list of attached packages, but TRUE or FALSE if logical.return is TRUE. When called as library() it returns an object of class "libraryIQR", and for library(help=), one of class "packageInfo".

require returns (invisibly) a logical indicating whether the required package is available.

Conflicts

Handling of conflicts depends on the setting of the conflicts.policy option. If this option is not set, then conflicts result in warning messages if the argument warn.conflicts is TRUE. If the option is set to the character string "strict", then all unresolved conflicts signal errors. Conflicts can be resolved using the mask.ok, exclude, and include.only arguments to library and require. Defaults for mask.ok and exclude can be specified using conflictRules.

If the conflicts.policy option is set to the string "depends.ok" then conflicts resulting from attaching declared dependencies will not produce errors, but other conflicts will. This is likely to be the best setting for most users wanting some additional protection against unexpected conflicts.

The policy can be tuned further by specifying the conflicts.policy option as a named list with the following fields:

error: logical; if TRUE treat unresolved conflicts as errors.
warn: logical; unless FALSE issue a warning message when conflicts are found.
generics.ok: logical; if TRUE ignore conflicts created by defining S4 generics for functions on the search path.
depends.ok: logical; if TRUE do not treat conflicts with required packages as errors.
can.mask: character vector of names of packages that are allowed to be masked. These would typically be base packages attached by default.

Licenses

Some packages have restrictive licenses, and there is a mechanism to allow users to be aware of such licenses. If getOption("checkPackageLicense") == TRUE, then at first use of a namespace of a package with a not-known-to-be-FOSS (see below) license the user is asked to view and accept
the license: a list of accepted licenses is stored in file ‘~/R/licensed’. In a non-interactive session it is an error to use such a package whose license has not already been recorded as accepted.

Free or Open Source Software (FOSS, e.g. https://en.wikipedia.org/wiki/FOSS) packages are determined by the same filters used by available.packages but applied to just the current package, not its dependencies.

There can also be a site-wide file ‘R_HOME/etc/licensed.site’ of packages (one per line).

**Formal methods**

library takes some further actions when package methods is attached (as it is by default). Packages may define formal generic functions as well as re-defining functions in other packages (notably base) to be generic, and this information is cached whenever such a namespace is loaded after methods and re-defined functions (implicit generics) are excluded from the list of conflicts. The caching and check for conflicts require looking for a pattern of objects; the search may be avoided by defining an object .noGenerics (with any value) in the namespace. Naturally, if the package does have any such methods, this will prevent them from being used.

**Note**

library and require can only load/attach an installed package, and this is detected by having a ‘DESCRIPTION’ file containing a ‘Built:’ field.

Under Unix-alikes, the code checks that the package was installed under a similar operating system as given by R.version$platform (the canonical name of the platform under which R was compiled), provided it contains compiled code. Packages which do not contain compiled code can be shared between Unix-alikes, but not to other OSes because of potential problems with line endings and OS-specific help files. If sub-architectures are used, the OS similarity is not checked since the OS used to build may differ (e.g. i386-pc-linux-gnu code can be built on an x86_64-unknown-linux-gnu OS).

The package name given to library and require must match the name given in the package’s ‘DESCRIPTION’ file exactly, even on case-insensitive file systems such as are common on Windows and macOS.

**References**


**See Also**

.libPaths, .packages, attach, detach, search, objects, autoload, requireNamespace, library.dynam, data, install.packages and installed.packages; INSTALL, REMOVE.

The initial set of packages attached is set by options(defaultPackages=): see also Startup.

**Examples**

```r
library() # list all available packages
library(lib.loc = .Library) # list all packages in the default library
library(help = splines) # documentation on package 'splines'
library(splines) # attach package 'splines'
require(splines) # the same
search() # "splines", too
```
library.dynam

Loading DLLs from Packages

Description

Load the specified file of compiled code if it has not been loaded already, or unloads it.

Usage

library.dynam(chname, package, lib.loc,
              verbose = getOption("verbose"),
              file.ext = .Platform$dynlib.ext, ...)

library.dynam.unload(chname, libpath,
                       verbose = getOption("verbose"),
                       file.ext = .Platform$dynlib.ext)

.dynLibs(new)

Arguments

chname a character string naming a DLL (also known as a dynamic shared object or library) to load.
package a character vector with the name of package.
lib.loc a character vector describing the location of R library trees to search through.
libpath the path to the loaded package whose DLL is to be unloaded.
verbose a logical value indicating whether an announcement is printed on the console before loading the DLL. The default value is taken from the verbose entry in the system options.
file.ext the extension (including "." if used) to append to the file name to specify the library to be loaded. This defaults to the appropriate value for the operating system.
... additional arguments needed by some libraries that are passed to the call to dyn.load to control how the library and its dependencies are loaded.
new a list of "DLLInfo" objects corresponding to the DLLs loaded by packages. Can be missing.
Details

See `dyn.load` for what sort of objects these functions handle.

`library.dynam` is designed to be used inside a package rather than at the command line, and should really only be used inside `.onLoad`. The system-specific extension for DLLs (e.g., `.so` or `.sl` on Unix-alike systems, `.dll` on Windows) should not be added.

`library.dynam.unload` is designed for use in `.onUnload`: it unloads the DLL and updates the value of `.dynLibs()`.

`.dynLibs` is used for getting (with no argument) or setting the DLLs which are currently loaded by packages (using `library.dynam`).

Value

If `chname` is not specified, `library.dynam` returns an object of class "DLLInfoList" corresponding to the DLLs loaded by packages.

If `chname` is specified, an object of class "DLLInfo" that identifies the DLL and which can be used in future calls is returned invisibly. Note that the class "DLLInfo" has a method for `$` which can be used to resolve native symbols within that DLL.

`library.dynam.unload` invisibly returns an object of class "DLLInfo" identifying the DLL successfully unloaded.

`.dynLibs` returns an object of class "DLLInfoList" corresponding to its current value.

Warning

Do not use `dyn.unload` on a DLL loaded by `library.dynam`: use `library.dynam.unload` to ensure that `.dynLibs` gets updated. Otherwise a subsequent call to `library.dynam` will be told the object is already loaded.

Note that whether or not it is possible to unload a DLL and then reload a revised version of the same file is OS-dependent: see the 'Value' section of the help for `dyn.unload`.

References


See Also

`getLoadedDLLs` for information on "DLLInfo" and "DLLInfoList" objects.

`onLoad`, `library`, `dyn.load`, `.packages`, `.libPaths`

`SHLIB` for how to create suitable DLLs.

Examples

```r
## Which DLLs were dynamically loaded by packages?
library.dynam()

## More on library.dynam.unload():
require(nlme)
nlme::.onUnload # shows library.dynam.unload() call
detach("package:nlme") # by default, unload=FALSE, so,
tail(library.dynam(), 2)# nlme still there
```
## How to unload the DLL ?
## Best is to unload the namespace, unloadNamespace("nlme")
## If we need to do it separately which should be exceptional:
pd.file <- attr(packageDescription("nlme"), "file")
library.dynam.unload("nlme", libpath = sub("/Meta.*", ",", pd.file))
tail(library.dynam(), 2) # 'nlme' is gone now
unloadNamespace("nlme") # now gives warning

---

### Description

The license terms under which R is distributed.

### Usage

- `license()`
- `licence()`

### Details

R is distributed under the terms of the GNU GENERAL PUBLIC LICENSE, either Version 2, June 1991 or Version 3, June 2007. A copy of the version 2 license is in file `$R_HOME/doc/COPYING` and can be viewed by RShowDoc("COPYING"). Version 3 of the license can be displayed by RShowDoc("GPL-3").

A small number of files (some of the API header files) are distributed under the LESSER GNU GENERAL PUBLIC LICENSE, version 2.1 or later. A copy of this license is in file `$R_SHARE_DIR/licenses/LGPL-2.1` and can be viewed by RShowDoc("LGPL-2.1"). Version 3 of the license can be displayed by RShowDoc("LGPL-3").

---

### list

#### Lists – Generic and Dotted Pairs

### Description

Functions to construct, coerce and check for both kinds of R lists.

### Usage

- `list(...)`
- `pairlist(...)`
- `as.list(x, ...)`
- `as.pairlist(x)`
- `is.list(x)`
- `is.pairlist(x)`
- `alist(...)`
Arguments

... objects, possibly named.

x object to be coerced or tested.

all.names a logical indicating whether to copy all values or (default) only those whose

names do not begin with a dot.

sorted a logical indicating whether the names of the resulting list should be sorted (increasingly). Note that this is somewhat costly, but may be useful for comparison of environments.

Details

Almost all lists in R internally are Generic Vectors, whereas traditional dotted pair lists (as in LISP) remain available but rarely seen by users (except as formals of functions).

The arguments to list or pairlist are of the form value or tag = value. The functions return a list or dotted pair list composed of its arguments with each value either tagged or untagged, depending on how the argument was specified.

alist handles its arguments as if they described function arguments. So the values are not evaluated, and tagged arguments with no value are allowed whereas list simply ignores them. alist is most often used in conjunction with formals.

as.list attempts to coerce its argument to a list. For functions, this returns the concatenation of the list of formal arguments and the function body. For expressions, the list of constituent elements is returned. as.list is generic, and as the default method calls as.vector(mode = "list") for a non-list, methods for as.vector may be invoked. as.list turns a factor into a list of one-element factors, keeping names. Other attributes may be dropped unless the argument already is a list or expression. (This is inconsistent with functions such as as.character which always drop attributes, and is for efficiency since lists can be expensive to copy.)

is.list returns TRUE if and only if its argument is a list or a pairlist of length > 0. is.pairlist returns TRUE if and only if the argument is a pairlist or NULL (see below).

The "environment" method for as.list copies the name-value pairs (for names not beginning with a dot) from an environment to a named list. The user can request that all named objects are copied. Unless sorted = TRUE, the list is in no particular order (the order depends on the order of creation of objects and whether the environment is hashed). No enclosing environments are searched. (Objects copied are duplicated so this can be an expensive operation.) Note that there is an inverse operation, the as.environment() method for list objects.

An empty pairlist, pairlist() is the same as NULL. This is different from list(): some but not all operations promote an empty pairlist to an empty list.

as.pairlist is implemented as as.vector(x, "pairlist"), and hence will dispatch methods for the generic function as.vector. Lists are copied element-by-element into a pairlist and the names of the list used as tags for the pairlist: the return value for other types of argument is undocumented.

list, is.list and is.pairlist are primitive functions.

References

See Also

vector("list", length) for creation of a list with empty components; c, for concatenation;
formals.unlist is an approximate inverse to as.list().

'plotmath' for the use of list in plot annotation.

Examples

require(graphics)

# create a plotting structure
pts <- list(x = cars[,1], y = cars[,2])
plot(pts)

is.pairlist(.Options)  # a user-level pairlist

## "pre-allocate" an empty list of length 5
vector("list", 5)

# Argument lists
f <- function() x
# Note the specification of a "..." argument:
formals(f) <- al <- alist(x = , y = 2+3, ... = )
f
al

## environment->list coercion

e1 <- new.env()
e1$a <- 10
e1$b <- 20
as.list(e1)

---

list.files

List the Files in a Directory/Folder

Description

These functions produce a character vector of the names of files or directories in the named directory.

Usage

list.files(path = ".", pattern = NULL, all.files = FALSE,
full.names = FALSE, recursive = FALSE,
ignore.case = FALSE, include.dirs = FALSE, no.. = FALSE)

dir(path = ".", pattern = NULL, all.files = FALSE,
full.names = FALSE, recursive = FALSE,
ignore.case = FALSE, include.dirs = FALSE, no.. = FALSE)

list.dirs(path = ".", full.names = TRUE, recursive = TRUE)
**Arguments**

- **path**: a character vector of full path names; the default corresponds to the working directory, `getwd()`. Tilde expansion (see `path.expand`) is performed. Missing values will be ignored. Elements with a marked encoding will be converted to the native encoding (and if that fails, considered non-existent).

- **pattern**: an optional regular expression. Only file names which match the regular expression will be returned.

- **all.files**: a logical value. If FALSE, only the names of visible files are returned (following Unix-style visibility, that is files whose name does not start with a dot). If TRUE, all file names will be returned.

- **full.names**: a logical value. If TRUE, the directory path is prepended to the file names to give a relative file path. If FALSE, the file names (rather than paths) are returned.

- **recursive**: logical. Should the listing recurse into directories?

- **ignore.case**: logical. Should pattern-matching be case-insensitive?

- **include.dirs**: logical. Should subdirectory names be included in recursive listings? (They always are in non-recursive ones).

- **no..**: logical. Should both "." and ".." be excluded also from non-recursive listings?

**Value**

A character vector containing the names of the files in the specified directories (empty if there were no files). If a path does not exist or is not a directory or is unreadable it is skipped.

The files are sorted in alphabetical order, on the full path if full.names = TRUE.

`list.files` implicitly has all.files = TRUE, and if recursive = TRUE, the answer includes path itself (provided it is a readable directory).

`dir` is an alias for `list.files`.

**Note**

File naming conventions are platform dependent. The pattern matching works with the case of file names as returned by the OS.

On a POSIX filesystem recursive listings will follow symbolic links to directories.

**Author(s)**

Ross Ihaka, Brian Ripley

**See Also**

- `file.info`, `file.access` and `files` for many more file handling functions and `file.choose` for interactive selection.
- `glob2rx` to convert wildcards (as used by system file commands and shells) to regular expressions.
- `Sys.glob` for wildcard expansion on file paths. `basename` and `dirname`, useful for splitting paths into non-directory (aka ‘filename’) and directory parts.
Examples

```r
list.files(R.home())
## Only files starting with a-l or r
## Note that a-l is locale-dependent, but using case-insensitive
## matching makes it unambiguous in English locales
dir("../..", pattern = "^[a-lr]", full.names = TRUE, ignore.case = TRUE)

dir(R.home("doc"))
lst.dirs(R.home("doc"), full.names = FALSE)
```

list2DF

**Create Data Frame From List**

Description

Create a data frame from a list of variables.

Usage

```r
list2DF(x = list(), nrow = 0)
```

Arguments

- `x` A list of same-length variables for the data frame.
- `nrow` An integer giving the desired number of rows for the data frame in case `x` gives no variables (i.e., has length zero).

Details

Note that all list elements are taken “as is”.

Value

A data frame with the given variables.

See Also

`data.frame`

Examples

```r
## Create a data frame holding a list of character vectors and the corresponding lengths:
x <- list(character(), "A", c("B", "C"))
n <- lengths(x)
list2DF(list(x = x, n = n))

## Create data frames with no variables and the desired number of rows:
list2DF()
list2DF(nrow = 3L)
```
list2env From A List, Build or Add To an Environment

Description

From a named list x, create an environment containing all list components as objects, or “multi-assign” from x into a pre-existing environment.

Usage

list2env(x, envir = NULL, parent = parent.frame(),
         hash = (length(x) > 100), size = max(29L, length(x)))

Arguments

x a list, where names(x) must not contain empty (""") elements.
envir an environment or NULL.
parent (for the case envir = NULL): a parent frame aka enclosing environment, see new.env.
hash (for the case envir = NULL): logical indicating if the created environment should use hashing, see new.env.
size (in the case envir = NULL, hash = TRUE): hash size, see new.env.

Details

This will be very slow for large inputs unless hashing is used on the environment.

Environments must have uniquely named entries, but named lists need not: where the list has duplicate names it is the last element with the name that is used. Empty names throw an error.

Value

An environment, either newly created (as by new.env) if the envir argument was NULL, otherwise the updated environment envir. Since environments are never duplicated, the argument envir is also changed.

Author(s)

Martin Maechler

See Also

environment, new.env, as.environment; further, assign.

The (semantical) “inverse”: as.list.environment.
**Examples**

L <- list(a = 1, b = 2:4, p = pi, ff = gl(3, 4, labels = LETTERS[1:3]))
e <- list2env(L)
ls(e)
stopifnot(ls(e) == sort(names(L)),
          identical(L$b, e$b)) # "$" working for environments as for lists

## consistency, when we do the inverse:
l1 <- as.list(e) # -> dispatching to the as.list.environment() method
rbind(names(L), names(l1)) # not in the same order, typically,
# but the same content:
stopifnot(identical(L [sort.list(names(L ))],
l1[sort.list(names(l1))]))

## now add to e -- can be seen as a fast "multi-assign":
list2env(list(abc = LETTERS, note = "just an example",
             df = data.frame(x = rnorm(20), y = rbinom(20, 1, prob = 0.2)),
             envir = e)
utils::ls.str(e)

---

**load**

Reload Saved Datasets

**Description**

Reload datasets written with the function save.

**Usage**

load(file, envir = parent.frame(), verbose = FALSE)

**Arguments**

- **file**: a (readable binary-mode) connection or a character string giving the name of the file to load (when tilde expansion is done).
- **envir**: the environment where the data should be loaded.
- **verbose**: should item names be printed during loading?

**Details**

load can load R objects saved in the current or any earlier format. It can read a compressed file (see save) directly from a file or from a suitable connection (including a call to ur1).

A not-open connection will be opened in mode "rb" and closed after use. Any connection other than a gzfile or gzcon connection will be wrapped in gzcon to allow compressed saves to be handled: note that this leaves the connection in an altered state (in particular, binary-only), and that it needs to be closed explicitly (it will not be garbage-collected).

Only R objects saved in the current format (used since R 1.4.0) can be read from a connection. If no input is available on a connection a warning will be given, but any input not in the current format will result in an error.

Loading from an earlier version will give a warning about the ‘magic number’: magic numbers 1971:1977 are from R < 0.99.0, and RD[ABX]1 from R 0.99.0 to R 1.3.1. These are all obsolete, and you are strongly recommended to re-save such files in a current format.
The verbose argument is mainly intended for debugging. If it is TRUE, then as objects from the file are loaded, their names will be printed to the console. If verbose is set to an integer value greater than one, additional names corresponding to attributes and other parts of individual objects will also be printed. Larger values will print names to a greater depth.

Objects can be saved with references to namespaces, usually as part of the environment of a function or formula. Such objects can be loaded even if the namespace is not available: it is replaced by a reference to the global environment with a warning. The warning identifies the first object with such a reference (but there may be more than one).

**Value**

A character vector of the names of objects created, invisibly.

**Warning**

Saved R objects are binary files, even those saved with ascii = TRUE, so ensure that they are transferred without conversion of end of line markers. load tries to detect such a conversion and gives an informative error message.

load(<file>) replaces all existing objects with the same names in the current environment (typically your workspace, .GlobalEnv) and hence potentially overwrites important data. It is considerably safer to use envir = to load into a different environment, or to attach(file) which load()s into a new entry in the search path.

**See Also**

save, download.file; further attach as wrapper for load().

For other interfaces to the underlying serialization format, see unserialize and readRDS.

**Examples**

```r
## save all data
xx <- pi # to ensure there is some data
save(list = ls(all.names = TRUE), file = "all.rda")
rm(xx)

## restore the saved values to the current environment
local({
  load("all.rda")
  ls()
})

xx <- exp(1:3)  # restore the saved values to the user's workspace
load("all.rda")  # which is here *equivalent* to
## load("all.rda",.GlobalEnv)
# This however annihilates all objects in .GlobalEnv with the same names!
xx # no longer exp(1:3)
rm(xx)
attach("all.rda") # safer and will warn about masked objects w/ same name in .GlobalEnv
ls(pos = 2)
## also typically need to cleanup the search path:
detach("file:all.rda")
```
## clean up (the example):
unlink("all.rda")

## Not run:
con <- url("http://some.where.net/R/data/example.rda")
## print the value to see what objects were created.
print(load(con))
close(con) # url() always opens the connection

## End(Not run)

### locales

**Query or Set Aspects of the Locale**

**Description**

Get details of or set aspects of the locale for the R process.

**Usage**

```r
Sys.getlocale (category = "LC_ALL")
Sys.setlocale (category = "LC_ALL", locale = "")
```

**Arguments**

- `category` character string. The following categories should always be supported:
  "LC_ALL", "LC_COLLATE", "LC_CTYPE", "LC_MONETARY", "LC_NUMERIC" and "LC_TIME". Some systems (not Windows) will also support "LC_MESSAGES", "LC_PAPER" and "LC_MEASUREMENT". These category names are available in `.LC.categories`; even when not supported, `Sys.getlocale(.)` will return "", e.g., for the "LC_PAPER" example on Windows.

- `locale` character string. A valid locale name on the system in use. Normally "" (the default) will pick up the default locale for the system.

**Details**

The locale describes aspects of the internationalization of a program. Initially most aspects of the locale of R are set to "C" (which is the default for the C language and reflects North-American usage – also known as "POSIX"). R sets "LC_CTYPE" and "LC_COLLATE", which allow the use of a different character set and alphabetic comparisons in that character set (including the use of `sort`), "LC_MONETARY" (for use by `Sys.localeconv`) and "LC_TIME" may affect the behaviour of `as.POSIXlt` and `strptime` and functions which use them (but not `date`).

The first seven categories described here are those specified by POSIX. "LC_MESSAGES" will be "C" on systems that do not support message translation, and is not supported on Windows, where you must use the `LANGUAGE` environment variable for message translation, see below and the `Sys.setLanguage()` utility. Trying to use an unsupported category is an error for `Sys.setlocale`.

Note that setting category "LC_ALL" sets only categories "LC_COLLATE", "LC_CTYPE", "LC_MONETARY" and "LC_TIME".
Attempts to set an invalid locale are ignored. There may or may not be a warning, depending on the OS.

Attempts to change the character set (by `Sys.setlocale("LC_CTYPE", )` if that implies a different character set) during a session may not work and are likely to lead to some confusion.

Note that the `LANGUAGE` environment variable has precedence over "LC_MESSAGES" in selecting the language for message translation on most R platforms.

On platforms where ICU is used for collation the locale used for collation can be reset by `icuSetCollate`. Except on Windows, the initial setting is taken from the "LC_COLLATE" category, and it is reset when this is changed by a call to `Sys.setlocale`.

### Value

A character string of length one describing the locale in use (after setting for `Sys.setlocale`), or an empty character string if the current locale settings are invalid or NULL if locale information is unavailable.

For `category = "LC_ALL"` the details of the string are system-specific: it might be a single locale name or a set of locale names separated by "/" (macOS) or ";" (Windows, Linux). For portability, it is best to query categories individually: it is not necessarily the case that the result of `foo <- Sys.getlocale()` can be used in `Sys.setlocale("LC_ALL", locale = foo)`.

### Available locales

On most Unix-alikes the POSIX shell command `locale -a` will list the ‘available public’ locales. What that means is platform-dependent. On recent Linuxen this may mean ‘available to be installed’ as on some RPM-based systems the locale data is in separate RPMs. On Debian/Ubuntu the set of available locales is managed by OS-specific facilities such as `locale-gen` and `locale -a` lists those currently enabled.

For Windows, Microsoft moves its documentation frequently so a Web search is the best way to find current information. From R 4.2, UCRT locale names should be used. The character set should match the system/ANSI codepage (`l10n_info()$codepage` be the same as `l10n_info()$system.codepage`). Setting it to any other value results in a warning and may cause encoding problems. As from R 4.2 on recent Windows the system codepage is 65001 and one should always use locale names ending with ".UTF-8" (except for "C" and ""), otherwise Windows may add a different character set.

### Warning

Setting "LC_NUMERIC" to any value other than "C" may cause R to function anomalously, so gives a warning. Input conversions in R itself are unaffected, but the reading and writing of ASCII save files will be, as may packages which do their own input/output.

Setting it temporarily on a Unix-alike to produce graphical or text output may work well enough, but `options(OutDec)` is often preferable.

Almost all the output routines used by R itself under Windows ignore the setting of "LC_NUMERIC" since they make use of the Trio library which is not internationalized.

### Note

Changing the values of locale categories whilst R is running ought to be noticed by the OS services, and usually is but exceptions have been seen (usually in collation services).

Do not use the value of `Sys.getlocale("LC_CTYPE")` to attempt to find the character set – for example UTF-8 locales can have suffix ‘.UTF-8’ or ‘.utf8’ (more common on Linux than
locales

'UTF-8') or none (as on macOS) and Latin-9 locales can have suffix ‘ISO8859-15’, ‘iso885915’, ‘iso885915@euro’ or ‘ISO8859-15@euro’. Use `n_info` instead.

See Also

`strptime` for uses of category = "LC_TIME". `localeconv` for details of numerical and monetary representations.

`n_info` gives some summary facts about the locale and its encoding (including if it is UTF-8).

The ‘R Installation and Administration’ manual for background on locales and how to find out locale names on your system.

Examples

Sys.getlocale()

## Date-time related:
Sys.getlocale("LC_TIME") -> olcT
then <- as.POSIXlt("2001-01-01 01:01:01", tz = "UTC+1")
## Not run:
c(m = months(then), wd = weekdays(then)) # locale specific
Sys.setlocale("LC_TIME", "de") # Solaris: details are OS-dependent
Sys.setlocale("LC_TIME", "de_DE") # Many Unix-alikes
Sys.setlocale("LC_TIME", "de_DE.UTF-8") # Linux, macOS, other Unix-alikes
Sys.setlocale("LC_TIME", "de_DE.utf8") # some Linux versions
Sys.setlocale("LC_TIME", "German.UTF-8") # Windows
Sys.getlocale("LC_TIME") # the last one successfully set above
c(m = months(then), wd = weekdays(then)) # in C_TIME locale ‘cT’; typically German

## End(Not run)
Sys.setlocale("LC_TIME", "C")
c(m = months(then), wd = weekdays(then)) # "standard" (still platform specific ?)
Sys.setlocale("LC_TIME", olcT) # reset to previous

## Other locales
Sys.getlocale("LC_PAPER") # may or may not be set
.LC.categories # of length 9 on all platforms

## Not run: Sys.setlocale("LC_COLLATE", "C") # turn off locale-specific sorting,
# usually (but not on all platforms)
Sys.setenv("LANGUAGE" = "es") # set the language for error/warning messages

## End(Not run)
## some nice formatting; should work on most platforms:
sys <- Sys.info()[["sysname"]]
sep <- switch(sys,
  "Darwin" = ", "SunOS" = "/",
  "Linux" =, "Windows" = ";")
##' show a "full" Sys.getlocale() nicely:
showL <- function(loc) {
  sl <- strsplit(strsplit(loc, sep)[[1]], ")
  setNames(sapply(sl, `[`, 2L), sapply(sl, `[`, 1L))
}
print.Dlist(lloc <- showL(Sys.getlocale()))
## R-supported ones (but LC_ALL):
lloc [.LC.categories[-1]]
**log**

*Logarithms and Exponentials*

**Description**

log computes logarithms, by default natural logarithms, log10 computes common (i.e., base 10) logarithms, and log2 computes binary (i.e., base 2) logarithms. The general form log(x, base) computes logarithms with base base.

log1p(x) computes log(1 + x) accurately also for |x| ≪ 1.

exp computes the exponential function.

expm1(x) computes exp(x) − 1 accurately also for |x| ≪ 1.

**Usage**

```r
log(x, base = exp(1))
logb(x, base = exp(1))
log10(x)
log2(x)
log1p(x)
exp(x)
expm1(x)
```

**Arguments**

- **x**: a numeric or complex vector.
- **base**: a positive or complex number: the base with respect to which logarithms are computed. Defaults to e = exp(1).

**Details**

All except logb are generic functions: methods can be defined for them individually or via the *Math* group generic.

log10 and log2 are only convenience wrappers, but logs to bases 10 and 2 (whether computed via log or the wrappers) will be computed more efficiently and accurately where supported by the OS. Methods can be set for them individually (and otherwise methods for log will be used).

logb is a wrapper for log for compatibility with S. If (S3 or S4) methods are set for log they will be dispatched. Do not set S4 methods on logb itself.

All except log are primitive functions.

**Value**

A vector of the same length as x containing the transformed values. log(0) gives -Inf, and log(x) for negative values of x is NaN. exp(-Inf) is 0.

For complex inputs to the log functions, the value is a complex number with imaginary part in the range [−π, π]: which end of the range is used might be platform-specific.
S4 methods

exp, expm1, log, log10, log2 and log1p are S4 generic and are members of the Math group generic. Note that this means that the S4 generic for log has a signature with only one argument, x, but that base can be passed to methods (but will not be used for method selection). On the other hand, if you only set a method for the Math group generic then base argument of log will be ignored for your class.

Source

log1p and expm1 may be taken from the operating system, but if not available there then they are based on the Fortran subroutine dlnrel by W. Fullerton of Los Alamos Scientific Laboratory (see https://netlib.org/slatec/fnlib/dlnrel.f) and (for small x) a single Newton step for the solution of log1p(y) = x respectively.

References


See Also

Trig, sqrt, Arithmetic.

Examples

log(exp(3))
log10(1e7) # = 7
x <- 10^-((1+2*1:9)
cbind(deparse.level=2, # to get nice column names
     x, log(1+x), log1p(x), exp(x)-1, expm1(x))

Logic Logical Operators

Description

These operators act on raw, logical and number-like vectors.

Usage

! x
x & y
x && y
x | y
x || y
xor(x, y)
isTRUE (x)
isFALSE(x)
Arguments

\(x, y\) raw, logical or ‘number-like’ vectors (i.e., of types double (class numeric), integer and complex), or objects for which methods have been written.

Details

! indicates logical negation (NOT).
& and && indicate logical AND and | and || indicate logical OR. The shorter forms performs elementwise comparisons in much the same way as arithmetic operators. The longer forms evaluates left to right, proceeding only until the result is determined. The longer form is appropriate for programming control-flow and typically preferred in if clauses.

Using vectors of more than one element in && or || will give an error.
xor indicates elementwise exclusive OR.
isTRUE(x) is the same as { is.logical(x) && length(x) == 1 && !is.na(x) && x ); isFALSE() is defined analogously. Consequently, if(isTRUE(cond)) may be preferable to if(cond) because of NAs.
In earlier \texttt{R} versions, isTRUE <- function(x) identical(x, TRUE), had the drawback to be false e.g., for x <- c(val = TRUE).
Numeric and complex vectors will be coerced to logical values, with zero being false and all non-zero values being true. Raw vectors are handled without any coercion for !, & and | and xor, with these operators being applied bitwise (so ! is the 1s-complement).
The operators !, & and | are generic functions: methods can be written for them individually or via the \texttt{Ops} (or S4 Logic, see below) group generic function. (See \texttt{Ops} for how dispatch is computed.)
\texttt{NA} is a valid logical object. Where a component of \(x\) or \(y\) is \texttt{NA}, the result will be \texttt{NA} if the outcome is ambiguous. In other words \texttt{NA \& TRUE} evaluates to \texttt{NA}, but \texttt{NA \& FALSE} evaluates to \texttt{FALSE}. See the examples below.

See \texttt{Syntax} for the precedence of these operators: unlike many other languages (including S) the AND and OR operators do not have the same precedence (the AND operators have higher precedence than the OR operators).

Value

For !, a logical or raw vector(for raw \(x\)) of the same length as \(x\): names, dims and dimnames are copied from \(x\), and all other attributes (including class) if no coercion is done.

For \(|\), \& and xor a logical or raw vector. If involving a zero-length vector the result has length zero. Otherwise, the elements of shorter vectors are recycled as necessary (with a warning when they are recycled only fractionally). The rules for determining the attributes of the result are rather complicated. Most attributes are taken from the longer argument, the first if they are of the same length. Names will be copied from the first if it is the same length as the answer, otherwise from the second if that is. For time series, these operations are allowed only if the series are compatible, when the class and tsp attribute of whichever is a time series (the same, if both are) are used. For arrays (and an array result) the dimensions and dimnames are taken from first argument if it is an array, otherwise the second.

For ||, && and isTRUE, a length-one logical vector.

S4 methods

!, & and | are S4 generics, the latter two part of the Logic group generic (and hence methods need argument names \(e1, e2\)).
logical

Note

The elementwise operators are sometimes called as functions as e.g. `&` \((x, y)\): see the description of how argument-matching is done in \texttt{Ops}.

References


See Also

\texttt{TRUE} or \texttt{logical}.
\texttt{any} and \texttt{all} for OR and AND on many scalar arguments.
\texttt{Syntax} for operator precedence.
\texttt{bitwAnd} for bitwise versions for integer vectors.

Examples

\begin{verbatim}
y <- 1 + (x <- stats::rpois(50, lambda = 1.5) / 4 - 1)
x[(x > 0) & (x < 1)] # all x values between 0 and 1
if (any(x == 0) || any(y == 0)) "zero encountered"

## construct truth tables :
x <- c(NA, FALSE, TRUE)
names(x) <- as.character(x)
outer(x, x, `&`) ## AND table
outer(x, x, `|`) ## OR table
\end{verbatim}

---

**Logical Vectors**

Description

Create or test for objects of type "logical", and the basic logical constants.

Usage

\begin{verbatim}
TRUE
FALSE
T; F
logical(length = 0)
as.logical(x, ...)
is.logical(x)
\end{verbatim}

Arguments

\begin{verbatim}
length A non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
x object to be coerced or tested.
... further arguments passed to or from other methods.
\end{verbatim}
TRUE and FALSE are reserved words denoting logical constants in the R language, whereas T and F are global variables whose initial values set to these. All four are logical(1) vectors.

Logical vectors are coerced to integer vectors in contexts where a numerical value is required, with TRUE being mapped to 1L, FALSE to 0L and NA to NA_integer_.

Value

`logical` creates a logical vector of the specified length. Each element of the vector is equal to FALSE.

`as.logical` attempts to coerce its argument to be of logical type. In numeric and complex vectors, zeros are FALSE and non-zero values are TRUE. For factors, this uses the `levels` (labels). Like `as.vector` it strips attributes including names. Character strings `c("T", "TRUE", "True", "true")` are regarded as true, `c("F", "FALSE", "False", "false")` as false, and all others as NA.

`is.logical` returns TRUE or FALSE depending on whether its argument is of logical type or not.

References


See Also

`NA`, the other logical constant. Logical operators are documented in `Logic`.

Examples

```r
## non-zero values are TRUE
as.logical(c(pi,0))
if (length(letters)) cat("26 is TRUE\n")

## logical interpretation of particular strings
charvec <- c("FALSE", "F", "false", "false", "False", "false", "FAlse", "0", "TRUE", "T", "True", "true", "tRue", "1")
as.logical(charvec)

## factors are converted via their levels, so string conversion is used
as.logical(factor(charvec))
as.logical(factor(c(0,1))) # "0" and "1" give NA
```

---

**Long Vectors**

Vectors of $2^{31}$ or more elements were added in R 3.0.0.
Details

Prior to R 3.0.0, all vectors in R were restricted to at most $2^{31} - 1$ elements and could be indexed by integer vectors.

Currently all atomic (raw, logical, integer, numeric, complex, character) vectors, lists and expressions can be much longer on 64-bit platforms: such vectors are referred to as ‘long vectors’ and have a slightly different internal structure. In theory they can contain up to $2^{52}$ elements, but address space limits of current CPUs and OSes will be much smaller. Such objects will have a length that is expressed as a double, and can be indexed by double vectors.

Arrays (including matrices) can be based on long vectors provided each of their dimensions is at most $2^{31} - 1$: thus there are no 1-dimensional long arrays.

R code typically only needs minor changes to work with long vectors, maybe only checking that \texttt{as.integer} is not used unnecessarily for e.g. lengths. However, compiled code typically needs quite extensive changes. Note that the \texttt{.C} and \texttt{.Fortran} interfaces do not accept long vectors, so \texttt{.Call} (or similar) has to be used.

Because of the storage requirements (a minimum of 64 bytes per character string), character vectors are only going to be usable if they have a small number of distinct elements, and even then factors will be more efficient (4 bytes per element rather than 8). So it is expected that most of the usage of long vectors will be integer vectors (including factors) and numeric vectors.

Matrix algebra

It is now possible to use $m \times n$ matrices with more than 2 billion elements. Whether matrix algebra (including \texttt{\%\%}, \texttt{crossprod}, \texttt{svd}, \texttt{qr}, \texttt{solve} and \texttt{eigen}) will actually work is somewhat implementation dependent, including the Fortran compiler used and if an external BLAS or LAPACK is used.

An efficient parallel BLAS implementation will often be important to obtain usable performance. For example on one particular platform \texttt{chol} on a 47,000 square matrix took about 5 hours with the internal BLAS, 21 minutes using an optimized BLAS on one core, and 2 minutes using an optimized BLAS on 16 cores.

lower.tri

\textit{Lower and Upper Triangular Part of a Matrix}

Description

Returns a matrix of logicals the same size of a given matrix with entries \texttt{TRUE} in the lower or upper triangle.

Usage

\begin{verbatim}
lower.tri(x, diag = FALSE)
upper.tri(x, diag = FALSE)
\end{verbatim}

Arguments

- \texttt{x} \hspace{1cm} a matrix or other R object with \texttt{length(dim(x))} == 2. For back compatibility reasons, when the above is not fulfilled, \texttt{as.matrix(x)} is called first.
- \texttt{diag} \hspace{1cm} logical. Should the diagonal be included?
See Also
diag.matrix; further row and col on which lower.tri() and upper.tri() are built.

Examples

(m2 <- matrix(1:20, 4, 5))
lower.tri(m2)
m2[lower.tri(m2)] <- NA
m2

ls  
List Objects

Description

ls and objects return a vector of character strings giving the names of the objects in the specified environment. When invoked with no argument at the top level prompt, ls shows what data sets and functions a user has defined. When invoked with no argument inside a function, ls returns the names of the function’s local variables: this is useful in conjunction with browser.

Usage

ls(name, pos = -1L, envir = as.environment(pos),
   all.names = FALSE, pattern, sorted = TRUE)
objects(name, pos = -1L, envir = as.environment(pos),
   all.names = FALSE, pattern, sorted = TRUE)

Arguments

name which environment to use in listing the available objects. Defaults to the current environment. Although called name for back compatibility, in fact this argument can specify the environment in any form; see the ‘Details’ section.
pos an alternative argument to name for specifying the environment as a position in the search list. Mostly there for back compatibility.
envir an alternative argument to name for specifying the environment. Mostly there for back compatibility.
all.names a logical value. If TRUE, all object names are returned. If FALSE, names which begin with a ‘.’ are omitted.
pattern an optional regular expression. Only names matching pattern are returned. glob2rx can be used to convert wildcard patterns to regular expressions.
sorted logical indicating if the resulting character should be sorted alphabetically. Note that this is part of ls() may take most of the time.

Details

The name argument can specify the environment from which object names are taken in one of several forms: as an integer (the position in the search list); as the character string name of an element in the search list; or as an explicit environment (including using sys.frame to access the currently active function calls). By default, the environment of the call to ls or objects is used. The pos
and `envir` arguments are an alternative way to specify an environment, but are primarily there for back compatibility.

Note that the order of strings for `sorted = TRUE` is locale dependent, see `Sys.getlocale`. If `sorted = FALSE` the order is arbitrary, depending if the environment is hashed, the order of insertion of objects, .....

References


See Also

`glob2rx` for converting wildcard patterns to regular expressions.

`ls.str` for a long listing based on `str.aappropos` (or `find`) for finding objects in the whole search path; `grep` for more details on 'regular expressions'; `class`, `methods`, etc., for object-oriented programming.

Examples

```r
.Ob <- 1
ls(pattern = "O")
ls(pattern = "O", all.names = TRUE)  # also shows ".[foo]"

# shows an empty list because inside myfunc no variables are defined
myfunc <- function() {ls()}
myfunc()

# define a local variable inside myfunc
myfunc <- function() {y <- 1; ls()}
myfunc()

# shows "y"
```

---

**make.names**

**Make Syntactically Valid Names**

**Description**

Make syntactically valid names out of character vectors.

**Usage**

`make.names(names, unique = FALSE, allow_ = TRUE)`

**Arguments**

- `names`: character vector to be coerced to syntactically valid names. This is coerced to character if necessary.
- `unique`: logical; if TRUE, the resulting elements are unique. This may be desired for, e.g., column names.
- `allow_`: logical. For compatibility with R prior to 1.9.0.
make.names

Details

A syntactically valid name consists of letters, numbers and the dot or underline characters and starts with a letter or the dot not followed by a number. Names such as ".2way" are not valid, and neither are the reserved words.

The definition of a letter depends on the current locale, but only ASCII digits are considered to be digits.

The character "X" is prepended if necessary. All invalid characters are translated to ".". A missing value is translated to "NA". Names which match R keywords have a dot appended to them. Duplicated values are altered by make.unique.

Value

A character vector of same length as names with each changed to a syntactically valid name, in the current locale’s encoding.

Warning

Some OSes, notably FreeBSD, report extremely incorrect information about which characters are alphabetic in some locales (typically, all multi-byte locales including UTF-8 locales). However, R provides substitutes on Windows, macOS and AIX.

Note

Prior to R version 1.9.0, underscores were not valid in variable names, and code that relies on them being converted to dots will no longer work. Use allow_ = FALSE for back-compatibility.

allow_ = FALSE is also useful when creating names for export to applications which do not allow underline in names (for example, S-PLUS and some DBMSes).

See Also

make.unique, names, character, data.frame.

Examples

make.names(c("a and b", "a-and-b"), unique = TRUE)
# "a.and.b" "a.and.b.1"
make.names(c("a and b", "a_and_b"), unique = TRUE)
# "a.and.b" "a_and_b"
make.names(c("a and b", "a_and_b"), unique = TRUE, allow_ = FALSE)
# "a.and.b" "a.and.b.1"
make.names(c("", "X"), unique = TRUE)
# "X.1" "X" currently; R up to 3.0.2 gave "X" "X.1"

state.name[make.names(state.name) != state.name] # those 10 with a space
**Description**

Makes the elements of a character vector unique by appending sequence numbers to duplicates.

**Usage**

```r
make.unique(names, sep = ".")
```

**Arguments**

- `names`: a character vector
- `sep`: a character string used to separate a duplicate name from its sequence number.

**Details**

The algorithm used by `make.unique` has the property that `make.unique(c(A, B)) == make.unique(c(make.unique(A), B)).` In other words, you can append one string at a time to a vector, making it unique each time, and get the same result as applying `make.unique` to all of the strings at once.

If character vector `A` is already unique, then `make.unique(c(A, B))` preserves `A`.

**Value**

A character vector of same length as `names` with duplicates changed, in the current locale’s encoding.

**Author(s)**

Thomas P. Minka

**See Also**

`make.names`

**Examples**

```r
make.unique(c("a", "a", "a"))
make.unique(c(make.unique(c("a", "a")), "a"))
make.unique(c("a", "a", "a.2", "a"))
make.unique(c(make.unique(c("a", "a")), "a.2", "a"))
## Now show a bit where this is used:
trace(make.unique)
## Applied in data.frame() constructions:
(d1 <- data.frame(x = 1, x = 2, x = 3)) # direct
d2 <- data.frame(data.frame(x = 1, x = 2), x = 3) # pairwise
stopifnot(identical(d1, d2),
           colnames(d1) == c("x", "x.1", "x.2"))
untrace(make.unique)
```
mapply

Apply a Function to Multiple List or Vector Arguments

Description

mapply is a multivariate version of sapply. mapply applies FUN to the first elements of each ...
argument, the second elements, the third elements, and so on. Arguments are recycled if neces-
sary.
.mapply() is a bare-bones version of mapply(), e.g., to be used in other functions.

Usage

mapply(FUN, ..., MoreArgs = NULL, SIMPLIFY = TRUE, 
USE.NAMES = TRUE)
.mapply(FUN, dots, MoreArgs)

Arguments

FUN function to apply, found via match.fun.
... arguments to vectorize over, will be recycled to common length (zero if one of 
them is). See also ‘Details’.
dots list or pairlist of arguments to vectorize over, see ... above.
MoreArgs a list of other arguments to FUN.
SIMPLIFY logical or character string; attempt to reduce the result to a vector, matrix or 
higher dimensional array; see the simplify argument of sapply.
USE.NAMES logical; use the names of the first ... argument, or if that is an unnamed character 
vector, use that vector as the names.

Details

mapply calls FUN for the values of ... (re-cycled to the length of the longest, unless any have 
length zero where recycling to zero length will return list()), followed by the arguments given in 
MoreArgs. The arguments in the call will be named if ... or MoreArgs are named.

For the arguments in ... (or components in dots) class specific subsetting (such as []) and length 
methods will be used where applicable.

Value

A list, or for SIMPLIFY = TRUE, a vector, array or list.

See Also

sapply, after which mapply() is modelled.
outer, which applies a vectorized function to all combinations of two arguments.
Examples

```r
mapply(rep, 1:4, 4:1)
mapply(rep, times = 1:4, x = 4:1)
mapply(rep, times = 1:4, MoreArgs = list(x = 42))
mapply(function(x, y) seq_len(x) + y,
c(a = 1, b = 2, c = 3), # names from first
c(A = 10, B = 0, C = -10))
word <- function(C, k) paste(rep.int(C, k), collapse = "")
## names from the first, too:
utils::str(L <- mapply(word, LETTERS[1:6], 6:1, SIMPLIFY = FALSE))
mapply(word, "A", integer()) # gave Error, now list()
```

marginSums

Compute table margins

Description

For a contingency table in array form, compute the sum of table entries for a given margin or set of margins.

Usage

```r
marginSums(x, margin = NULL)
margin.table(x, margin = NULL)
```

Arguments

- `x`: an array
- `margin`: a vector giving the margins to compute sums for. E.g., for a matrix 1 indicates rows, 2 indicates columns, c(1, 2) indicates rows and columns. When `x` has named dimnames, it can be a character vector selecting dimension names.

Value

The relevant marginal table, or just the sum of all entries if `margin` has length zero. The class of `x` is copied to the output table if `margin` is non-NULL.

Note

`margin.table` is an earlier name, retained for back-compatibility.

Author(s)

Peter Dalgaard

See Also

`proportions` and `addmargins`.
Examples

```r
m <- matrix(1:4, 2)
marginSums(m, 1)
marginSums(m, 2)
```

```r
DF <- as.data.frame(UCBAdmissions)
tbl <- xtabs(Freq ~ Gender + Admit, DF)

marginSums(tbl, "Gender")
proportions(tbl, "Gender")
```

---

### mat.or.vec

Create a Matrix or a Vector

**Description**

`mat.or.vec` creates an `nr` by `nc` zero matrix if `nc` is greater than 1, and a zero vector of length `nr` if `nc` equals 1.

**Usage**

```r
mat.or.vec(nr, nc)
```

**Arguments**

- `nr`, `nc` numbers of rows and columns.

**Examples**

```r
mat.or.vec(3, 1)
mat.or.vec(3, 2)
```

---

### match

Value Matching

**Description**

`match` returns a vector of the positions of (first) matches of its first argument in its second.

`%in%` is a more intuitive interface as a binary operator, which returns a logical vector indicating if there is a match or not for its left operand.

**Usage**

```r
match(x, table, nomatch = NA_integer_, incomparables = NULL)
```

```r
x %in% table
```
Arguments

x  vector or NULL: the values to be matched. Long vectors are supported.
table  vector or NULL: the values to be matched against. Long vectors are not supported.
nomatch  the value to be returned in the case when no match is found. Note that it is coerced to integer.
incomparables  a vector of values that cannot be matched. Any value in x matching a value in this vector is assigned the nomatch value. For historical reasons, FALSE is equivalent to NULL.

Details

%in% is currently defined as

"%in%" <- function(x, table) match(x, table, nomatch = 0) > 0

Factors, raw vectors and lists are converted to character vectors, internally classed objects are transformed via mtfrm, and then x and table are coerced to a common type (the later of the two types in R’s ordering, logical < integer < numeric < complex < character) before matching. If incomparables has positive length it is coerced to the common type.

Matching for lists is potentially very slow and best avoided except in simple cases.

Exactly what matches what is to some extent a matter of definition. For all types, NA matches NA and no other value. For real and complex values, NaN values are regarded as matching any other NaN value, but not matching NA, where for complex x, real and imaginary parts must match both (unless containing at least one NA).

Character strings will be compared as byte sequences if any input is marked as "bytes", and otherwise are regarded as equal if they are in different encodings but would agree when translated to UTF-8 (see Encoding).

That %in% never returns NA makes it particularly useful in if conditions.

Value

A vector of the same length as x.

match: An integer vector giving the position in table of the first match if there is a match, otherwise nomatch.

If x[i] is found to equal table[j] then the value returned in the i-th position of the return value is j, for the smallest possible j. If no match is found, the value is nomatch.

%in%: A logical vector, indicating if a match was located for each element of x: thus the values are TRUE or FALSE and never NA.

References


See Also

pmatch and charmatch for (partial) string matching, match.arg, etc for function argument matching. findInterval similarly returns a vector of positions, but finds numbers within intervals, rather than exact matches.

is.element for an S-compatible equivalent of %in%.
**match.arg**

**Argument Verification Using Partial Matching**

**Description**

`match.arg` matches a character `arg` against a table of candidate values as specified by `choices`.

**Usage**

`match.arg(arg, choices, several.ok = FALSE)`
**match.arg**

Arguments

- **arg**: a character vector (of length one unless several.ok is TRUE) or NULL which means to take choices[1].
- **choices**: a character vector of candidate values, often missing, see ‘Details’.
- **several.ok**: logical specifying if arg should be allowed to have more than one element.

Details

In the one-argument form `match.arg(arg)`, the choices are obtained from a default setting for the formal argument arg of the function from which `match.arg` was called. (Since default argument matching will set arg to choices, this is allowed as an exception to the ‘length one unless several.ok is TRUE’ rule, and returns the first element.)

Matching is done using `pmatch`, so arg may be abbreviated and the empty string (“”) never matches, not even itself, see `pmatch`.

Value

The unabbreviated version of the exact or unique partial match if there is one; otherwise, an error is signalled if several.ok is false, as per default. When several.ok is true and (at least) one element of arg has a match, all unabbreviated versions of matches are returned.

Warning

The error messages given are liable to change and did so in R 4.2.0. Do not test them in packages.

See Also

`pmatch`, `match.fun`, `match.call`.

Examples

```r
require(stats)
## Extends the example for 'switch'
center <- function(x, type = c("mean", "median", "trimmed")) {
  type <- match.arg(type)
  switch(type,
    mean = mean(x),
    median = median(x),
    trimmed = mean(x, trim = .1))
}
x <- rcauchy(10)
center(x, "t")  # Works
center(x, "med")  # Works
try(center(x, "m"))  # Error
stopifnot(identical(center(x), center(x, "mean")),
          identical(center(x, NULL), center(x, "mean")))
```

```r
## Allowing more than one 'arg' and hence more than one match:
match.arg(c("gauss", "rect", "ep"),
          c("gaussian", "epanechnikov", "rectangular", "triangular"),
          several.ok = TRUE)
match.arg(c("a", ""), c("", NA, "bb", "abc"), several.ok=TRUE) # |--> "abc"
```
match.call

Argument Matching

Description

match.call returns a call in which all of the specified arguments are specified by their full names.

Usage

match.call(definition = sys.function(sys.parent()),
           call = sys.call(sys.parent()),
           expand.dots = TRUE,
           envir = parent.frame(2L))

Arguments

definition a function, by default the function from which match.call is called. See details.
call an unevaluated call to the function specified by definition, as generated by call.
expand.dots logical. Should arguments matching ... in the call be included or left as a ... argument?
envir an environment, from which the ... in call are retrieved, if any.

Details

‘function’ on this help page means an interpreted function (also known as a ‘closure’): match.call does not support primitive functions (where argument matching is normally positional). match.call is most commonly used in two circumstances:

- To record the call for later re-use: for example most model-fitting functions record the call as element call of the list they return. Here the default expand.dots = TRUE is appropriate.
- To pass most of the call to another function, often model.frame. Here the common idiom is that expand.dots = FALSE is used, and the ... element of the matched call is removed. An alternative is to explicitly select the arguments to be passed on, as is done in lm.

Calling match.call outside a function without specifying definition is an error.

Value

An object of class call.

References


See Also

sys.call() is similar, but does not expand the argument names; call, pmatch, match.arg, match.fun.
Examples
match.call(get, call("get", "abc", i = FALSE, p = 3))
## -> get(x = "abc", pos = 3, inherits = FALSE)
fun <- function(x, lower = 0, upper = 1) {
  structure((x - lower) / (upper - lower), CALL = match.call())
}
fun(4 * atan(1), u = pi)

match.fun

Extract a Function Specified by Name

Description
When called inside functions that take a function as argument, extract the desired function object while avoiding undesired matching to objects of other types.

Usage
match.fun(FUN, descend = TRUE)

Arguments
FUN item to match as function: a function, symbol or character string. See ‘Details’. descend logical; control whether to search past non-function objects.

Details
match.fun is not intended to be used at the top level since it will perform matching in the parent of the caller.

If FUN is a function, it is returned. If it is a symbol (for example, enclosed in backquotes) or a character vector of length one, it will be looked up using get in the environment of the parent of the caller. If it is of any other mode, it is attempted first to get the argument to the caller as a symbol (using substitute twice), and if that fails, an error is declared.

If descend = TRUE, match.fun will look past non-function objects with the given name; otherwise if FUN points to a non-function object then an error is generated.

This is used in base functions such as apply, lapply, outer, and sweep.

Value
A function matching FUN or an error is generated.

Bugs
The descend argument is a bit of misnomer and probably not actually needed by anything. It may go away in the future.

It is impossible to fully foolproof this. If one attaches a list or data frame containing a length-one character vector with the same name as a function, it may be used (although namespaces will help).

Author(s)
Peter Dalgaard and Robert Gentleman, based on an earlier version by Jonathan Rougier.
MathFun

Miscellaneous Mathematical Functions

Description
abs(x) computes the absolute value of x, sqrt(x) computes the (principal) square root of x, $\sqrt{x}$.

The naming follows the standard for computer languages such as C or Fortran.

Usage
abs(x)
sqrt(x)

Arguments
x  a numeric or complex vector or array.

Details
These are internal generic primitive functions: methods can be defined for them individually or via the Math group generic. For complex arguments (and the default method), z, abs(z) == Mod(z) and sqrt(z) == z^0.5.

abs(x) returns an integer vector when x is integer or logical.

S4 methods
Both are S4 generic and members of the Math group generic.

References

See Also
Arithmetic for simple, log for logarithmic, sin for trigonometric, and Special for special mathematical functions.

'plotmath' for the use of sqrt in plot annotation.
Examples

```r
require(stats) # for spline
require(graphics)
xx <- -9:9
plot(xx, sqrt(abs(xx)), col = "red")
lines(spline(xx, sqrt(abs(xx)), n=101), col = "pink")
```

Description

Multiplies two matrices, if they are conformable. If one argument is a vector, it will be promoted to either a row or column matrix to make the two arguments conformable. If both are vectors of the same length, it will return the inner product (as a matrix).

Usage

```r
x %*% y
```

Arguments

- `x`, `y`: numeric or complex matrices or vectors.

Details

When a vector is promoted to a matrix, its names are not promoted to row or column names, unlike `as.matrix`.

Promotion of a vector to a 1-row or 1-column matrix happens when one of the two choices allows `x` and `y` to get conformable dimensions.

This operator is a generic function: methods can be written for it individually or via the `matOps` group generic function; it dispatches to S3 and S4 methods. Methods need to be written for a function that takes two arguments named `x` and `y`.

Value

A double or complex matrix product. Use `drop` to remove dimensions which have only one level.

Note

The propagation of NaN/Inf values, precision, and performance of matrix products can be controlled by `options("matprod")`.

References


See Also

For matrix crossproducts, `crossprod()` and `tcrossprod()` are typically preferable. `matrix`, `Arithmetic`, `diag`. 
Examples

```r
x <- 1:4
(z <- x %*% x) # scalar ("inner") product (1 x 1 matrix)
drop(z) # as scalar

y <- diag(x)
z <- matrix(1:12, ncol = 3, nrow = 4)
y %*% z
y %*% x
x %*% z
```

matrix  

Matrices

Description

matrix creates a matrix from the given set of values.
as.matrix attempts to turn its argument into a matrix.
is.matrix tests if its argument is a (strict) matrix.

Usage

```r
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE,
       dimnames = NULL)
as.matrix(x, ...)  
## S3 method for class 'data.frame'
as.matrix(x, rownames.force = NA, ...)
is.matrix(x)
```

Arguments

data an optional data vector (including a list or expression vector). Non-atomic classed R objects are coerced by as.vector and all attributes discarded.
nrow the desired number of rows.
ncol the desired number of columns.
byrow logical. If FALSE (the default) the matrix is filled by columns, otherwise the matrix is filled by rows.

```r
dimnames A dimnames attribute for the matrix: NULL or a list of length 2 giving the row and column names respectively. An empty list is treated as NULL, and a list of length one as row names. The list can be named, and the list names will be used as names for the dimensions.
```
x an R object.

... additional arguments to be passed to or from methods.

rownames.force logical indicating if the resulting matrix should have character (rather than NULL) rownames. The default, NA, uses NULL rownames if the data frame has \( \text{automatic} \) row.names or for a zero-row data frame.
Details

If one of nrow or ncol is not given, an attempt is made to infer it from the length of data and the other parameter. If neither is given, a one-column matrix is returned.

If there are too few elements in data to fill the matrix, then the elements in data are recycled. If data has length zero, NA of an appropriate type is used for atomic vectors (0 for raw vectors) and NULL for lists.

is.matrix returns TRUE if x is a vector and has a "dim" attribute of length 2 and FALSE otherwise. Note that a data.frame is not a matrix by this test. The function is generic: you can write methods to handle specific classes of objects, see InternalMethods.

as.matrix is a generic function. The method for data frames will return a character matrix if there is only atomic columns and any non-(numeric/logical/complex) column, applying as.vector to factors and format to other non-character columns. Otherwise, the usual coercion hierarchy (logical < integer < double < complex) will be used, e.g., all-logical data frames will be coerced to a logical matrix, mixed logical-integer will give a integer matrix, etc.

The default method for as.matrix calls as.vector(x), and hence e.g. coerces factors to character vectors.

When coercing a vector, it produces a one-column matrix, and promotes the names (if any) of the vector to the rownames of the matrix.

is.matrix is a primitive function.

The print method for a matrix gives a rectangular layout with dimnames or indices. For a list matrix, the entries of length not one are printed in the form 'integer,7' indicating the type and length.

Note

If you just want to convert a vector to a matrix, something like

```r
dim(x) <- c(nx, ny)
dimnames(x) <- list(row_names, col_names)
```

will avoid duplicating x and preserve class(x) which may be useful, e.g., for Date objects.

References


See Also

data.matrix, which attempts to convert to a numeric matrix.

A matrix is the special case of a two-dimensional array, inherits(m, "array") is true for a matrix m.

Examples

```r
is.matrix(as.matrix(1:10))
!is.matrix(warpbreaks)  # data.frame, NOT matrix!
warpbreaks[1:10,]
as.matrix(warpbreaks[1:10,])  # using as.matrix.data.frame(.) method
```

## Example of setting row and column names
maxCol

Find Maximum Position in Matrix

Description

Find the maximum position for each row of a matrix, breaking ties at random.

Usage

max.col(m, ties.method = c("random", "first", "last"))

Arguments

m  
numerical matrix

ties.method  
a character string specifying how ties are handled, "random" by default; can be abbreviated; see 'Details'.

Details

When ties.method = "random", as per default, ties are broken at random. In this case, the determination of a tie assumes that the entries are probabilities: there is a relative tolerance of $10^{-5}$, relative to the largest (in magnitude, omitting infinity) entry in the row.

If ties.method = "first", max.col returns the column number of the first of several maxima in every row, the same as `unnname(apply(m, 1, which.max))` if m has no missing values. Correspondingly, ties.method = "last" returns the last of possibly several indices.

Value

index of a maximal value for each row, an integer vector of length nrow(m).

References


See Also

which.max for vectors.
mean

Examples

```r
table(mc <- max.col(swiss))  # mostly "1" and "5", 5 x "2" and once "4"
swiss[unique(print(mr <- max.col(t(swiss)))), ]  # 3 33 45 45 33 6

set.seed(1)  # reproducible example:
(mm <- rbind(x = round(2*stats::runif(12)),
y = round(5*stats::runif(12)),
z = round(8*stats::runif(12))))

## Not run:
x 1 1 1 2 0 2 2 1 1 0 0 0
y 3 2 4 2 4 5 2 4 5 1 3 1
z 2 3 0 3 7 3 4 5 4 1 7 5

## End(Not run)
## column indices of all row maxima :
utils::str(lapply(1:3, function(i) which(mm[i,] == max(mm[i,]))))
max.col(mm) ; max.col(mm)  # "random"
max.col(mm, "first")  # -> 4 6 5
max.col(mm, "last")  # -> 7 9 11
```

mean

### Arithmetic Mean

**Description**

Generic function for the (trimmed) arithmetic mean.

**Usage**

```r
mean(x, ...)
```

#### Default S3 method:

```r
mean(x, trim = 0, na.rm = FALSE, ...)
```

**Arguments**

- **x**
  
  An R object. Currently there are methods for numeric/logical vectors and date, date-time and time interval objects. Complex vectors are allowed for `trim = 0`, only.

- **trim**
  
  the fraction (0 to 0.5) of observations to be trimmed from each end of `x` before the mean is computed. Values of trim outside that range are taken as the nearest endpoint.

- **na.rm**
  
  a logical evaluating to TRUE or FALSE indicating whether NA values should be stripped before the computation proceeds.

- **...**
  
  further arguments passed to or from other methods.
Value

If `trim` is zero (the default), the arithmetic mean of the values in `x` is computed, as a numeric or complex vector of length one. If `x` is not logical (coerced to numeric), numeric (including integer) or complex, `NA_real_` is returned, with a warning.

If `trim` is non-zero, a symmetrically trimmed mean is computed with a fraction of `trim` observations deleted from each end before the mean is computed.

References


See Also

`weighted.mean`, `mean.POSIXct`, `colMeans` for row and column means.

Examples

```r
x <- c(0:10, 50)
xm <- mean(x)
c(xm, mean(x, trim = 0.10))
```

memCompress

**In-memory Compression and Decompression**

Description

In-memory compression or decompression for raw vectors.

Usage

```r
memCompress(from, type = c("gzip", "bzip2", "xz", "none"))
memDecompress(from, 
    type = c("unknown", "gzip", "bzip2", "xz", "none"),
    asChar = FALSE)
```

Arguments

- **from**: A raw vector. For `memCompress` a character vector will be converted to a raw vector with character strings separated by "\n". Types except "bzip2" support long raw vectors.
- **type**: character string, the type of compression. May be abbreviated to a single letter, defaults to the first of the alternatives.
- **asChar**: logical: should the result be converted to a character string? NB: character strings have a limit of $2^{31} - 1$ bytes, so raw vectors should be used for large inputs.
### Details

type = "none" passes the input through unchanged, but may be useful if type is a variable.

type = "unknown" attempts to detect the type of compression applied (if any): this will always succeed for bzip2 compression, and will succeed for other forms if there is a suitable header. If no type of compression is detected this is the same as type = "none" but a warning is given.

gzip compression uses whatever is the default compression level of the underlying library (usually 6). This supports the RFC 1950 format, sometimes known as ‘zlib’ format, for compression and decompression and for decompression only RFC 1952, the ‘gzip’ format (which wraps the ‘zlib’ format with a header and footer).

bzip2 compression always adds a header ("BZh"). The underlying library only supports in-memory (de)compression of up to \(2^{31} - 1\) elements. Compression is equivalent to bzip2 -9 (the default).

Compressing with type = "xz" is equivalent to compressing a file with xz -9e (including adding the ‘magic’ header): decompression should cope with the contents of any file compressed by xz version 4.999 and later, as well as by some versions of lzma. There are other versions, in particular ‘raw’ streams, that are not currently handled.

All the types of compression can expand the input: for "gzip" and "bzip2" the maximum expansion is known and so memCompress can always allocate sufficient space. For "xz" it is possible (but extremely unlikely) that compression will fail if the output would have been too large.

### Value

A raw vector or a character string (if asChar = TRUE).

### See Also

connections.

extSoftVersion for the versions of the zlib, bzip2 and xz libraries in use.

https://en.wikipedia.org/wiki/Data_compression for background on data compression,

### Examples

txt <- readLines(file.path(R.home("doc"), "COPYING"))
sum(nchar(txt))
txt.gz <- memCompress(txt, "g")
length(txt.gz)
txt2 <- strsplit(memDecompress(txt.gz, "g", asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt2))
txt.bz2 <- memCompress(txt, "b")
length(txt.bz2)
## can auto-detect bzip2:
txt3 <- strsplit(memDecompress(txt.bz2, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))

## xz compression is only worthwhile for large objects
txt.xz <- memCompress(txt, "x")
length(txt.xz)
txt3 <- strsplit(memDecompress(txt.xz, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))
### memlimits

#### Query and Set Heap Size Limits

**Description**

Query and set the maximal size of the vector heap and the maximal number of heap nodes for the current R process.

**Usage**

- `mem.maxVSize(vsize = 0)`
- `mem.maxNSize(nsize = 0)`

**Arguments**

- `vsize` numeric; new size limit in Mb.
- `nsize` numeric; new maximal node number.

**Details**

New Limits lower than current usage are ignored. Specifying a size of `Inf` sets the limit to the maximal possible value for the platform.

The default maximal values are unlimited on most platforms, but can be adjusted using environment variables as described in `Memory`. On macOS a lower default vector heap limit is used to protect against the R process being killed when macOS over-commits memory.

Adjusting the maximal number of nodes is rarely necessary. Adjusting the vector heap size limit can be useful on macOS in particular but should be done with caution.

**Value**

The current or new value, in Mb for `mem.maxVSize`. Inf is returned if the current value is unlimited.

**See Also**

`Memory`. 

```r
## test decompressing a gzip-ed file
tf <- tempfile(fileext = ".gz")
con <- gzfile(tf, "w")
writeLines(txt, con)
close(con)
(nf <- file.size(tf))
# if (nzchar(Sys.which("file"))) system2("file", tf)
foo <- readBin(tf, "raw", n = nf)
unlink(tf)
## will detect the gzip header and choose type = "gzip"
txt3 <- strsplit(memDecompress(foo, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))
```
Description

How R manages its workspace.

Details

R has a variable-sized workspace. There are (rarely-used) command-line options to control its minimum size, but no longer any to control the maximum size.

R maintains separate areas for fixed and variable sized objects. The first of these is allocated as an array of cons cells (Lisp programmers will know what they are, others may think of them as the building blocks of the language itself, parse trees, etc.), and the second are thrown on a heap of Vcells of 8 bytes each. Each cons cell occupies 28 bytes on a 32-bit build of R, (usually) 56 bytes on a 64-bit build.

The default values are (currently) an initial setting of 350k cons cells and 6Mb of vector heap. Note that the areas are not actually allocated initially: rather these values are the sizes for triggering garbage collection. These values can be set by the command line options '--min-nsize' and '--min-vsize' (or if they are not used, the environment variables R_NSIZE and R_VSIZE) when R is started. Thereafter R will grow or shrink the areas depending on usage, never decreasing below the initial values. The maximal vector heap size can be set with the environment variable R_MAX_VSIZE.

How much time R spends in the garbage collector will depend on these initial settings and on the trade-off the memory manager makes, when memory fills up, between collecting garbage to free up unused memory and growing these areas. The strategy used for growth can be specified by setting the environment variable R_GC_MEM_GROW to an integer value between 0 and 3. This variable is read at start-up. Higher values grow the heap more aggressively, thus reducing garbage collection time but using more memory.

You can find out the current memory consumption (the heap and cons cells used as numbers and megabytes) by typing gc() at the R prompt. Note that following gcinfo(TRUE), automatic garbage collection always prints memory use statistics.

The command-line option '--max-ppsize' controls the maximum size of the pointer protection stack. This defaults to 50000, but can be increased to allow deep recursion or large and complicated calculations to be done. Note that parts of the garbage collection process goes through the full reserved pointer protection stack and hence becomes slower when the size is increased. Currently the maximum value accepted is 500000.

See Also

An Introduction to R for more command-line options.
Memory-limits for the design limitations.
gc for information on the garbage collector and total memory usage, object.size(a) for the (approximate) size of R object a. memory.profile for profiling the usage of cons cells.
Memory-limits

Memory Limits in R

Description

R holds objects it is using in virtual memory. This help file documents the current design limitations on large objects: these differ between 32-bit and 64-bit builds of R.

Details

Currently R runs on 32- and 64-bit operating systems, and most 64-bit OSes (including Linux, Solaris, Windows and macOS) can run either 32- or 64-bit builds of R. The memory limits depends mainly on the build, but for a 32-bit build of R on Windows they also depend on the underlying OS version.

R holds all objects in virtual memory, and there are limits based on the amount of memory that can be used by all objects:

- There may be limits on the size of the heap and the number of cons cells allowed – see Memory – but these are usually not imposed.
- There is a limit on the (user) address space of a single process such as the R executable. This is system-specific, and can depend on the executable.
- The environment may impose limitations on the resources available to a single process: Windows’ versions of R do so directly.

Error messages beginning cannot allocate vector of size indicate a failure to obtain memory, either because the size exceeded the address-space limit for a process or, more likely, because the system was unable to provide the memory. Note that on a 32-bit build there may well be enough free memory available, but not a large enough contiguous block of address space into which to map it.

There are also limits on individual objects. The storage space cannot exceed the address limit, and if you try to exceed that limit, the error message begins cannot allocate vector of length. The number of bytes in a character string is limited to $2^{31} - 1 \approx 2 \times 10^9$, which is also the limit on each dimension of an array.

Unix

The address-space limit is system-specific: 32-bit OSes imposes a limit of no more than 4Gb: it is often 3Gb. Running 32-bit executables on a 64-bit OS will have similar limits: 64-bit executables will have an essentially infinite system-specific limit (e.g., 128Tb for Linux on x86_64 cpus).

See the OS/shell’s help on commands such as limit or ulimit for how to impose limitations on the resources available to a single process. For example a bash user could use

```bash
ulimit -t 600 -v 4000000
```

whereas a csh user might use

```csh
limit cputime 10m
limit vmemmyuse 4096m
```

to limit a process to 10 minutes of CPU time and (around) 4Gb of virtual memory. (There are other options to set the RAM in use, but they are not generally honoured.)
Windows

The address-space limit is 2Gb under 32-bit Windows unless the OS’s default has been changed to allow more (up to 3Gb). See [https://docs.microsoft.com/en-gb/windows/desktop/Memory/physical-address-extension](https://docs.microsoft.microsoft.com/en-gb/windows/desktop/Memory/physical-address-extension) and [https://docs.microsoft.com/en-gb/windows/desktop/Memory/4-gigabyte-tuning](https://docs.microsoft.com/en-gb/windows/desktop/Memory/4-gigabyte-tuning). Under most 64-bit versions of Windows the limit for a 32-bit build of R is 4Gb: for the oldest ones it is 2Gb. The limit for a 64-bit build of R (imposed by the OS) is 8Tb.

It is not normally possible to allocate as much as 2Gb to a single vector in a 32-bit build of R even on 64-bit Windows because of preallocations by Windows in the middle of the address space.

See Also

`object.size(a)` for the (approximate) size of R object a.

---

memory.profile Profile the Usage of Cons Cells

Description

Lists the usage of the cons cells by SEXP type.

Usage

`memory.profile()`

Details

The current types and their uses are listed in the include file ‘Rinternals.h’.

Value

A vector of counts, named by the types. See `typeof` for an explanation of types.

See Also

`gc` for the overall usage of cons cells. Rprofmem and tracemem allow memory profiling of specific code or objects, but need to be enabled at compile time.

Examples

`memory.profile()`
merge Two Data Frames

Description

Merge two data frames by common columns or row names, or do other versions of database join operations.

Usage

merge(x, y, ...)

## Default S3 method:
merge(x, y, ...)

## S3 method for class 'data.frame'
merge(x, y, by = intersect(names(x), names(y)),
      by.x = by, by.y = by, all = FALSE, all.x = all, all.y = all,
      sort = TRUE, suffixes = c(".x",".y"), no.dups = TRUE,
      incomparables = NULL, ...)

Arguments

x, y       data frames, or objects to be coerced to one.
by, by.x, by.y specifications of the columns used for merging. See ‘Details’.
all        logical; all = L is shorthand for all.x = L and all.y = L, where L is either TRUE or FALSE.
all.x      logical; if TRUE, then extra rows will be added to the output, one for each row in x that has no matching row in y. These rows will have NAs in those columns that are usually filled with values from y. The default is FALSE, so that only rows with data from both x and y are included in the output.
all.y      logical; analogous to all.x.
sort       logical. Should the result be sorted on the by columns?
suffixes   a character vector of length 2 specifying the suffixes to be used for making unique the names of columns in the result which are not used for merging (appearing in by etc).
no.dups    logical indicating that suffixes are appended in more cases to avoid duplicated column names in the result. This was implicitly false before R version 3.5.0.
incomparables values which cannot be matched. See match. This is intended to be used for merging on one column, so these are incomparable values of that column.
... arguments to be passed to or from methods.

Details

merge is a generic function whose principal method is for data frames: the default method coheres its arguments to data frames and calls the "data.frame" method.

By default the data frames are merged on the columns with names they both have, but separate specifications of the columns can be given by by.x and by.y. The rows in the two data frames that
match on the specified columns are extracted, and joined together. If there is more than one match, all possible matches contribute one row each. For the precise meaning of ‘match’, see `match`.

Columns to merge on can be specified by name, number or by a logical vector: the name "row.names" or the number 0 specifies the row names. If specified by name it must correspond uniquely to a named column in the input.

If by or both by.x and by.y are of length 0 (a length zero vector or NULL), the result, r, is the Cartesian product of x and y, i.e., dim(r) = c(nrow(x)*nrow(y), ncol(x) + ncol(y)).

If all.x is true, all the non matching cases of x are appended to the result as well, with NA filled in the corresponding columns of y; analogously for all.y.

If the columns in the data frames not used in merging have any common names, these have suffixes (".x" and ".y" by default) appended to try to make the names of the result unique. If this is not possible, an error is thrown.

If a by.x column name matches one of y, and if no.dups is true (as by default), the y version gets suffixed as well, avoiding duplicate column names in the result.

The complexity of the algorithm used is proportional to the length of the answer.

In SQL database terminology, the default value of all = FALSE gives a natural join, a special case of an inner join. Specifying all.x = TRUE gives a left (outer) join, all.y = TRUE a right (outer) join, and both (all = TRUE) a (full) outer join. DBMSes do not match NULL records, equivalent to incomparables = NA in R.

Value

A data frame. The rows are by default lexicographically sorted on the common columns, but for sort = FALSE are in an unspecified order. The columns are the common columns followed by the remaining columns in x and then those in y. If the matching involved row names, an extra character column called Row.names is added at the left, and in all cases the result has ‘automatic’ row names.

Note

This is intended to work with data frames with vector-like columns: some aspects work with data frames containing matrices, but not all.

Currently long vectors are not accepted for inputs, which are thus restricted to less than 2^31 rows. That restriction also applies to the result for 32-bit platforms.

See Also

data.frame, by, cbind.
dendrogram for a class which has a merge method.

Examples

```r
authors <- data.frame(
  ## I(*) : use character columns of names to get sensible sort order
  surname = I(c("Tukey", "Venables", "Tierney", "Ripley", "McNeil")),
  nationality = c("US", "Australia", "US", "UK", "Australia"),
  deceased = c("yes", rep("no", 4)))
authorN <- within(authors, { name <- surname; rm(surname) })
books <- data.frame(
  name = I(c("Tukey", "Venables", "Tierney", "Ripley", "Ripley", "McNeil", "R Core")),
  title = c("Exploratory Data Analysis",
```
"Modern Applied Statistics ...",
"LISP-STAT",
"Spatial Statistics", "Stochastic Simulation",
"Interactive Data Analysis",
"An Introduction to R"),
other.author = c(NA, "Ripley", NA, NA, NA, NA,
   "Venables & Smith")

(m0 <- merge(authorN, books))
(m1 <- merge(authors, books, by.x = "surname", by.y = "name"))
m2 <- merge(books, authors, by.x = "name", by.y = "surname")
stopifnot(exprs = {
    identical(m0, m2[, names(m0)])
    as.character(m1[, 1]) == as.character(m2[, 1])
    all.equal(m1[, -1], m2[, -1][ names(m1)[-1] ])
    identical(dim(merge(m1, m2, by = NULL)),
        c(nrow(m1)*nrow(m2), ncol(m1)+ncol(m2)))
})

## "R core" is missing from authors and appears only here :
merge(authors, books, by.x = "surname", by.y = "name", all = TRUE)

## example of using 'incomparables'
x <- data.frame(k1 = c(NA,NA,3,4,5), k2 = c(1,NA,NA,4,5), data = 1:5)
y <- data.frame(k1 = c(NA,2,NA,4,5), k2 = c(NA,NA,3,4,5), data = 1:5)
merge(x, y, by = c("k1","k2")) # NA's match
merge(x, y, by = "k1") # NA's match, so 6 rows
merge(x, y, by = "k2", incomparables = NA) # 2 rows

---

### Diagnostic Messages

Generate a diagnostic message from its arguments.

#### Usage

```r
message(..., domain = NULL, appendLF = TRUE)
suppressMessages(expr, classes = "message")

packageStartupMessage(..., domain = NULL, appendLF = TRUE)
suppressPackageStartupMessages(expr)

.makeMessage(..., domain = NULL, appendLF = FALSE)
```

#### Arguments

- `...`: zero or more objects which can be coerced to character (and which are pasted together with no separator) or (for `message` only) a single condition object.
- `domain`: see `gettext`. If NA, messages will not be translated, see also the note in `stop`.
- `appendLF`: logical: should messages given as a character string have a newline appended?
**missing**

Does a Formal Argument have a Value?

### Description

*missing* can be used to test whether a value was specified as an argument to a function.

### Examples

```r
message("ABC", "DEF")
suppressMessages(message("ABC"))

testit <- function() {
  message("testing package startup messages")
  packageStartupMessage("initializing ...", appendLF = FALSE)
  Sys.sleep(1)
  packageStartupMessage(" done")
}

testit()
suppressPackageStartupMessages(testit())
suppressMessages(testit())
```
Usage

missing(x)

Arguments

x a formal argument.

Details

missing(x) is only reliable if x has not been altered since entering the function: in particular it will always be false after x <- match.arg(x).

The example shows how a plotting function can be written to work with either a pair of vectors giving x and y coordinates of points to be plotted or a single vector giving y values to be plotted against their indices.

Currently missing can only be used in the immediate body of the function that defines the argument, not in the body of a nested function or a local call. This may change in the future.

This is a ‘special’ primitive function: it must not evaluate its argument.

References


See Also

substitute for argument expression; NA for missing values in data.

Examples

myplot <- function(x, y) {
  if(missing(y)) {
    y <- x
    x <- 1:length(y)
  }
  plot(x, y)
}

mode The (Storage) Mode of an Object

Description

Get or set the ‘mode’ (a kind of ‘type’), or the storage mode of an R object.

Usage

mode(x)
mode(x) <- value
storage.mode(x)
storage.mode(x) <- value
Arguments

- \textit{x} any \texttt{R} object.
- \textit{value} a character string giving the desired mode or ‘storage mode’ (type) of the object.

Details

Both \texttt{mode} and \texttt{storage.mode} return a character string giving the (storage) mode of the object — often the same — both relying on the output of \texttt{typeof(x)}, see the example below.

\texttt{mode(x) <- "newmode"} changes the mode of object \texttt{x} to \texttt{newmode}. This is only supported if there is an appropriate \texttt{as.newmode} function, for example “logical”, “integer”, “double”, “complex”, “raw”, “character”, “list”, “expression”, “name”, “symbol” and “function”. Attributes are preserved (but see below).

\texttt{storage.mode(x) <- "newmode"} is a more efficient \texttt{primitive} version of \texttt{mode<-}, which works for “newmode” which is one of the internal types (see \texttt{typeof}), but not for “single”. Attributes are preserved.

As storage mode “single” is only a pseudo-mode in \texttt{R}, it will not be reported by \texttt{mode} or \texttt{storage.mode}: use \texttt{attr(object, "Csingle")} to examine this. However, \texttt{mode<-} can be used to set the mode to “single”, which sets the real mode to “double” and the “Csingle” attribute to \texttt{TRUE}. Setting any other mode will remove this attribute.

Note (in the examples below) that some \texttt{calls} have mode “(“ which is \texttt{S} compatible.

Mode names

Modes have the same set of names as types (see \texttt{typeof}) except that

- types “integer” and “double” are returned as “numeric”.
- types “special”, “builtin” and “closure” are returned as “function”.
- type “symbol” is called mode “name”.
- type “language” is returned as “(" or “call”.

References


See Also

\texttt{typeof} for the \texttt{R}-internal ‘mode’ or ‘type’, \texttt{type.convert}, \texttt{attributes}.

Examples

\begin{verbatim}
require(stats)
sapply(options(), mode)

cex3 <- c("NULL", "1", "1:1", "1i", "list()", "data.frame(x = 1)",  
  "pairlist(pi)", "c", "lm", "formals(lm)[[1]]", "formals(lm)[[2]]", 
  "y ~ x", "expression(())[[1]]", "(y ~ x)[[1]]",  
  "expression(x <- pi)[[1]][[1]][[1]]")
lex3 <- sapply(cex3, function(x) eval(str2lang(x)))
mex3 <- t(sapply(lex3, 
  function(x) c(typeof(x), storage.mode(x), mode(x))))
\end{verbatim}
dimnames(mex3) <- list(cex3, c("typeof(.)","storage.mode(.)","mode(.)"))  
mex3
## This also makes a local copy of 'pi':
storage.mode(pi) <- "complex"
storage.mode(pi)
rm(pi)

---

**mtfrm**  
**Auxiliary Function for Matching**

**Description**

Transform objects for matching via `match()`, think “match form” -> "mtfrm". **base** provides the S3 generic and a default plus "POSIXct" and "POSIXlt" methods.

**Usage**

`mtfrm(x)`

**Arguments**

- `x`  
an R object

**Details**

Matching via `match` will use `mtfrm` to transform internally classed objects (see `is.object`) to a vector representation appropriate for matching. The default method performs `as.character` if this preserves the length.

Ideally, methods for `mtfrm` should ensure that comparisons of same-classed objects via `match` are consistent with those employed by methods for `duplicated/unique` and `==/!=` (where applicable).

**Value**

A vector of the same length as `x`.

---

**NA**  
**‘Not Available’ / Missing Values**

**Description**

`NA` is a logical constant of length 1 which contains a missing value indicator. `NA` can be coerced to any other vector type except raw. There are also constants `NA_integer_`, `NA_real_`, `NA_complex_` and `NA_character_` of the other atomic vector types which support missing values: all of these are reserved words in the R language.

The generic function `is.na` indicates which elements are missing.

The generic function `is.na<-` sets elements to `NA`.

The generic function `anyNA` implements `any(is.na(x))` in a possibly faster way (especially for atomic vectors).
Usage

is.na(x)
anyNA(x, recursive = FALSE)

## S3 method for class 'data.frame'
is.na(x)
is.na(x) <- value

Arguments

x
an R object to be tested: the default method for is.na and anyNA handle atomic vectors, lists, pairlists, and NULL.
recursive
logical: should anyNA be applied recursively to lists and pairlists?
value
a suitable index vector for use with x.

Details

The NA of character type is distinct from the string "NA". Programmers who need to specify an explicit missing string should use NA_character_ (rather than "NA") or set elements to NA using is.na<-.

is.na and anyNA are generic: you can write methods to handle specific classes of objects, see InternalMethods.

Function is.na<- may provide a safer way to set missingness. It behaves differently for factors, for example.

Numerical computations using NA will normally result in NA: a possible exception is where NaN is also involved, in which case either might result (which may depend on the R platform). However, this is not guaranteed and future CPUs and/or compilers may behave differently. Dynamic binary translation may also impact this behavior (with valgrind, computations using NA may result in NaN even when no NaN is involved).

Logical computations treat NA as a missing TRUE/FALSE value, and so may return TRUE or FALSE if the expression does not depend on the NA operand.

The default method for anyNA handles atomic vectors without a class and NULL. It calls any(is.na(x)) on objects with classes and for recursive = FALSE, on lists and pairlists.

Value

The default method for is.na applied to an atomic vector returns a logical vector of the same length as its argument x, containing TRUE for those elements marked NA or, for numeric or complex vectors, NaN, and FALSE otherwise. (A complex value is regarded as NA if either its real or imaginary part is NA or NaN) dim, dimnames and names attributes are copied to the result.

The default methods also work for lists and pairlists:
For is.na, elementwise the result is false unless that element is a length-one atomic vector and the single element of that vector is regarded as NA or NaN (note that any is.na method for the class of the element is ignored).
anyNA(recursive = FALSE) works the same way as is.na; anyNA(recursive = TRUE) applies anyNA (with method dispatch) to each element.

The data frame method for is.na returns a logical matrix with the same dimensions as the data frame, and with dimnames taken from the row and column names of the data frame.
anyNA(NULL) is false; is.na(NULL) is logical(0) (no longer warning since R version 3.5.0).

References


See Also

NaN, is.nan, etc., and the utility function complete.cases.

na.action, na.omit, na.fail on how methods can be tuned to deal with missing values.

Examples

is.na(c(1, NA)) #> FALSE TRUE
is.na(paste(c(1, NA))) #> FALSE FALSE

(xx <- c(0:4))
is.na(xx) <- c(2, 4)
x #> 0 NA 2 NA 4
anyNA(xx) # TRUE

# Some logical operations do not return NA
c(TRUE, FALSE) & NA
(c(TRUE, FALSE) | NA)

## Measure speed difference in a favourable case:
## the difference depends on the platform, on most ca 3x.
x <- 1:10000; x[5000] <- NaN # coerces x to be double
if(require("microbenchmark")) { # does not work reliably on all platforms
  print(microbenchmark(any(is.na(x)), anyNA(x)))
} else {
  nSim <- 2^13
  print(rbind(is.na = system.time(replicate(nSim, any(is.na(x)))),
              anyNA = system.time(replicate(nSim, anyNA(x)))))
}

## anyNA() can work recursively with list()s:
LL <- list(1:5, c(NA, 5:8), c("A","NA"), c("a", NA_character_))
L2 <- LL[c(1,3)]
sapply(LL, anyNA); c(anyNA(LL), anyNA(LL, TRUE))
sapply(L2, anyNA); c(anyNA(L2), anyNA(L2, TRUE))

## ... lists, and hence data frames, too:
dN <- dd <- USJudgeRatings; dN[3,6] <- NA
anyNA(dd) # FALSE
anyNA(dN) # TRUE
Names and Symbols

Description
A ‘name’ (also known as a ‘symbol’) is a way to refer to R objects by name (rather than the value of the object, if any, bound to that name).
as.name and as.symbol are identical: they attempt to coerce the argument to a name.
is.symbol and the identical is.name return TRUE or FALSE depending on whether the argument is a name or not.

Usage

as.symbol(x)

is.symbol(x)

as.name(x)

is.name(x)

Arguments
x object to be coerced or tested.

Details
Names are limited to 10,000 bytes (and were to 256 bytes in versions of R before 2.13.0).
as.name first coerces its argument internally to a character vector (so methods for as.character are not used). It then takes the first element and provided it is not "", returns a symbol of that name (and if the element is NA_character_, the name is "NA").
as.name is implemented as as.vector(x, "symbol"), and hence will dispatch methods for the generic function as.vector.
is.name and is.symbol are primitive functions.

Value
For as.name and as.symbol, an R object of type "symbol" (see typeof).
For is.name and is.symbol, a length-one logical vector with value TRUE or FALSE.

Note
The term ‘symbol’ is from the LISP background of R, whereas ‘name’ has been the standard S term for this.

References
See Also
call, is.language. For the internal object mode, typeof.
plotmath for another use of `symbol`.

Examples

```r
an <- as.name("arrg")
is.name(an) # TRUE
mode(an) # name
typeof(an) # symbol
```

names  The Names of an Object

Description

Functions to get or set the names of an object.

Usage

```r
names(x)
names(x) <- value
```

Arguments

- `x`: an R object.
- `value`: a character vector of up to the same length as `x`, or NULL.

Details

names is a generic accessor function, and names<- is a generic replacement function. The default methods get and set the "names" attribute of a vector (including a list) or pairlist.

For an environment `env`, `names(env)` gives the names of the corresponding list, i.e., `names(as.list(env, all.names = TRUE))` which are also given by `ls(env, all.names = TRUE, sorted = FALSE)`. If the environment is used as a hash table, `names(env)` are its "keys".

If `value` is shorter than `x`, it is extended by character NAs to the length of `x`.

It is possible to update just part of the names attribute via the general rules: see the examples. This works because the expression there is evaluated as `z <- "names<-"(z, "[<"(names(z), 3, "c2"))`.

The name "" is special: it is used to indicate that there is no name associated with an element of a (atomic or generic) vector. Subscripting by "" will match nothing (not even elements which have no name).

A name can be character NA, but such a name will never be matched and is likely to lead to confusion. Both are primitive functions.
names

Value

For names, NULL or a character vector of the same length as x. (NULL is given if the object has no names, including for objects of types which cannot have names.) For an environment, the length is the number of objects in the environment but the order of the names is arbitrary.

For names<-, the updated object. (Note that the value of names(x) <- value is that of the assignment, value, not the return value from the left-hand side.)

Note

For vectors, the names are one of the attributes with restrictions on the possible values. For pairlists, the names are the tags and converted to and from a character vector.

For a one-dimensional array the names attribute really is dimnames[[1]].

Formally classed aka “S4” objects typically have slotNames() (and no names()).

References


See Also

slotNames, dimnames.

Examples

# print the names attribute of the islands data set
names(islands)

# remove the names attribute
names(islands) <- NULL
islands
rm(islands) # remove the copy made

z <- list(a = 1, b = "c", c = 1:3)
names(z)
# change just the name of the third element.
names(z)[3] <- "c2"

z <- 1:3
names(z)
## assign just one name
names(z)[2] <- "b"

z
**nargs**

*The Number of Arguments to a Function*

**Description**

When used inside a function body, `nargs()` returns the number of arguments supplied to that function, including positional arguments left blank.

**Usage**

`nargs()`

**Details**

The count includes empty (missing) arguments, so that `foo(x, , z)` will be considered to have three arguments (see 'Examples'). This can occur in rather indirect ways, so for example `x[]` might dispatch a call to `.`.some_method`(x, ,)` which is considered to have two arguments.

This is a primitive function.

**References**


**See Also**

`args`, `formals` and `sys.call`.

**Examples**

```r
tst <- function(a, b = 3, ...) { nargs() }
tst() # 0
tst(clicketyclack) # 1 (even non-existing)
tst(c1, a2, rr3) # 3

foo <- function(x, y, z, w) {
  cat("call was ", deparse(match.call()), 
      "\n", sep = "")
  nargs()
}
foo() # 0
foo(, , 3) # 3
foo(z = 3) # 1, even though this is the same call

nargs() # not really meaningful
```
Description

nchar takes a character vector as an argument and returns a vector whose elements contain the sizes of the corresponding elements of x. Internally, it is a generic, for which methods can be defined (see InternalMethods).

nzchar is a fast way to find out if elements of a character vector are non-empty strings.

Usage

nchar(x, type = "chars", allowNA = FALSE, keepNA = NA)
nzchar(x, keepNA = FALSE)

Arguments

x character vector, or a vector to be coerced to a character vector. Giving a factor is an error.
type character string: partial matching to one of c("bytes", "chars", "width"). See ‘Details’.
allowNA logical: should NA be returned for invalid multibyte strings or "bytes"-encoded strings (rather than throwing an error)?
keepNA logical: should NA be returned when x is NA? If false, nchar() returns 2, as that is the number of printing characters used when strings are written to output, and nzchar() is TRUE. The default for nchar(), NA, means to use keepNA = TRUE unless type is "width".

Details

The ‘size’ of a character string can be measured in one of three ways (corresponding to the type argument):

bytes The number of bytes needed to store the string (plus in C a final terminator which is not counted).
chars The number of characters.
width The number of columns cat will use to print the string in a monospaced font. The same as chars if this cannot be calculated.

These will often be the same, and usually will be in single-byte locales (but note how type determines the default for keepNA). There will be differences between the first two with multibyte character sequences, e.g. in UTF-8 locales.

The internal equivalent of the default method of as.character is performed on x (so there is no method dispatch). If you want to operate on non-vector objects passing them through deparse first will be required.
Value

For `nchar`, an integer vector giving the sizes of each element. For missing values (i.e., `NA`, i.e., `NA_character_`), `nchar()` returns `NA_integer_` if `keepNA` is true, and 2, the number of printing characters, if false.

`type = "width"` gives (an approximation to) the number of columns used in printing each element in a terminal font, taking into account double-width, zero-width and ‘composing’ characters. The approximation is likely to be poor when there are unassigned or non-printing characters.

If `allowNA = TRUE` and an element is detected as invalid in a multi-byte character set such as UTF-8, its number of characters and the width will be `NA`. Otherwise the number of characters will be non-negative, so `!is.na(nchar(x, "chars", TRUE))` is a test of validity.

A character string marked with "bytes" encoding (see `Encoding`) has a number of bytes, but neither a known number of characters nor a width, so the latter two types are `NA` if `allowNA = TRUE`, otherwise an error.

Names, dims and dimnames are copied from the input.

For `nzchar`, a logical vector of the same length as `x`, true if and only if the element has non-zero size; if the element is `NA`, `nzchar()` is true when `keepNA` is false (the default) or `NA`, and `NA` otherwise.

Note

This does not by default give the number of characters that will be used to `print()` the string. Use `encodeString` to find that. Where character strings have been marked as UTF-8, the number of characters and widths will be computed in UTF-8, even though printing may use escapes such as `<\u2642>` in a non-UTF-8 locale.

The concept of ‘width’ is a slippery one even in a monospaced font. Some human languages have the concept of combining characters, in which two or more characters are rendered together: an example would be “y\u386”, which is two characters of width one: combining characters are given width zero, and there are other zero-width characters such as the zero-width space “\u200b”.

Some East Asian languages have ‘wide’ characters, ideographs which are conventionally printed across two columns when mixed with ASCII and other ‘narrow’ characters in those languages. The problem is that whether a computer prints wide characters over two or one columns depends on the font, with it not being uncommon to use two columns in a font intended for East Asian users and a single column in a ‘Western’ font. Unicode has encodings for ‘fullwidth’ versions of ASCII characters and ‘halfwidth’ versions of Katakana (Japanese) and Hangul (Korean) characters. Then there is the ‘East Asian Ambiguous class’ (Greek, Cyrillic, signs, some accented Latin chars, etc), for which the historical practice was to use two columns in East Asia and one elsewhere. The width quoted by `nchar` for characters in that class (and some others) depends on the locale, being one except in some East Asian locales on some OSes (notably Windows).

Control characters are usually given width zero: this includes CR and LF. Computing the width of a string containing control characters should be avoided (and may depend on the OS and R version).

References


Unicode Standard Annex #11: East Asian Width. [https://www.unicode.org/reports/tr11/](https://www.unicode.org/reports/tr11/)

See Also

`strwidth` giving width of strings for plotting; `paste`, `substr`, `strsplit`
Examples

```r
x <- c("asfed", "qwerty", "yuiop[", "b", "stuff.blah.yech")
nchar(x)
# 5 6 6 1 15
nchar(deparse(mean))
# 18 17 <-- unless mean differs from base::mean

## NA behaviour as function of keepNA=* :
logi <- setNames(, c(FALSE, NA, TRUE))
sapply(logi, \(k) data.frame(nchar = nchar (NA, keepNA=k),
nzchar = nzchar(NA, keepNA=k)))
x[3] <- NA; x
nchar(x, keepNA= TRUE) # 5 6 NA 1 15
nchar(x, keepNA=FALSE) # 5 6 2 1 15
stopifnot(identical(nchar(x ), nchar(x, keepNA= TRUE)),
  identical(nchar(x, "w"), nchar(x, keepNA=FALSE)),
  identical(is.na(x), is.na(nchar(x))))
```

##' nchar() for all three types :
nchars <- function(x, ...)  
  vapply(c("chars", "bytes", "width"),
  function(tp) nchar(x, tp, ...), integer(length(x)))
nchars("\u200b") # in R versions (>= 2015-09-xx):
## chars bytes width
## 1 3 0
data.frame(x, nchars(x)) ## all three types : same unless for NA
## force the same by forcing 'keepNA':
(ncT <- nchars(x, keepNA = TRUE)) ## .... NA NA NA ....
(ncF <- nchars(x, keepNA = FALSE))## .... 2 2 2 ....
stopifnot(apply(ncT, 1, function(.) length(unique(.))) == 1,
  apply(ncF, 1, function(.) length(unique(.))) == 1)

---

### nlevels

**The Number of Levels of a Factor**

**Description**

Return the number of levels which its argument has.

**Usage**

`nlevels(x)`

**Arguments**

- `x`  
  an object, usually a factor.

**Details**

This is usually applied to a factor, but other objects can have levels.

The actual factor levels (if they exist) can be obtained with the `levels` function.
noquote

Value

The length of levels(x), which is zero if x has no levels.

See Also

levels, factor.

Examples

nlevels(gl(3, 7)) # = 3

description

Class for ‘no quote’ Printing of Character Strings

Description

Print character strings without quotes.

Usage

noquote(obj, right = FALSE)

## S3 method for class 'noquote'
print(x, quote = FALSE, right = FALSE, ...)

## S3 method for class 'noquote'
c(..., recursive = FALSE)

Arguments

obj any R object, typically a vector of character strings.

right optional logical eventually to be passed to print(), used by print.default(), indicating whether or not strings should be right aligned.

x an object of class "noquote".

quote, ... further options passed to next methods, such as print.

recursive for compatibility with the generic c function.

Details

noquote returns its argument as an object of class "noquote". There is a method for c() and subscript method("[.noquote") which ensures that the class is not lost by subsetting. The print method (print.noquote) prints character strings without quotes ("...." is printed as ....).

If right is specified in a call print(x, right=*) it takes precedence over a possible right setting of x, e.g., created by x <- noquote(*, right=TRUE).

These functions exist both as utilities and as an example of using (S3) class and object orientation.

Author(s)

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norm

Compute the Norm of a Matrix

Description

Computes a matrix norm of \( x \) using LAPACK. The norm can be the one ("O") norm, the infinity ("I") norm, the Frobenius ("F") norm, the maximum modulus ("M") among elements of a matrix, or the “spectral” or \( 2 \)-norm, as determined by the value of type.

Usage

\[
\text{norm}(x, \text{type} = c("O", "I", "F", "M", "2"))
\]

Arguments

- **x**: numeric matrix; note that packages such as Matrix define more norm() methods.
- **type**: character string, specifying the type of matrix norm to be computed. A character indicating the type of norm desired.
  - "O", "o" or "1" specifies the one norm, (maximum absolute column sum);
  - "I" or "i" specifies the infinity norm (maximum absolute row sum);
  - "F", "f", "E" or "e" specifies the Frobenius norm (the Euclidean norm of \( x \) treated as if it were a vector);
  - "M" or "m" specifies the maximum modulus of all the elements in \( x \); and
  - "2" specifies the “spectral” or \( 2 \)-norm, which is the largest singular value (svd) of \( x \).

The default is "O". Only the first character of type[1] is used.
Details

The base method of norm() calls the LAPACK function dlange.

Note that the 1-, Inf- and "M" norm is faster to calculate than the Frobenius one.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Value

The matrix norm, a non-negative number. Zero for a 0-extent (empty) matrix.

Source

Except for norm = "2", the LAPACK routine DLANGE.
LAPACK is from https://netlib.org/lapack/.

References


See Also

rcond for the (reciprocal) condition number.

Examples

```r
(x1 <- cbind(1, 1:10))
norm(x1)
norm(x1, "I")
norm(x1, "M")
stopifnot(all.equal(norm(x1, "F"),
                   sqrt(sum(x1^2))))

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
h9 <- hilbert(9)
## all 5 (4 different) types of norm:
(nTyp <- eval(formals(base::norm)$type))
sapply(nTyp, norm, x = h9)
stopifnot(exprs = { # 0-extent matrices:
sapply(nTyp, norm, x = matrix(, 1,0)) == 0
  sapply(nTyp, norm, x = matrix(, 0,0)) == 0
})
```

normalizePath

Express File Paths in Canonical Form

Description

Convert file paths to canonical form for the platform, to display them in a user-understandable form and so that relative and absolute paths can be compared.
Usage

normalizePath(path, winslash = "\\", mustWork = NA)

Arguments

- **path**: character vector of file paths.
- **winslash**: the separator to be used on Windows – ignored elsewhere. Must be one of `c("/", \\)`.
- **mustWork**: logical: if TRUE then an error is given if the result cannot be determined; if NA then a warning.

Details

Tilde-expansion (see `path.expand`) is first done on paths.

Where the Unix-alike platform supports it attempts to turn paths into absolute paths in their canonical form (no '.', '..', nor symbolic links). It relies on the POSIX system function `realpath`: if the platform does not have that (we know of no current example) then the result will be an absolute path but might not be canonical. Even where `realpath` is used the canonical path need not be unique, for example via hard links or multiple mounts.

On Windows it converts relative paths to absolute paths, resolves symbolic links, converts short names for path elements to long names and ensures the separator is that specified by `winslash`. It will match each path element case-insensitively or case-sensitively as during the usual name lookup and return the canonical case. It relies on Windows API function `GetFinalPathNameByHandle` and in case of an error (such as insufficient permissions) it currently falls back to the R 3.6 (and older) implementation, which relies on `GetFullPathName` and `GetLongPathName` with limitations described in the Notes section. An attempt is made not to introduce UNC paths in presence of mapped drives or symbolic links: if `GetFinalPathNameByHandle` returns a UNC path, but `GetLongPathName` returns a path starting with a drive letter, R falls back to the R 3.6 (and older) implementation. UTF-8-encoded paths not valid in the current locale can be used.

mustWork = FALSE is useful for expressing paths for use in messages.

Value

A character vector.

If an input is not a real path the result is system-dependent (unless mustWork = TRUE, when this should be an error). It will be either the corresponding input element or a transformation of it into an absolute path.

Converting to an absolute file path can fail for a large number of reasons. The most common are:

- One of more components of the file path does not exist.
- A component before the last is not a directory, or there is insufficient permission to read the directory.
- For a relative path, the current directory cannot be determined.
- A symbolic link points to a non-existent place or links form a loop.
- The canonicalized path would be exceed the maximum supported length of a file path.
Note

The canonical form of paths may not be what you expect. For example, on macOS absolute paths such as `/tmp` and `/var` are symbolic links. On Linux, a path produced by bash process substitution is a symbolic link (such as `/proc/fd/63`) to a pipe and there is no canonical form of such path. In R 3.6 and older on Windows, symlinks will not be resolved and the long names for path elements will be returned with the case in which they are in path, which may not be canonical in case-insensitive folders.

Examples

```r
# random tempdir
cat(normalizePath(c(R.home(), tempdir())), sep = "\n")
```

Description

In order to pinpoint missing functionality, the R core team uses these functions for missing R functions and not yet used arguments of existing R functions (which are typically there for compatibility purposes).

You are very welcome to contribute your code ...

Usage

```r
.NotYetImplemented()
.NotYetUsed(arg, error = TRUE)
```

Arguments

- `arg` an argument of a function that is not yet used.
- `error` a logical. If TRUE, an error is signalled; if FALSE; only a warning is given.

See Also

the contrary, Deprecated and Defunct for outdated code.

Examples

```r
require(graphics)
barplot(1:5, inside = TRUE) # 'inside' is not yet used
```
**nrow**

The Number of Rows/Columns of an Array

**Description**

\( \text{nrow} \) and \( \text{ncol} \) return the number of rows or columns present in \( x \). \( \text{NCOL} \) and \( \text{NROW} \) do the same treating a vector as 1-column matrix, even a 0-length vector, compatibly with \( \text{as.matrix()} \) or \( \text{cbind()} \), see the example.

**Usage**

\[
\begin{align*}
\text{nrow}(x) \\
\text{ncol}(x) \\
\text{NCOL}(x) \\
\text{NROW}(x)
\end{align*}
\]

**Arguments**

- \( x \) a vector, array, data frame, or \text{NULL}.

**Value**

an integer of length 1 or \text{NULL}, the latter only for \text{ncol} and \text{nrow}.

**References**


**See Also**

\( \text{dim} \) which returns all dimensions, and \( \text{length} \) which gives a number (a ‘count’) also in cases where \( \text{dim}() \) is \text{NULL}, and hence \text{nrow()} and \text{ncol()} return \text{NULL}; \text{array}, \text{matrix}.

**Examples**

\[
\begin{align*}
\text{ma} & \leftarrow \text{matrix}(1:12, 3, 4) \\
\text{nrow}(\text{ma}) & \quad # 3 \\
\text{ncol}(\text{ma}) & \quad # 4
\end{align*}
\]

\[
\begin{align*}
\text{ncol}(\text{array}(1:24, \text{dim} = 2:4)) & \quad # 3, \text{the second dimension} \\
\text{NCOL}(1:12) & \quad # 1 \\
\text{NROW}(1:12) & \quad # 12, \text{the length()} \text{of the vector}
\end{align*}
\]

###

\[
\begin{align*}
\text{dim}(\text{as.matrix}(\text{numeric}())) & \quad # \emptyset 1 \\
\text{dim}(\text{cbind}(\text{numeric}())) & \quad # \text{ditto}
\end{align*}
\]

###

\[
\begin{align*}
\text{NCOL}(\text{numeric}()) & \quad # 1 \text{ and hence} \\
\text{NCOL}(\text{NULL}) & \quad # 1
\end{align*}
\]
Double Colon and Triple Colon Operators

Description

Accessing exported and internal variables, i.e. \texttt{R} objects (including lazy loaded data sets) in a namespace.

Usage

\begin{verbatim}
 pkg::name
 pkg:::name
\end{verbatim}

Arguments

\begin{verbatim}
 pkg  package name: symbol or literal character string.
 name variable name: symbol or literal character string.
\end{verbatim}

Details

For a package \texttt{pkg}, \texttt{pkg::name} returns the value of the exported variable \texttt{name} in namespace \texttt{pkg}, whereas \texttt{pkg:::name} returns the value of the internal variable \texttt{name}. The package namespace will be loaded if it was not loaded before the call, but the package will not be attached to the search path.

Specifying a variable or package that does not exist is an error.

Note that \texttt{pkg::name} does \textbf{not} access the objects in the environment \texttt{package:pkg} (which does not exist until the package’s namespace is attached): the latter may contain objects not exported from the namespace. It can access datasets made available by lazy-loading.

Note

It is typically a design mistake to use ::: in your code since the corresponding object has probably been kept internal for a good reason. Consider contacting the package \texttt{maintainer} if you feel the need to access the object for anything but mere inspection.

See Also

get to access an object masked by another of the same name. loadNamespace, asNamespace for more about namespaces.

Examples

\begin{verbatim}
 base::log
 base::"*

 ## Beware -- use ':::' at your own risk! (see "Details")
 stats:::coef.default
\end{verbatim}
Description

Packages can supply functions to be called when loaded, attached, detached or unloaded.

Usage

.onLoad(libname, pkgname)
.onAttach(libname, pkgname)
.onUnload(libpath)
.onDetach(libpath)
.Last.lib(libpath)

Arguments

libname a character string giving the library directory where the package defining the
 namespace was found.

pkgname a character string giving the name of the package.

libpath a character string giving the complete path to the package.

Details

After loading, loadNamespace looks for a hook function named .onLoad and calls it (with two
unnamed arguments) before sealing the namespace and processing exports.

When the package is attached (via library or attachNamespace), the hook function .onAttach
is looked for and if found is called (with two unnamed arguments) before the package environment
is sealed.

If a function .onDetach is in the namespace or .Last.lib is exported from the package, it will be
called (with a single argument) when the package is detached. Beware that it might be called if
.onAttach has failed, so it should be written defensively. (It is called within tryCatch, so errors
will not stop the package being detached.)

If a namespace is unloaded (via unloadNamespace), a hook function .onUnload is run (with a
single argument) before final unloading.

Note that the code in .onLoad and .onUnload should not assume any package except the base
package is on the search path. Objects in the current package will be visible (unless this is circum-
vented), but objects from other packages should be imported or the double colon operator should
be used.

.onLoad, .onUnload, .onAttach and .onDetach are looked for as internal objects in the names-
space and should not be exported (whereas .Last.lib should be).

Note that packages are not detached nor namespaces unloaded at the end of an R session unless the
user安排s to do so (e.g., via .Last).

Anything needed for the functioning of the namespace should be handled at load/unload times by the
.onLoad and .onUnload hooks. For example, DLLs can be loaded (unless done by a useDynLib
directive in the ‘NAMESPACE’ file) and initialized in .onLoad and unloaded in .onUnload. Use
.onAttach only for actions that are needed only when the package becomes visible to the user (for
example a start-up message) or need to be run after the package environment has been created.
**Good practice**

Loading a namespace should where possible be silent, with startup messages given by `.onAttach`. These messages (and any essential ones from `.onLoad`) should use `packageStartupMessage` so they can be silenced where they would be a distraction.

There should be no calls to `library` nor `require` in these hooks. The way for a package to load other packages is via the ‘Depends’ field in the ‘DESCRIPTION’ file: this ensures that the dependence is documented and packages are loaded in the correct order. Loading a namespace should not change the search path, so rather than attach a package, dependence of a namespace on another package should be achieved by (selectively) importing from the other package’s namespace.

Uses of `library` with argument `help` to display basic information about the package should use `format` on the computed package information object and pass this to `packageStartupMessage`.

There should be no calls to `installed.packages` in startup code: it is potentially very slow and may fail in versions of R before 2.14.2 if package installation is going on in parallel. See its help page for alternatives.

Compiled code should be loaded (e.g., via `library.dynam`) in `.onLoad` or a `useDynLib` directive in the ‘NAMESPACE’ file, and not in `.onAttach`. Similarly, compiled code should not be unloaded (e.g., via `library.dynam.unload`) in `.Last.lib` nor `.onDetach`, only in `.onUnload`.

**See Also**

`setHook` shows how users can set hooks on the same events, and lists the sequence of events involving all of the hooks.

`reg.finalizer` for hooks to be run at the end of a session.

`loadNamespace` for more about namespaces.
Arguments

- **ns**: string or name space object.
- **pos**: integer specifying position to attach.
- **depends**: NULL or a character vector of dependencies to be recorded in object .Depends in the package.
- **package**: string naming the package/name space to load.
- **lib.loc**: character vector specifying library search path (the location of R library trees to search through).
- **keep.source**: Now ignored except during package installation.
- **keep.parse.data**: Ignored except during package installation.
- **partial**: logical; if true, stop just after loading code.
- **versionCheck**: NULL or a version specification (a list with components op and version).
- **quietly**: logical: should progress and error messages be suppressed?
- **name**: string or ‘name’, see as.symbol, of a package, e.g., "stats".
- **exclude, include.only**: character vectors; see library.
- **...**: further arguments to be passed to loadNamespace.

Details

The functions loadNamespace and attachNamespace are usually called implicitly when library is used to load a name space and any imports needed. However it may be useful at times to call these functions directly.

loadNamespace loads the specified name space and registers it in an internal data base. A request to load a name space when one of that name is already loaded has no effect. The arguments have the same meaning as the corresponding arguments to library, whose help page explains the details of how a particular installed package comes to be chosen. After loading, loadNamespace looks for a hook function named .onLoad as an internal variable in the name space (it should not be exported). Partial loading is used to support installation with lazy-loading.

Optionally the package licence is checked during loading: see section ‘Licenses’ in the help for library. loadNamespace does not attach the name space it loads to the search path. attachNamespace can be used to attach a frame containing the exported values of a name space to the search path (but this is almost always done via library). The hook function .onAttach is run after the name space exports are attached.

requireNamespace is a wrapper for loadNamespace analogous to require that returns a logical value.

loadedNamespaces returns a character vector of the names of the loaded name spaces.

isNamespaceLoaded(pkg) is equivalent to but more efficient than pkg %in% loadedNamespaces().

unloadNamespace can be used to attempt to force a name space to be unloaded. If the name space is attached, it is first detached, thereby running a .onDetach or .Last.lib function in the name space if one is exported. An error is signaled and the name space is not unloaded if the name space is imported by other loaded name spaces. If defined, a hook function .onUnload is run before removing the name space from the internal registry.

See the comments in the help for detach about some issues with unloading and reloading name spaces.
Value

attachNamespace returns invisibly the package environment it adds to the search path.
loadNamespace returns the name space environment, either one already loaded or the one the function causes to be loaded.
requireNamespace returns TRUE if it succeeds or FALSE.
loadedNamespaces returns a character vector.
unloadNamespace returns NULL, invisibly.

Tracing

As from R 4.1.0 the operation of loadNamespace can be traced, which can help track down the causes of unexpected messages (including which package(s) they come from since loadNamespace is called in many ways including from itself and by :: and can be called by load). Setting the environment variable _R_TRACE_LOADNAMESPACE_ to a numerical value will generate additional messages on progress. Non-zero values, e.g. 1, report which namespace is being loaded and when loading completes: values 2 to 4 report in increasing detail. Negative values are reserved for tracing specific features and their current meanings are documented in source-code comments.

Loading standard packages is never traced.

Author(s)

Luke Tierney and R-core

References

The ‘Writing R Extensions’ manual, section “Package namespaces”.

See Also

gNamespace, asNamespace, topenv, .onLoad (etc); further environment.

Examples

(lns <- loadedNamespaces())
statL <- isNamespaceLoaded("stats")
stopifnot( identical(statL, "stats" %in% lns ) )

## The string "foo" and the symbol 'foo' can be used interchangeably here:
stopifnot( identical(isNamespaceLoaded( "foo" ), FALSE),
identical(isNamespaceLoaded(quote(foo)), FALSE),
identical(isNamespaceLoaded(quote(stats)), statL))

hasS <- isNamespaceLoaded("splines") # (to restore if needed)
Sns <- asNamespace("splines") # loads it if not already
stopifnot( ! isNamespaceLoaded("splines") )
if (is.null(try(unloadNamespace(Sns)))) # try unloading the NS 'object'
stopifnot( ! isNamespaceLoaded("splines") )
if (hasS) loadNamespace("splines") # (restoring previous state)
### ns-topenv

**Description**

Finding the top level environment from an environment `envir` and its enclosing environments.

**Usage**

```r
topenv(envir = parent.frame(),
       matchThisEnv = getOption("topLevelEnvironment"))
```

**Arguments**

- `envir` environment.
- `matchThisEnv` return this environment, if it matches before any other criterion is satisfied. The default, the option `'topLevelEnvironment'`, is set by `sys.source`, which treats a specific environment as the top level environment. Supplying the argument as `NULL` or `emptyenv()` means it will never match.

**Details**

topenv returns the first top level environment found when searching `envir` and its enclosing environments. If no top level environment is found, `.GlobalEnv` is returned. An environment is considered top level if it is the internal environment of a namespace, a package environment in the search path, or `.GlobalEnv`.

**See Also**

- `environment`, notably `parent.env()` on “enclosing environments”; `loadNamespace` for more on namespaces.

**Examples**

```r
topenv(.GlobalEnv)
topenv(new.env())  # also global env
topenv(environment(ls))# namespace:base
topenv(environment(lm))# namespace:stats
```

### NULL

**The Null Object**

**Description**

NULL represents the null object in R: it is a reserved word. NULL is often returned by expressions and functions whose value is undefined.
Usage

NULL
as.null(x, ...)
is.null(x)

Arguments

x an object to be tested or coerced.
... ignored.

Details

NULL can be indexed (see Extract) in just about any syntactically legal way: apart from NULL[[]] which is an error, the result is always NULL. Objects with value NULL can be changed by replacement operators and will be coerced to the type of the right-hand side.

NULL is also used as the empty pairlist: see the examples. Because pairlists are often promoted to lists, you may encounter NULL being promoted to an empty list.

Objects with value NULL cannot have attributes as there is only one null object: attempts to assign them are either an error (attr) or promote the object to an empty list with attribute(s) (attributes and structure).

Value

as.null ignores its argument and returns NULL.
is.null returns TRUE if its argument’s value is NULL and FALSE otherwise.

Note

is.null is a primitive function.

References


Examples

is.null(list()) # FALSE (on purpose!)
is.null(pairlist()) # TRUE
is.null(integer(0)) # FALSE
is.null(logical(0)) # FALSE
as.null(list(a = 1, b = "c"))
**numeric**

**Numeric Vectors**

**Description**

Creates or coerces objects of type "numeric". `is.numeric` is a more general test of an object being interpretable as numbers.

**Usage**

```r
numeric(length = 0)
as.numeric(x, ...)
is.numeric(x)
```

**Arguments**

- `length`: A non-negative integer specifying the desired length. Double values will be coerced to integer: supplying an argument of length other than one is an error.
- `x`: object to be coerced or tested.
- `...`: further arguments passed to or from other methods.

**Details**

`numeric` is identical to `double`. It creates a double-precision vector of the specified length with each element equal to 0.

`as.numeric` is a generic function, but S3 methods must be written for `as.double`. It is identical to `as.double`.

`is.numeric` is an **internal generic** primitive function: you can write methods to handle specific classes of objects, see **InternalMethods**. It is **not** the same as `is.double`. Factors are handled by the default method, and there are methods for classes "Date", "POSIXt" and "difftime" (all of which return false). Methods for `is.numeric` should only return true if the base type of the class is `double` or `integer` and values can reasonably be regarded as numeric (e.g., arithmetic on them makes sense, and comparison should be done via the base type).

**Value**

for numeric and `as.numeric` see `double`.

The default method for `is.numeric` returns TRUE if its argument is of mode "numeric" (type "double" or type "integer") and not a factor, and FALSE otherwise. That is, `is.integer(x) || is.double(x), or (mode(x) == "numeric") && !is.factor(x).

**Warning**

If `x` is a `factor`, `as.numeric` will return the underlying numeric (integer) representation, which is often meaningless as it may not correspond to the `factor` `levels`, see the ‘Warning’ section in `factor` (and the 2nd example below).
S4 methods

as.numeric and is.numeric are internally S4 generic and so methods can be set for them via setMethod.

To ensure that as.numeric and as.double remain identical, S4 methods can only be set for as.numeric.

Note on names

It is a historical anomaly that R has two names for its floating-point vectors, double and numeric (and formerly had real).

double is the name of the type. numeric is the name of the mode and also of the implicit class. As an S4 formal class, use "numeric".

The potential confusion is that R has used mode "numeric" to mean ‘double or integer’, which conflicts with the S4 usage. Thus is.numeric tests the mode, not the class, but as.numeric (which is identical to as.double) coerces to the class.

References


See Also
double, integer, storage.mode.

Examples

## Conversion does trim whitespace; non-numeric strings give NA + warning
as.numeric(c("-.1"," 2.7 ","B"))

## Numeric values are sometimes accidentally converted to factors.
## Converting them back to numeric is trickier than you'd expect.
f <- factor(5:10)
as.numeric(f) # not what you might expect, probably not what you want
## what you typically meant and want:
as.numeric(as.character(f))
## the same, considerably more efficient (for long vectors):
as.numeric(levels(f))[f]
Details

R parses numeric constants in its input in a very similar way to C99 floating-point constants. Inf and NaN are numeric constants (with typeof(.) "double"). In text input (e.g., in scan and as.double), these are recognized ignoring case as is infinity as an alternative to Inf. NA_real_ and NA_integer_ are constants of types "double" and "integer" representing missing values. All other numeric constants start with a digit or period and are either a decimal or hexadecimal constant optionally followed by L.

Hexadecimal constants start with 0x or 0X followed by a nonempty sequence from 0-9 a-f A-F. which is interpreted as a hexadecimal number, optionally followed by a binary exponent. A binary exponent consists of a P or p followed by an optional plus or minus sign followed by a non-empty sequence of (decimal) digits, and indicates multiplication by a power of two. Thus 0x123p456 is $291 \times 2^{456}$.

Decimal constants consist of a nonempty sequence of digits possibly containing a period (the decimal point), optionally followed by a decimal exponent. A decimal exponent consists of an E or e followed by an optional plus or minus sign followed by a non-empty sequence of digits, and indicates multiplication by a power of ten.

Values which are too large or too small to be representable will overflow to Inf or underflow to 0.0.

A numeric constant immediately followed by i is regarded as an imaginary complex number.

A numeric constant immediately followed by L is regarded as an integer number when possible (and with a warning if it contains a ".").

Only the ASCII digits 0–9 are recognized as digits, even in languages which have other representations of digits. The ‘decimal separator’ is always a period and never a comma.

Note that a leading plus or minus is not regarded by the parser as part of a numeric constant but as a unary operator applied to the constant.

Note

When a string is parsed to input a numeric constant, the number may or may not be representable exactly in the C double type used. If not one of the nearest representable numbers will be returned. R’s own C code is used to convert constants to binary numbers, so the effect can be expected to be the same on all platforms implementing full IEC 600559 arithmetic (the most likely area of difference being the handling of numbers less than .Machine$double.xmin). The same code is used by scan.

See Also

Syntax. For complex numbers, see complex. Quotes for the parsing of character constants, Reserved for the “reserved words” in R.

Examples

## You can create numbers using fixed or scientific formatting.
2.1
2.1e10
-2.1E-10

## The resulting objects have class numeric and type double.
class(2.1)
typeof(2.1)
## This holds even if what you typed looked like an integer.
class(2)
typeof(2)

## If you actually wanted integers, use an "L" suffix.
class(2L)
typeof(2L)

## These are equal but not identical
2 == 2L
identical(2, 2L)

## You can write numbers between 0 and 1 without a leading "0"
## (but typically this makes code harder to read)
.1234

sqrt(1i) # remember elementary math?
utils::str(0xA0)
identical(1L, as.integer(1))

## You can combine the "0x" prefix with the "L" suffix :
identical(0xFL, as.integer(15))

## Numeric Versions
### Description
A simple S3 class for representing numeric versions including package versions, and associated methods.

### Usage
numeric_version(x, strict = TRUE)
package_version(x, strict = TRUE)
R_system_version(x, strict = TRUE)
getRversion()
as.numeric_version(x)
as.package_version(x)
is.numeric_version(x)
is.package_version(x)

### Arguments
- **x** for the creators, a character vector with suitable numeric version strings (see 'Details'); for package_version, alternatively an R version object as obtained by R.version. For as.numeric_version and as.package_version, suitable character vectors as above, or numeric version objects. For is.numeric_version and is.package_version, arbitrary R objects.
- **strict** a logical indicating whether invalid numeric versions should results in an error (default) or not.
Details

Numeric versions are sequences of one or more non-negative integers, usually (e.g., in package 'DESCRIPTION' files) represented as character strings with the elements of the sequence concatenated and separated by single '.' or '-' characters. R package versions consist of at least two such integers, an R system version of exactly three (major, minor and patchlevel).

Functions numeric_version, package_version and R_system_version create a representation from such strings (if suitable) which allows for coercion and testing, combination, comparison, summaries (min/max), inclusion in data frames, subscripting, and printing. The classes can hold a vector of such representations.

getRversion returns the version of the running R as an R system version object.

The [[ operator extracts or replaces a single version. To access the integers of a version use two indices: see the examples.

See Also

compareVersion; packageVersion for the version of a specific R package. R.version etc for the version of R (and the information underlying getRversion()).

Examples

```r
x <- package_version(c("1.2-4", "1.2-3", "2.1"))
x < "1.4-2.3"
c(min(x), max(x))
x[2, 2]
x$major
x$minor

if(getRversion() <= "2.5.0") { ## work around missing feature
  cat("Your version of R, ", as.character(getRversion()), 
      ", is outdated.\n", "Now trying to work around that ...
", sep = "")
}

x[[c(1, 3)]] # '4' as a numeric vector, same as x[1, 3]
x[1, 3]    # 4 as an integer
x[[2, 3]] <- 0  # zero the patchlevel
x[[c(2, 3)]] <- 0  # same
x
x[[3]] <- "2.2.3"; x
x <- c(x, package_version("0.0"))
is.na(x)[4] <- TRUE
stopifnot(identical(is.na(x), c(rep(FALSE,3), TRUE)), anyNA(x))
```

octmode

Integer Numbers Displayed in Octal

Description

Integers which are displayed in octal (base-8 number system) format, with as many digits as are needed to display the largest, using leading zeroes as necessary.

Arithmetic works as for integers, and non-integer valued mathematical functions typically work by truncating the result to integer.
Usage

as.octmode(x)

## S3 method for class 'octmode'
as.character(x, keepStr = FALSE, ...)

## S3 method for class 'octmode'
format(x, width = NULL, ...)

## S3 method for class 'octmode'
print(x, ...)

Arguments

x

an object, for the methods inheriting from class "octmode".

keepStr

a logical indicating that names and dimensions should be kept; set TRUE for back compatibility, if needed.

width

NULL or a positive integer specifying the minimum field width to be used, with padding by leading zeroes.

... further arguments passed to or from other methods.

Details

"octmode" objects are integer vectors with that class attribute, used primarily to ensure that they are printed in octal notation, specifically for Unix-like file permissions such as 755. Subsetting ([) works too, as do arithmetic or other mathematical operations, albeit truncated to integer.

as.character(x) drops all attributes (unless when keepStr=TRUE where it keeps, dim, dimnames and names for back compatibility) and converts each entry individually, hence with no leading zeroes, whereas in format(), when width = NULL (the default), the output is padded with leading zeroes to the smallest width needed for all the non-missing elements.

as.octmode can convert integers (of type "integer" or "double") and character vectors whose elements contain only digits 0-7 (or are NA) to class "octmode".

There is a ! method and methods for | and &:
these recycle their arguments to the length of the longer and then apply the operators bitwise to each element.

See Also

These are auxiliary functions for file.info.

hexmode, sprintf for other options in converting integers to octal, strtoI to convert octal strings to integers.

Examples

(on <- as.octmode(c(16, 32, 127:129))) # "020" "040" "177" "200" "201"

unclass(on[3:4]) # subsetting

## manipulate file modes
fmode <- as.octmode("170")
(fmode | "644") & "755"
umask <- Sys.umask(NA) # depends on platform
fmode <- c("666", "755") & !umask

om <- as.octmode(1:12)
om # print()s via format()
stopifnot(nchar(format(om)) == 2)

om1 <- as.octmode(c(1:10, 60:70))

## Integer arithmetic (remaining "octmode"):
om^2
om * 64
-om

(fac <- factorial(om)) # !1, !2, !3, !4 .. in hexadecimal
as.integer(fac) # indeed the same as factorial(1:12)

---

### on.exit

**Function Exit Code**

<table>
<thead>
<tr>
<th>on.exit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Function Exit Code</td>
</tr>
</tbody>
</table>

**Description**

on.exit records the expression given as its argument as needing to be executed when the current function exits (either naturally or as the result of an error). This is useful for resetting graphical parameters or performing other cleanup actions.

If no expression is provided, i.e., the call is on.exit(), then the current on.exit code is removed.

**Usage**

on.exit(expr = NULL, add = FALSE, after = TRUE)

**Arguments**

- **expr**
  - an expression to be executed.
- **add**
  - if TRUE, add expr to be executed after any previously set expressions (or before if after is FALSE); otherwise (the default) expr will overwrite any previously set expressions.
- **after**
  - if add is TRUE and after is FALSE, then expr will be added on top of the expressions that were already registered. The resulting last in first out order is useful for freeing or closing resources in reverse order.

**Details**

The expr argument passed to on.exit is recorded without evaluation. If it is not subsequently removed/replaced by another on.exit call in the same function, it is evaluated in the evaluation frame of the function when it exits (including during standard error handling). Thus any functions
or variables in the expression will be looked for in the function and its environment at the time of
exit: to capture the current value in expr use substitute or similar.
If multiple on.exit expressions are set using add = TRUE then all expressions will be run even if
one signals an error.
This is a `special` primitive function: it only evaluates the arguments add and after.

Value
Invisible NULL.

References
Brooks/Cole.

See Also
sys.on.exit which returns the expression stored for use by on.exit() in the function in which
sys.on.exit() is evaluated.

Examples

```r
require(graphics)
opar <- par(mai = c(1,1,1,1))
on.exit(par(opar))
```

---

**Ops.Date**

*Operators on the Date Class*

Description

Operators for the "Date" class.

There is an Ops method and specific methods for + and - for the Date class.

Usage

```
date + x
x + date
date - x
date1 lop date2
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>date</td>
<td>date objects</td>
</tr>
<tr>
<td>date1, date2</td>
<td>date objects or character vectors. (Character vectors are converted by as.Date.)</td>
</tr>
<tr>
<td>x</td>
<td>a numeric vector (in days) or an object of class &quot;difftime&quot;, rounded to the nearest whole day.</td>
</tr>
<tr>
<td>lop</td>
<td>One of ==, !=, &lt;, &lt;=, &gt; or &gt;=.</td>
</tr>
</tbody>
</table>
**options**

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**Details**

x does not need to be integer if specified as a numeric vector, but see the comments about fractional days in the help for Dates.

**Examples**

(z <- Sys.Date())
z + 10
z < c("2009-06-01", "2010-01-01", "2015-01-01")

---

**options**

*Options Settings*

---

**Description**

Allow the user to set and examine a variety of global options which affect the way in which R computes and displays its results.

**Usage**

options(...)

getOption(x, default = NULL)

.Options

**Arguments**

... any options can be defined, using name = value. However, only the ones below are used in base R.

Options can also be passed by giving a single unnamed argument which is a named list.

x a character string holding an option name.

default if the specified option is not set in the options list, this value is returned. This facilitates retrieving an option and checking whether it is set and setting it separately if not.

**Details**

Invoking options() with no arguments returns a list with the current values of the options. Note that not all options listed below are set initially. To access the value of a single option, one should use, e.g., getOption("width") rather than options("width") which is a list of length one.

**Value**

For getOption, the current value set for option x, or default (which defaults to NULL) if the option is unset.

For options(), a list of all set options sorted by name. For options(name), a list of length one containing the set value, or NULL if it is unset. For uses setting one or more options, a list with the previous values of the options changed (returned invisibly).
Options used in base R

add.smooth: typically logical, defaulting to TRUE. Could also be set to an integer for specifying how many (simulated) smooths should be added. This is currently only used by plot.lm.

askYesNo: a function (typically set by a front-end) to ask the user binary response functions in a consistent way, or a vector of strings used by askYesNo to use as default responses for such questions.

browserNLdisabled: logical: whether newline is disabled as a synonym for “n” in the browser.

checkPackageLicense: logical, not set by default. If true, loadNamespace asks a user to accept any non-standard license at first load of the package.

check.bounds: logical, defaulting to FALSE. If true, a warning is produced whenever a vector (atomic or list) is extended, by something like x <- 1:3; x[5] <- 6.

CBoundsCheck: logical, controlling whether .C and .Fortran make copies to check for array overruns on the atomic vector arguments.

Initially set from value of the environment variable R_C_BOUNDS_CHECK (set to yes to enable).

conflicts.policy: character string or list controlling handling of conflicts found in calls to library or require. See library for details.

continue: a non-empty string setting the prompt used for lines which continue over one line.

defaultPackages: the packages that are attached by default when R starts up. Initially set from value of the environment variable R_DEFAULT_PACKAGES, or if that is unset to c("datasets", "utils", "grDevices", "graphics", "stats", "methods"). (Set R_DEFAULT_PACKAGES to NULL or a comma-separated list of package names.) It will not work to set this in a ‘.Rprofile’ file, as its value is consulted before that file is read.

deparse.cutoff: integer value controlling the printing of language constructs which are deparsed. Default 60.

deparse.max.lines: controls the number of lines used when deparsing in browser, upon entry to a function whose debugging flag is set, and if option traceback.max.lines is unset, of traceback(). Initially unset, and only used if set to a positive integer.

traceback.max.lines: controls the number of lines used when deparsing in traceback, if set. Initially unset, and only used if set to a positive integer.

digits: controls the number of significant (see signif) digits to print when printing numeric values. It is a suggestion only. Valid values are 1...22 with default 7. See the note in print.default about values greater than 15.

digits.secs: controls the maximum number of digits to print when formatting time values in seconds. Valid values are 0...6 with default 0 (equivalent to NULL which is used when it is undefined as on vanilla startup). See strftime.

download.file.extra: Extra command-line argument(s) for non-default methods: see download.file.

download.file.method: Method to be used for download.file. Currently download methods "internal", "wininet" (Windows only), "libcurl", "wget" and "curl" are available. If not set, method = "auto" is chosen: see download.file.

echo: logical. Only used in non-interactive mode, when it controls whether input is echoed. Command-line option ‘--no-echo’ sets this to FALSE, but otherwise it starts the session as TRUE.

encoding: The name of an encoding, default "native.enc". See connections.
error: either a function or an expression governing the handling of non-catastrophic errors such as those generated by `stop` as well as by signals and internally detected errors. If the option is a function, a call to that function, with no arguments, is generated as the expression. By default the option is not set: see `stop` for the behaviour in that case. The functions `dump.frames` and `recover` provide alternatives that allow post-mortem debugging. Note that these need to be specified as e.g. `options(error = utils::recover)` in startup files such as `.Rprofile`.

expressions: sets a limit on the number of nested expressions that will be evaluated. Valid values are 25…500000 with default 5000. If you increase it, you may also want to start R with a larger protection stack; see `--max-ppsize` in `Memory`. Note too that you may cause a segfault from overflow of the C stack, and on OSes where it is possible you may want to increase that. Once the limit is reached an error is thrown. The current number under evaluation can be found by calling `Cstack_info`.

interrupt: a function taking no arguments to be called on a user interrupt if the interrupt condition is not otherwise handled.

keep.parse.data: When internally storing source code (keep.source is TRUE), also store parse data. Parse data can then be retrieved with `getParseData()` and used e.g. for spell checking of string constants or syntax highlighting. The value has effect only when internally storing source code (see `keep.source`). The default is TRUE.

keep.parse.data.pkgs: As for `keep.parse.data`, used only when packages are installed. Defaults to FALSE unless the environment variable `R_KEEP_PKG_PARSE_DATA` is set to yes. The space overhead of parse data can be substantial even after compression and it causes performance overhead when loading packages.

keep.source: When TRUE, the source code for functions (newly defined or loaded) is stored internally allowing comments to be kept in the right places. Retrieve the source by printing or using `deparse(fn, control = "useSource")`. The default is `interactive()`, i.e., TRUE for interactive use.

keep.source.pkgs: As for `keep.source`, used only when packages are installed. Defaults to FALSE unless the environment variable `R_KEEP_PKG_SOURCE` is set to yes.

matprod: a string selecting the implementation of the matrix products `%*%`, `crossprod`, and `tcrossprod` for double and complex vectors:

- "internal" uses an unoptimized 3-loop algorithm which correctly propagates NaN and Inf values and is consistent in precision with other summation algorithms inside R like `sum` or `colSums` (which now means that it uses a long double accumulator for summation if available and enabled, see `capabilities`).
- "default" uses BLAS to speed up computation, but to ensure correct propagation of NaN and Inf values it uses an unoptimized 3-loop algorithm for inputs that may contain NaN or Inf values. When deemed beneficial for performance, "default" may call the 3-loop algorithm unconditionally, i.e., without checking the input for NaN/Inf values. The 3-loop algorithm uses (only) a double accumulator for summation, which is consistent with the reference BLAS implementation.
- "blas" uses BLAS unconditionally without any checks and should be used with extreme caution. BLAS libraries do not propagate NaN or Inf values correctly and for inputs with NaN/Inf values the results may be undefined.
- "default SIMD" is experimental and will likely be removed in future versions of R. It provides the same behavior as "default", but the check whether the input contains NaN/Inf values is faster on some SIMD hardware. On older systems it will run correctly, but may be much slower than "default".

max.print: integer, defaulting to 99999. `print` or `show` methods can make use of this option, to limit the amount of information that is printed, to something in the order of (and typically slightly less than) `max.print` entries.
OutDec: character string containing a single character. The preferred character to be used as the decimal point in output conversions, that is in printing, plotting, `format` and `as.character` but not when deparsing nor by `sprintf` nor `formatC` (which are sometimes used prior to printing.)

`pager`: the command used for displaying text files by `file.show`, details depending on the platform:

On a unix-alike defaults to `{R_HOME}/bin/pager`, which is a shell script running the command-line specified by the environment variable `PAGER` whose default is set at configuration, usually to `less`.

On Windows defaults to “internal”, which uses a pager similar to the GUI console. Another possibility is “console” to use the console itself.

Can be a character string or an R function, in which case it needs to accept the arguments (files, header, title, delete.file) corresponding to the first four arguments of `file.show`.

papersize: the default paper format used by `postscript`; set by environment variable `R_PAPERSIZE` when R is started: if that is unset or invalid it defaults platform dependently on a unix-alike to a value derived from the locale category `LC_PAPER`, or if that is unavailable to a default set when R was built.

On Windows to "a4", or "letter" in US and Canadian locales.

`PCRE_limit_recursion`: Logical: should `grep(perl = TRUE)` and similar limit the maximal recursion allowed when matching? Only relevant for PCRE1 and PCRE2 <= 10.23. PCRE can be built not to use a recursion stack (see `pcre_config`), but it uses recursion by default with a recursion limit of 10000000 which potentially needs a very large C stack: see the discussion at `https://www.pcre.org/original/doc/html/pcrestack.html`. If true, the limit is reduced using R’s estimate of the C stack size available (if known), otherwise 10000. If NA, the limit is imposed only if any input string has 1000 or more bytes. The limit has no effect when PCRE’s Just-in-Time compiler is used.

`PCRE_study`: Logical or integer: should `grep(perl = TRUE)` and similar ‘study’ the patterns? Either logical or a numerical threshold for the minimum number of strings to be matched for the pattern to be studied (the default is 10). Missing values and negative numbers are treated as false. This option is ignored with PCRE2 (PCRE version >= 10.00) which does not have a separate study phase and patterns are automatically optimized when possible.

`PCRE_use_JIT`: Logical: should `grep(perl = TRUE)`, `strsplit(perl = TRUE)` and similar make use of PCRE’s Just-In-Time compiler if available? (This applies only to studied patterns with PCRE1.) Default: true. Missing values are treated as false.

`pdfviewer`: default PDF viewer. The default is set from the environment variable `R_PDFVIEWER`, the default value of which on a unix-alike is set when R is configured, and on Windows is the full path to `open.exe`, a utility supplied with R.

`printcmd`: the command used by `postscript` for printing; set by environment variable `R_PRINTCMD` when R is started. This should be a command that expects either input to be piped to ‘stdin’ or to be given a single filename argument. Usually set to “lpr” on a Unix-alike.

`prompt`: a non-empty string to be used for R’s prompt; should usually end in a blank (" ").

`rl_word_breaks`: (Unix only:) Used for the readline-based terminal interface. Default value " \t\n\"\'\">=<%;|&{()}. This is the set of characters use to break the input line into tokens for object- and file-name completion. Those who do not use spaces around operators may prefer " \t\n\"\'\">=+==%;|&{()}"
options

save.defaults, save.image.defaults: see save.

scipen: integer. A penalty to be applied when deciding to print numeric values in fixed or exponential notation. Positive values bias towards fixed and negative towards scientific notation: fixed notation will be preferred unless it is more than scipen digits wider.

setWidthOnResize: a logical. If set and TRUE, R run in a terminal using a recent readline library will set the width option when the terminal is resized.

showWarnCalls, showErrorCalls: a logical. Should warning and error messages show a summary of the call stack? By default error calls are shown in non-interactive sessions.

showNCalls: integer. Controls how long the sequence of calls must be (in bytes) before ellipses are used. Defaults to 50 and should be at least 30 and no more than 500.

show.error.locations: Should source locations of errors be printed? If set to TRUE or "top", the source location that is highest on the stack (the most recent call) will be printed. "bottom" will print the location of the earliest call found on the stack. Integer values can select other entries. The value 0 corresponds to "top" and positive values count down the stack from there. The value -1 corresponds to "bottom" and negative values count up from there.

show.error.messages: a logical. Should error messages be printed? Intended for use with try or a user-installed error handler.

texi2dvi: used by functions texi2dvi and texi2pdf in package tools.

unix-alike only: Set at startup from the environment variable R_TEXI2DVICMD, which defaults first to the value of environment variable TEXI2DVI, and then to a value set when R was installed (the full path to a texi2dvi script if one was found). If necessary, that environment variable can be set to "emulation".

timeout: positive integer. The timeout for some Internet operations, in seconds. Default 60 (seconds) but can be set from environment variable R_DEFAULT_INTERNET_TIMEOUT. (Invalid values of the option or the variable are silently ignored: non-integer numeric values will be truncated.) See download.file and connections.

topLevelEnvironment: see toplevel and sys.source.

url.method: character string: the default method for url. Normally unset, which is equivalent to "default", which is "internal" except on Windows.

useFancyQuotes: controls the use of directional quotes in sQuote, dQuote and in rendering text help (see Rd2txt in package tools). Can be TRUE, FALSE, "TeX" or "UTF-8".

verbose: logical. Should R report extra information on progress? Set to TRUE by the command-line option '--verbose'.

warn: integer value to set the handling of warning messages. If warn is negative all warnings are ignored. If warn is zero (the default) warnings are stored until the top-level function returns. If 10 or fewer warnings were signalled they will be printed otherwise a message saying how many were signalled. An object called last.warning is created and can be printed through the function warnings. If warn is one, warnings are printed as they occur. If warn is two (or larger, coercible to integer), all warnings are turned into errors.

warnPartialMatchArgs: logical. If true, warns if partial matching is used in argument matching.

warnPartialMatchAttr: logical. If true, warns if partial matching is used in extracting attributes via attr.

warnPartialMatchDollar: logical. If true, warns if partial matching is used for extraction by $.

warning.expression: an R code expression to be called if a warning is generated, replacing the standard message. If non-null it is called irrespective of the value of option warn.
warning.length: sets the truncation limit in bytes for error and warning messages. A non-negative integer, with allowed values 100…8170, default 1000.

nwarnings: the limit for the number of warnings kept when warn = 0, default 50. This will discard messages if called whilst they are being collected. If you increase this limit, be aware that the current implementation pre-allocates the equivalent of a named list for them, i.e., do not increase it to more than say a million.

width: controls the maximum number of columns on a line used in printing vectors, matrices and arrays, and when filling by cat.

Columns are normally the same as characters except in East Asian languages.

You may want to change this if you re-size the window that R is running in. Valid values are 10…10000 with default normally 80. (The limits on valid values are in file ‘Print.h’ and can be changed by re-compiling R.) Some R consoles automatically change the value when they are resized.

See the examples on Startup for one way to set this automatically from the terminal width when R is started.

The ‘factory-fresh’ default settings of some of these options are

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>add.smooth</td>
<td>TRUE</td>
</tr>
<tr>
<td>check.bounds</td>
<td>FALSE</td>
</tr>
<tr>
<td>continue</td>
<td>&quot;+ &quot;</td>
</tr>
<tr>
<td>digits</td>
<td>7</td>
</tr>
<tr>
<td>echo</td>
<td>TRUE</td>
</tr>
<tr>
<td>encoding</td>
<td>&quot;native.enc&quot;</td>
</tr>
<tr>
<td>error</td>
<td>NULL</td>
</tr>
<tr>
<td>expressions</td>
<td>5000</td>
</tr>
<tr>
<td>keep.source</td>
<td>interactive()</td>
</tr>
<tr>
<td>keep.source.pkgs</td>
<td>FALSE</td>
</tr>
<tr>
<td>max.print</td>
<td>99999</td>
</tr>
<tr>
<td>OutDec</td>
<td>&quot;. &quot;</td>
</tr>
<tr>
<td>prompt</td>
<td>&quot;&gt; &quot;</td>
</tr>
<tr>
<td>scipen</td>
<td>0</td>
</tr>
<tr>
<td>show.error.messages</td>
<td>TRUE</td>
</tr>
<tr>
<td>timeout</td>
<td>60</td>
</tr>
<tr>
<td>verbose</td>
<td>FALSE</td>
</tr>
<tr>
<td>warn</td>
<td>0</td>
</tr>
<tr>
<td>warning.length</td>
<td>1000</td>
</tr>
<tr>
<td>width</td>
<td>80</td>
</tr>
</tbody>
</table>

Others are set from environment variables or are platform-dependent.

**Options set in package grDevices**

These will be set when package grDevices (or its namespace) is loaded if not already set.

bitmapType: (Unix only, incl. macOS) character. The default type for the bitmap devices such as png. Defaults to "cairo" on systems where that is available, or to "quartz" on macOS where that is available.

device: a character string giving the name of a function, or the function object itself, which when called creates a new graphics device of the default type for that session. The value of this option defaults to the normal screen device (e.g., X11, windows or quartz) for an interactive
session, and pdf in batch use or if a screen is not available. If set to the name of a device, the
device is looked for first from the global environment (that is down the usual search path) and
then in the \texttt{grDevices} namespace.
The default values in interactive and non-interactive sessions are configurable via environment
variables \texttt{R\_INTERACTIVE\_DEVICE} and \texttt{R\_DEFAULT\_DEVICE} respectively.
The search logic for ‘the normal screen device’ is that this is windows on Windows, and
quartz if available on macOS (running at the console, and compiled into the build). Otherwise
\texttt{X11} is used if environment variable \texttt{DISPLAY} is set.

\texttt{device.\_ask\_default}: logical. The default for \texttt{devAskNewPage("ask")} when a device is opened.
\texttt{locatorBell}: logical. Should selection in \texttt{locator} and \texttt{identify} be confirmed by a bell? Default
\texttt{TRUE}. Honoured at least on \texttt{X11} and windows devices.
\texttt{windows\_Timeout}: (Windows-only) integer vector of length 2 representing two times in milliseconds.
These control the double-buffering of \texttt{windows} devices when that is enabled: the first
is the delay after plotting finishes (default 100) and the second is the update interval during
continuous plotting (default 500). The values at the time the device is opened are used.

\textbf{Other options used by package graphics}

\texttt{max}\_\texttt{contour}\_\texttt{segments}: positive integer, defaulting to \texttt{25000} if not set. A limit on the number of
segments in a single contour line in \texttt{contour} or \texttt{contourLines}.

\textbf{Options set in package stats}

These will be set when package \texttt{stats} (or its namespace) is loaded if not already set.
\texttt{contrasts}: the default \texttt{contrasts} used in model fitting such as with \texttt{aov} or \texttt{lm}. A character vector
of length two, the first giving the function to be used with unordered factors and the second the
function to be used with ordered factors. By default the elements are named \texttt{c("unordered",}
"ordered"), but the names are unused.
\texttt{na.action}: the name of a function for treating missing values (\texttt{NA}'s) for certain situations, see
\texttt{na.action} and \texttt{na.pass}.
\texttt{show}\_\texttt{coef}\_\texttt{Pvalues}: logical, affecting whether P values are printed in summary tables of coefficients.
See \texttt{printCoefmat}.
\texttt{show.nls.convergence}: logical, should \texttt{nls} convergence messages be printed for successful fits?
\texttt{show.signif.stars}: logical, should stars be printed on summary tables of coefficients? See
\texttt{printCoefmat}.
\texttt{ts.eps}: the relative tolerance for certain time series (\texttt{ts}) computations. Default \texttt{1e-05}.
\texttt{ts.S.compat}: logical. Used to select S compatibility for plotting time-series spectra. See the
description of argument \texttt{log} in \texttt{plot.spec}.

\textbf{Options set (or used) in package utils}

These will be set (apart from \texttt{Ncpus}) when package \texttt{utils} (or its namespace) is loaded if not already set.
\texttt{BioC\_mirror}: The URL of a Bioconductor mirror for use by \texttt{setRepositories},
e.g. the default “https://bioconductor.org” or the European mirror
“https://bioconductor.statistik.tu-dortmund.de”. Can be set by
\texttt{chooseBioCmirror}.
browser: The HTML browser to be used by `browseURL`. This sets the default browser on UNIX or a non-default browser on Windows. Alternatively, an R function that is called with a URL as its argument. See `browseURL` for further details.

ccaddress: default Cc: address used by `create.post` (and hence `bug.report` and `help.request`). Can be FALSE or "".

citation.bibtex.max: default 1; the maximal number of bibentries (bibentry) in a citation for which the bibtex version is printed in addition to the text one.

dc.cellwidth: integer: the cell widths (number of characters) to be used in the data editor `dataentry`. If this is unset (the default), 0, negative or NA, variable cell widths are used.

demo.ask: default for the ask argument of `demo`.

editor: a non-empty character string or an R function that sets the default text editor, e.g., for `edit` and `file.edit`. Set from the environment variable `EDITOR` on UNIX, or if unset `VISUAL` or `vi`. As a string it should specify the name of or path to an external command.

ewample.ask: default for the ask argument of `example`.

help.ports: optional integer vector for setting ports of the internal HTTP server, see `startDynamicHelp`.

help.search.types: default types of documentation to be searched by `help.search` and `??`.

help.try.all.packages: default for an argument of `help`.

help.type: default for an argument of `help`, used also as the help type by `?`.

help.htmlmath: default for the `texmath` argument of `Rd2HTML`, controlling how LaTeX-like mathematical equations are displayed in R help pages (if enabled). Useful values are "katex" (equivalent to NULL, the default) and "mathjax"; for all other values basic substitutions are used.

HTTPUserAgent: string used as the 'user agent' in HTTP(S) requests by `download.file`, `url` and `curlGetHeaders`, or NULL when requests will be made without a user agent header. The default is R (<version> <platform> <arch> <os>) except when 'libcurl' is used when it is libcurl/7.<xx>.<y> for the 'libcurl' version in use.

install.lock: logical: should per-directory package locking be used by `install.packages`?

install.packages.check.source: Used by `install.packages` (and indirectly `update.packages`) on platforms which support binary packages. Possible values "yes" and "no", with unset being equivalent to "yes".

install.packages.compile.from.source: Used by `install.packages` (type = "both") (and indirectly `update.packages`) on platforms which support binary packages. Possible values "never", "interactive" (which means ask in interactive use and "never" in batch use) and "always". The default is taken from environment variable R_COMPILE_AND_INSTALL_PACKAGES, with default "interactive" if unset. However, `install.packages` uses "never" unless a make program is found, consulting the environment variable `MAKE`.

mailer: default emailing method used by `create.post` and hence `bug.report` and `help.request`. 
menu.graphics: Logical: should graphical menus be used if available? Defaults to TRUE. Currently applies to `select.list`, `chooseCRANmirror`, `setRepositories` and to select from multiple (text) help files in `help`.

Ncpus: an integer \( n \geq 1 \), used in `install.packages` as default for the number of cpus to use in a potentially parallel installation, as `Ncpus = getOption("Ncpus", 1L)`, i.e., when unset is equivalent to a setting of 1.

pkgType: The default type of packages to be downloaded and installed – see `install.packages`. Possible values are platform dependently
- **on Windows** "win.binary", "source" and "both" (the default).
- **on Unix-alikes** "source" (the default except under a CRAN macOS build), "mac.binary" and "both" (the default for CRAN macOS builds). ("mac.binary.el-capitan", "mac.binary.mavericks", "mac.binary.leopard" and "mac.binary.universal" are no longer in use.)

Value "binary" is a synonym for the native binary type (if there is one); "both" is used by `install.packages` to choose between source and binary installs.

repos: character vector of repository URLs for use by `available.packages` and related functions. Initially set from entries marked as default in the 'repositories' file, whose path is configurable via environment variable `R_REPOSITORIES` (set this to `NULL` to skip initialization at startup). The ‘factory-fresh’ setting from the file in `R.home("etc")` is `c(CRAN="@CRAN@")`, a value that causes some utilities to prompt for a CRAN mirror. To avoid this do set the CRAN mirror, by something like
```r
local({
  r <- getOption("repos")
  r["CRAN"] <- "https://my.local.cran"
  options(repos = r)
})
```
in your `.Rprofile`, or use a personal 'repositories' file.

Note that you can add more repositories (Bioconductor, R-Forge, RForge.net, ...) for the current session using `setRepositories`.

str: a list of options controlling the default `str` display. Defaults to `strOptions()`.

SweaveHooks, SweaveSyntax: see Sweave.

unzip: a character string used by `unzip`: the path of the external program unzip or "internal". Defaults (platform dependently)
- **on unix-alikes** to the value of `R_UNZIPCMD`, which is set in `etc/Renviron` to the path of the unzip command found during configuration and otherwise to "".
- **on Windows** to "internal" when the internal unzip code is used.

**Options set in package parallel**

These will be set when package `parallel` (or its namespace) is loaded if not already set.

mc.cores: an integer giving the maximum allowed number of additional \( \mathcal{R} \) processes allowed to be run in parallel to the current \( \mathcal{R} \) process. Defaults to the setting of the environment variable `MC_CORES` if set. Most applications which use this assume a limit of 2 if it is unset.

**Options used on Unix only**

dvipscmd: character string giving a command to be used in the (deprecated) off-line printing of help pages via PostScript. Defaults to "dvips".
Options used on Windows only

warn.FPU: logical, by default undefined. If true, a warning is produced whenever dyn.load repairs the control word damaged by a buggy DLL.

Note

For compatibility with S there is a visible object .Options whose value is a pairlist containing the current options() (in no particular order). Assigning to it will make a local copy and not change the original. (Using it however is faster than calling options()).

An option set to NULL is indistinguishable from a non-existing option.

References


Examples

```r
op <- options(); utils::str(op) # op is a named list

getOption("width") == options()$width # the latter needs more memory
options(digits = 15)
pi

# set the editor, and save previous value
old.o <- options(editor = "nedit")
old.o

options(check.bounds = TRUE, warn = 1)
x <- NULL; x[4] <- "yes" # gives a warning

options(digits = 5)
print(1e5)
options(scipen = 3); print(1e5)

options(op) # reset (all) initial options
options("digits")

## Not run: ## set contrast handling to be like S
options(contrasts = c("contr.helmert", "contr.poly"))

## End(Not run)

## Not run: ## on error, terminate the R session with error status 66
options(error = quote(q("no", status = 66, runLast = FALSE)))
stop("test it")

## End(Not run)

## Not run: ## Set error actions for debugging:
## enter browser on error, see ?recover:
options(error = recover)
## allows to call debugger() afterwards, see ?debugger:
options(error = dump.frames)
## A possible setting for non-interactive sessions
```
options(error = quote({dump.frames(to.file = TRUE); q()}))

## End(Not run)

# Compare the two ways to get an option and use it
# accounting for the possibility it might not be set.
if(as.logical(getOption("performCleanup", TRUE)))
cat("do cleanup\n")

## Not run:
# a clumsier way of expressing the above w/o the default.
tmp <- getOption("performCleanup")
if(is.null(tmp))
tmp <- TRUE
if(tmp)
cat("do cleanup\n")

## End(Not run)

<table>
<thead>
<tr>
<th>order</th>
<th>Ordering Permutation</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Description</strong></td>
<td>order returns a permutation which rearranges its first argument into ascending or descending order, breaking ties by further arguments. sort.list does the same, using only one argument. See the examples for how to use these functions to sort data frames, etc.</td>
</tr>
</tbody>
</table>
| **Usage** | order(..., na.last = TRUE, decreasing = FALSE, method = c("auto", "shell", "radix"))

sort.list(x, partial = NULL, na.last = TRUE, decreasing = FALSE, method = c("auto", "shell", "quick", "radix")) |

| **Arguments** | |
| ... | a sequence of numeric, complex, character or logical vectors, all of the same length, or a classed R object. |
| x | an atomic vector for methods "shell" and "quick". When x is a non-atomic R object, the default "auto" and "radix" methods may work if order(x,...) does. |
| partial | vector of indices for partial sorting. (Non-NULL values are not implemented.) |
| decreasing | logical. Should the sort order be increasing or decreasing? For the "radix" method, this can be a vector of length equal to the number of arguments in ... and the elements are recycled as necessary. For the other methods, it must be length one. |
| na.last | for controlling the treatment of NAs. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed (see ‘Note’.) |
method is the method to be used: partial matches are allowed. The default ("auto") implies "radix" for numeric vectors, integer vectors, logical vectors and factors with fewer than \(2^{31}\) elements. Otherwise, it implies "shell". For details of methods "shell", "quick", and "radix", see the help for sort.

**Details**

In the case of ties in the first vector, values in the second are used to break the ties. If the values are still tied, values in the later arguments are used to break the tie (see the first example). The sort used is stable (except for method = "quick"), so any unresolved ties will be left in their original ordering.

Complex values are sorted first by the real part, then the imaginary part.

Except for method "radix", the sort order for character vectors will depend on the collating sequence of the locale in use: see Comparison.

The "shell" method is generally the safest bet and is the default method, except for short factors, numeric vectors, integer vectors and logical vectors, where "radix" is assumed. Method "radix" stably sorts logical, numeric and character vectors in linear time. It outperforms the other methods, although there are drawbacks, especially for character vectors (see sort). Method "quick" for sort.list is only supported for numeric \(x\) with na.last = NA, is not stable, and is slower than "radix".

partial = NULL is supported for compatibility with other implementations of S, but no other values are accepted and ordering is always complete.

For a classed R object, the sort order is taken from xtfm; as its help page notes, this can be slow unless a suitable method has been defined or is.numeric(\(x\)) is true. For factors, this sorts on the internal codes, which is particularly appropriate for ordered factors.

**Value**

An integer vector unless any of the inputs has \(2^{31}\) or more elements, when it is a double vector.

**Warning**

In programmatic use it is unsafe to name the ... arguments, as the names could match current or future control arguments such as decreasing. A sometimes-encountered unsafe practice is to call do.call('order', df_obj) where df_obj might be a data frame: copy df_obj and remove any names, for example using unname.

**Note**

sort.list can get called by mistake as a method for sort with a list argument: it gives a suitable error message for list \(x\).

There is a historical difference in behaviour for na.last = NA: sort.list removes the NAs and then computes the order amongst the remaining elements: order computes the order amongst the non-NA elements of the original vector. Thus

\[
x[\text{order}(x, \text{na.last} = \text{NA})]
\]
\[
z z <- x[\text{!is.na}(x)]; zz[\text{sort.list}(x, \text{na.last} = \text{NA})]
\]

both sort the non-NA values of \(x\).

Prior to R 3.3.0 method = "radix" was only supported for integers of range less than 100,000.
order

References


See Also

`sort`, `rank`, `xtfrm`.

Examples

```r
require(stats)

(ii <- order(x <- c(1,1,3:1,1:4,3), y <- c(9,9:1), z <- c(2,1:9)))
## 6 5 2 1 7 4 10 8 3 9
rbind(x, y, z)[,ii] # shows the reordering (ties via 2nd & 3rd arg)

## Suppose we wanted descending order on y.
## A simple solution for numeric 'y' is
rbind(x, y)[, order(x, -y, z)]
## More generally we can make use of xtfrm
cy <- as.character(y)
rbind(x, y, z)[, order(x, -xtfrm(cy), z)]
## The radix sort supports multiple 'decreasing' values:
rbind(x, y, z)[, order(x, cy, z, decreasing = c(FALSE, TRUE, FALSE),
method="radix")]

## Sorting data frames:
dd <- transform(data.frame(x, y, z),
  z = factor(z, labels = LETTERS[9:1]))
## Either as above (for factor 'z': using internal coding):
dd[ order(x, -y, z), ]
## or along 1st column, ties along 2nd, ... arbitrary* no.(columns):
dd[ do.call(order, dd), ]

set.seed(1) # reproducible example:
d4 <- data.frame(x = round( rnorm(100)), y = round(10*runif(100)),
  z = round( 8*rnorm(100)), u = round(50*runif(100)))
(d4s <- d4[ do.call(order, d4), ])
i <- which(diff(d4s[, 3]) == 0)
# in 2 places, needed 3 cols to break ties:
d4s[ rbind(i, i+1), ]

## rearrange matched vectors so that the first is in ascending order
x <- c(5:1, 6:8, 12:9)
y <- (x - 5)^2
o <- order(x)
rbind(x[o], y[o])

## tests of na.last
a <- c(4, 3, 2, NA, 1)
b <- c(4, NA, 2, 7, 1)
z <- cbind(a, b)
o <- order(a, b)); z[o, ]
o <- order(a, b, na.last = FALSE)); z[o, ]
```
(o <- order(a, b, na.last = NA)); z[o, ]

## speed examples on an average laptop for long vectors:
## factor/small-valued integers:
x <- factor(sample(letters, 1e7, replace = TRUE))
system.time(o <- sort.list(x, method = "quick", na.last = NA)) # 0.1 sec
stopifnot(!is.unsorted(x[o]))
system.time(o <- sort.list(x, method = "radix")) # 0.05 sec, 2X faster
stopifnot(!is.unsorted(x[o]))
## large-valued integers:
xx <- sample(1:200000, 1e7, replace = TRUE)
system.time(o <- sort.list(xx, method = "quick", na.last = NA)) # 0.3 sec
system.time(o <- sort.list(xx, method = "radix")) # 0.2 sec
## character vectors:
xx <- sample(state.name, 1e6, replace = TRUE)
system.time(o <- sort.list(xx, method = "shell")) # 2 sec
system.time(o <- sort.list(xx, method = "radix")) # 0.007 sec, 300X faster
## double vectors:
xx <- rnorm(1e6)
system.time(o <- sort.list(xx, method = "shell")) # 0.4 sec
system.time(o <- sort.list(xx, method = "quick", na.last = NA)) # 0.1 sec
system.time(o <- sort.list(xx, method = "radix")) # 0.05 sec, 2X faster

---

**outer**

### Outer Product of Arrays

**Description**

The outer product of the arrays X and Y is the array A with dimension `c(dim(X), dim(Y))` where element $A[c(arrayindex.x, arrayindex.y)] = FUN(X[arrayindex.x], Y[arrayindex.y], ...)$.

**Usage**

`outer(X, Y, FUN = "*", ...)`

`X %o% Y`

**Arguments**

- `X, Y` First and second arguments for function FUN. Typically a vector or array.
- `FUN` a function to use on the outer products, found via `match.fun` (except for the special case ".*").
- `...` optional arguments to be passed to FUN.

**Details**

X and Y must be suitable arguments for FUN. Each will be extended by `rep` to length the products of the lengths of X and Y before FUN is called.

FUN is called with these two extended vectors as arguments (plus any arguments in ...). It must be a vectorized function (or the name of one) expecting at least two arguments and returning a value with the same length as the first (and the second).
Where they exist, the [dim]names of \( X \) and \( Y \) will be copied to the answer, and a dimension assigned which is the concatenation of the dimensions of \( X \) and \( Y \) (or lengths if dimensions do not exist).

\( \text{FUN} = "*" \) is handled as a special case via \( \text{as\_vector}(X) \times \text{t}(\text{as\_vector}(Y)) \), and is intended only for numeric vectors and arrays.

\( \%o\% \) is binary operator providing a wrapper for \( \text{outer}(x, y, "*") \).

**Author(s)**

Jonathan Rougier

**References**


**See Also**

\( \%\times\% \) for usual (inner) matrix vector multiplication; \texttt{kronecker} which is based on \texttt{outer}; \texttt{Vectorize} for vectorizing a non-vectorized function.

**Examples**

```r
x <- 1:9; names(x) <- x
# Multiplication & Power Tables
x \%o\% x
y <- 2:8; names(y) <- paste(y,:", sep = ")
outer(y, x, "^")
outer(month.abb, 1999:2003, FUN = paste)
## three way multiplication table:
x \%o\% x \%o\% y[1:3]
```

---

**Paren**

**Parentheses and Braces**

**Description**

Open parenthesis, (, and open brace, {, are .Primitive functions in \( \mathcal{R} \).

Effectively, ( is semantically equivalent to the identity function(\( x \)) \( x \), whereas { is slightly more interesting, see examples.

**Usage**

```
( ... )
```

```
{ ... }
```

**Value**

For (, the result of evaluating the argument. This has visibility set, so will auto-print if used at top-level.

For {, the result of the last expression evaluated. This has the visibility of the last evaluation.
References


See Also

*if*, *return*, etc for other objects used in the R language itself.

Syntax for operator precedence.

Examples

```r
f <- get(""

```

```r
e <- expression(3 + 2 * 4)
identical(f(e), e)
```

```r
do <- get(""

```

```r
do(x <- 3, y <- 2*x-3, 6-x-y); x; y
```

```r
## note the differences
(2+3)
(2+3; 4+5)
(invisible(2+3))
(invisible(2+3))
```

Description

`parse()` returns the parsed but unevaluated expressions in an expression, a “list” of calls.

`str2expression()` and `str2lang()` return special versions of `parse(text=s, keep.source=FALSE)` and can therefore be regarded as transforming character strings `s` to expressions, calls, etc.

Usage

```r
parse(file = "", n = NULL, text = NULL, prompt = "?",
       keep.source = getOption("keep.source"), srcfile,
       encoding = "unknown")

str2lang(s)
str2expression(text)
```

Arguments

- `file` a connection, or a character string giving the name of a file or a URL to read the expressions from. If `file` is "" and `text` is missing or `NULL` then input is taken from the console.

- `n` integer (or coerced to integer). The maximum number of expressions to parse. If `n` is `NULL` or negative or `NA` the input is parsed in its entirety.
parse

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text character vector. The text to parse. Elements are treated as if they were lines of a file. Other R objects will be coerced to character if possible.
prompt the prompt to print when parsing from the keyboard. NULL means to use R’s prompt, getOption("prompt").
keep.source a logical value; if TRUE, keep source reference information.
srcfile NULL, a character vector, or a srcfile object. See the ‘Details’ section.
encoding encoding to be assumed for input strings. If the value is "latin1" or "UTF-8" it is used to mark character strings as known to be in Latin-1 or UTF-8; it is not used to re-encode the input. To do the latter, specify the encoding as part of the connection con or via options(encoding=): see the example under file. Arguments encoding = "latin1" and encoding = "UTF-8" are ignored with a warning when running in a MBCS locale.
s a character vector of length 1, i.e., a “string”.

Details

parse(....): If text has length greater than zero (after coercion) it is used in preference to file. All versions of R accept input from a connection with end of line marked by LF (as used on Unix), CRLF (as used on DOS/Windows) or CR (as used on classic Mac OS). The final line can be incomplete, that is missing the final EOL marker.
When input is taken from the console, n = NULL is equivalent to n = 1, and n < 0 will read until an EOF character is read. (The EOF character is Ctrl-Z for the Windows front-ends.) The line-length limit is 4095 bytes when reading from the console (which may impose a lower limit: see ‘An Introduction to R’). The default for srcfile is set as follows. If keep.source is not TRUE, srcfile defaults to a character string, either "<text>" or one derived from file. When keep.source is TRUE, if text is used, srcfile will be set to a srcfilecopy containing the text. If a character string is used for file, a srcfile object referring to that file will be used.
When srcfile is a character string, error messages will include the name, but source reference information will not be added to the result. When srcfile is a srcfile object, source reference information will be retained.
str2expression(s): for a character vector s, str2expression(s) corresponds to parse(text = s, keep.source=FALSE), which is always of type (typeof) and class expression.
str2lang(s): for a character string s, str2lang(s) corresponds to parse(text = s, keep.source=FALSE)[[1]] (plus a check that both s and the parse(*) result are of length one) which is typically a call but may also be a symbol aka name, NULL or an atomic constant such as 2, 1L, or TRUE. Put differently, the value of str2lang(.) is a call or one of its parts, in short “a call or simpler”.
Currently, encoding is not handled in str2lang() and str2expression().

Value

parse() and str2expression() return an object of type "expression", for parse() with up to n elements if specified as a non-negative integer.
str2lang(s), s a string, returns “a call or simpler”, see the ‘Details’ section.
When srcfile is non-NULL, a "srcref" attribute will be attached to the result containing a list of srcref records corresponding to each element, a "srcfile" attribute will be attached containing a copy of srcfile, and a "wholeSrcref" attribute will be attached containing a srcref record
corresponding to all of the parsed text. Detailed parse information will be stored in the "srcfile" attribute, to be retrieved by `getParseData`.

A syntax error (including an incomplete expression) will throw an error.

Character strings in the result will have a declared encoding if encoding is "latin1" or "UTF-8", or if text is supplied with every element of known encoding in a Latin-1 or UTF-8 locale.

**Partial parsing**

When a syntax error occurs during parsing, `parse` signals an error. The partial parse data will be stored in the `srcfile` argument if it is a `srcfile` object and the `text` argument was used to supply the text. In other cases it will be lost when the error is triggered.

The partial parse data can be retrieved using `getParseData` applied to the `srcfile` object. Because parsing was incomplete, it will typically include references to “parent” entries that are not present.

**Note**

Using `parse(text = *, ..)` or its simplified and hence more efficient versions `str2lang()` or `str2expression()` is at least an order of magnitude less efficient than `call( .. )` or `as.call()`.

**References**


**See Also**

`scan`, `source`, `eval`, `deparse`.

The source reference information can be used for debugging (see e.g. `setBreakpoint`) and profiling (see `Rprof`). It can be examined by `getSrcRef` and related functions. More detailed information is available through `getParseData`.

**Examples**

```r
fil <- tempfile(fileext = ".Rdmped")
cat("x <- c(1, 4)\n x ^ 3 -10 ; outer(1:7, 5:9)\n", file = fil)
# parse 3 statements from our temp file
parse(file = fil, n = 3)
unlink(fil)
```

```r
## str2lang(<string>) || str2expression(<character>) is at least an order of magnitude less efficient than call( .. ) or as.call().
```

```r
## A partial parse with a syntax error

txt <- "
```
x <- 1
an error
"sf <- srcfile("txt")
tryCatch(parse(text = txt, srcfile = sf), error = function(e) "Syntax error."
getParseData(sf)

---

**paste**

**Concatenate Strings**

**Description**

Concatenate vectors after converting to character. Concatenation happens in two basically different ways, determined by collapse being a string or not.

**Usage**

```r
paste (...; sep = " ", collapse = NULL, recycle0 = FALSE)
paste0(..., collapse = NULL, recycle0 = FALSE)
```

**Arguments**

- `...` one or more R objects, to be converted to character vectors.
- `sep` a character string to separate the terms. Not `NA_character_`.
- `collapse` an optional character string to separate the results. Not `NA_character_`. When collapse is a string, the result is always a string (character of length 1).
- `recycle0` logical indicating if zero-length character arguments should result in the zero-length `character(0)`. Note that when collapse is a string, `recycle0` does not recycle to zero-length, but to "".

**Details**

`paste` converts its arguments (via `as.character`) to character strings, and concatenates them (separating them by the string given by `sep`).

If the arguments are vectors, they are concatenated term-by-term to give a character vector result. Vector arguments are recycled as needed. Zero-length arguments are recycled as "" unless `recycle0` is TRUE and collapse is NULL.

Note that `paste()` coerces `NA_character_`, the character missing value, to "NA" which may seem undesirable, e.g., when pasting two character vectors, or very desirable, e.g. in `paste("the value of p is ", p)`.

`paste0(..., collapse)` is equivalent to `paste(..., sep = "", collapse)`, slightly more efficiently.

If a value is specified for `collapse`, the values in the result are then concatenated into a single string, with the elements being separated by the value of `collapse`. 
Value

A character vector of the concatenated values. This will be of length zero if all the objects are, unless collapse is non-NULL, in which case it is "" (a single empty string).

If any input into an element of the result is in UTF-8 (and none are declared with encoding "bytes", see Encoding), that element will be in UTF-8, otherwise in the current encoding in which case the encoding of the element is declared if the current locale is either Latin-1 or UTF-8, at least one of the corresponding inputs (including separators) had a declared encoding and all inputs were either ASCII or declared.

If an input into an element is declared with encoding "bytes", no translation will be done of any of the elements and the resulting element will have encoding "bytes". If collapse is non-NULL, this applies also to the second, collapsing, phase, but some translation may have been done in pasting object together in the first phase.

References


See Also

toString typically calls paste(*, collapse="", "). String manipulation with as.character, substr, nchar, strsplit; further, cat which concatenates and writes to a file, and sprintf for C like string construction.

'plotmath' for the use of paste in plot annotation.

Examples

```r
## When passing a single vector, paste0 and paste work like as.character.
paste0(1:12)
paste(1:12) # same
as.character(1:12) # same

## If you pass several vectors to paste0, they are concatenated in a
## vectorized way.
(nth <- paste0(1:12, c("st", "nd", "rd", rep("th", 9))))

## paste works the same, but separates each input with a space.
## Notice that the recycling rules make every input as long as the longest input.
paste(month.abb, "is the", nth, "month of the year.")
paste(month.abb, letters)

## You can change the separator by passing a sep argument
## which can be multiple characters.
paste(month.abb, "is the", nth, "month of the year.", sep = "_\_*")

## To collapse the output into a single string, pass a collapse argument.
paste0(nth, collapse = ", ")

## For inputs of length 1, use the sep argument rather than collapse
paste("1st", "2nd", "3rd", collapse = ", ") # probably not what you wanted
paste("1st", "2nd", "3rd", sep = ", ")

## You can combine the sep and collapse arguments together.
paste(month.abb, nth, sep = ": ", collapse = "; ")
```
## Using `paste()` in combination with `strwrap()` can be useful
## for dealing with long strings.
```
title <- paste(strwrap("Stopping distance of cars (ft) vs. speed (mph) from Ezekiel (1930)",
    width = 30), collapse = "\n"))
plot(dist ~ speed, cars, main = title)
```

## zero length arguments recycled as `'``' -- NB: `\{\}` `==>` `character(0)` here
```
paste(\{}, 1:2)
```

## `recycle0 = TRUE` allows standard vectorized behaviour, i.e., zero-length
## recycling resulting in zero-length result `character(0)`:
```
valid <- FALSE
val <- pi
paste("The value is", val[valid], "-- not so good!") # -> ".. value is -- not .."
paste("The value is", val[valid], "-- good: empty!", recycle0=TRUE) # -> `character(0)`
```

## When `collapse = <string>`), result is (length 1) string in all cases
```
paste("foo", {}, "bar", collapse = "|") # |--> "foo bar"
paste("foo", {}, collapse = ", recycle0 = TRUE) # |--> ""
```

## If all arguments are empty (and `collapse` a string), "" results always
```
paste( collapse = "|")
paste( collapse = "|", recycle0 = TRUE)
paste(\{}, collapse = "|")
paste(\{}, collapse = "|", recycle0 = TRUE)
```

### path.expand --- Expand File Paths

**Description**

Expand a path name, for example by replacing a leading tilde by the user’s home directory (if defined on that platform).

**Usage**

```
path.expand(path)
```

**Arguments**

- `path` character vector containing one or more path names.

**Details**

**On Unix - alikes:** On most builds of R a leading `~user` will expand to the home directory of user. There are possibly different concepts of ‘home directory’: that usually used is the setting of the environment variable `HOME`. The ‘path names’ need not exist nor be valid path names but they do need to be representable in the session encoding.

**On Windows:** The definition of the ‘home’ directory is in the ‘rw-FAQ’ Q2.14: it is taken from the `R_USER` environment variable when `path.expand` is first called in a session. The ‘path names’ need not exist nor be valid path names.
pcre_config

Value
A character vector of possibly expanded path names: where the home directory is unknown or none is specified the path is returned unchanged.
If the expansion would exceed the maximum path length the result may be truncated or the path may be returned unchanged.

See Also
basename, normalizePath, file.path.

Examples
path.expand("~/foo")

---

desc

Description
Report some of the configuration options of the version of PCRE in use in this R session.

Usage
pcre_config()

Value
A named logical vector, currently with elements

- UTF-8: Support for UTF-8 inputs. Required.
- Unicode properties: Support for \p{xx} and \P{xx} in regular expressions. Desirable and used by some CRAN packages. As of PCRE2, always present with support for UTF-8.
- JIT: Support for just-in-time compilation. Desirable for speed (but only available as a compile-time option on certain architectures, and may be unused as unreliable on some of those, e.g. arm64).
- stack: Does match recursion use a stack (TRUE, the default for PCRE1 and PCRE2 older than 10.30) or a heap? See the discussion at https://www.pcre.org/original/doc/html/pcrestack.html (Added in R 3.4.0.). No longer relevant and always FALSE in PCRE2 since version 10.30 which no longer uses function recursion to remember backtracking positions.

See Also
extSoftVersion for the PCRE version.

Examples
pcre_config()
**Description**

Pipe a value into a call expression or a function expression.

**Usage**

\[ lhs \, |> \, rhs \]

**Arguments**

- **lhs**: expression producing a value.
- **rhs**: a call expression.

**Details**

A pipe expression passes, or pipes, the result of the left-hand side expression `lhs` to the right-hand side expression `rhs`.

The `lhs` is inserted as the first argument in the call. So `x \, |> \, f(y)` is interpreted as `f(x, y)`.

To avoid ambiguities, functions in `rhs` calls may not be syntactically special, such as `+` or `if`.

It is also possible to use a named argument with the placeholder `_` in the `rhs` call to specify where the `lhs` is to be inserted. The placeholder can only appear once on the `rhs`.

As an experimental feature the placeholder can also be used as the first argument in an extraction call, such as `_.$coef`. More generally, it can be used as the head of a chain of extractions, such as `_.$coef[[2]]`, using a sequence of the extraction functions $, [, [[, or @.

Pipe notation allows a nested sequence of calls to be written in a way that may make the sequence of processing steps easier to follow.

Currently, pipe operations are implemented as syntax transformations. So an expression written as `x \, |> \, f(y)` is parsed as `f(x, y)`. It is worth emphasizing that while the code in a pipeline is written sequentially, regular R semantics for evaluation apply and so piped expressions will be evaluated only when first used in the `rhs` expression.

**Value**

Returns the result of evaluating the transformed expression.

**Background**

The forward pipe operator is motivated by the pipe introduced in the `magrittr` package, but is more streamlined. It is similar to the pipe or pipeline operators introduced in other languages, including F#, Julia, and JavaScript.
Examples

# simple uses:
mtcars |> head()  # same as head(mtcars)
mtcars |> head(2)  # same as head(mtcars, 2)
mtcars |> subset(cyl == 4) |> nrow()  # same as nrow(subset(mtcars, cyl == 4))

# to pass the lhs into an argument other than the first, either
# use the _ placeholder with a named argument:
mtcars |> subset(cyl == 4) |> lm(mpg ~ disp, data = _)
# or use an anonymous function:
mtcars |> subset(cyl == 4) |> (function(d) lm(mpg ~ disp, data = d))()
mtcars |> subset(cyl == 4) |> (\(d\) lm(mpg ~ disp, data = d))()
# or explicitly name the argument(s) before the "one":
mtcars |> subset(cyl == 4) |> lm(formula = mpg ~ disp)

# using the placeholder as the head of an extraction chain:
mtcars |> subset(cyl == 4) |> lm(formula = mpg ~ disp) |> _$coef[[2]]

# the pipe operator is implemented as a syntax transformation:
quote(mtcars |> subset(cyl == 4) |> nrow())

# regular R evaluation semantics apply
stop() |> (function(...) {})()  # stop() is not used on RHS so is not evaluated

plot

Generic X-Y Plotting

Description

Generic function for plotting of R objects.

For simple scatter plots, plot.default will be used. However, there are plot methods for many R objects, including functions, data.frames, density objects, etc. Use methods(plot) and the documentation for these. Most of these methods are implemented using traditional graphics (the graphics package), but this is not mandatory.

For more details about graphical parameter arguments used by traditional graphics, see par.

Usage

plot(x, y, ...)

Arguments

x the coordinates of points in the plot. Alternatively, a single plotting structure, function or any R object with a plot method can be provided.

y the y coordinates of points in the plot, optional if x is an appropriate structure.

... Arguments to be passed to methods, such as graphical parameters (see par).

Many methods will accept the following arguments:
type what type of plot should be drawn. Possible types are

• "p" for points,
• "l" for lines,
• "b" for both,
• "c" for the lines part alone of "b",
• "o" for both ‘overplotted’,
• "h" for ‘histogram’ like (or ‘high-density’) vertical lines,
• "s" for stair steps,
• "$S" for other steps, see ‘Details’ below,
• "n" for no plotting.
All other types give a warning or an error; using, e.g., type = "punkte" being equivalent to type = "p" for S compatibility. Note that some methods, e.g. plot.factor, do not accept this.

main an overall title for the plot: see title.
sub a subtitle for the plot: see title.
xlab a title for the x axis: see title.
ylab a title for the y axis: see title.
asp the y/x aspect ratio, see plot.window.

Details

The two step types differ in their x-y preference: Going from \((x_1, y_1)\) to \((x_2, y_2)\) with \(x_1 < x_2\), type = "s" moves first horizontal, then vertical, whereas type = "$S" moves the other way around.

Note

The plot generic was moved from the graphics package to the base package in R 4.0.0. It is currently re-exported from the graphics namespace to allow packages importing it from there to continue working, but this may change in future versions of R.

See Also

plot.default, plot.formula and other methods; points, lines, par. For thousands of points, consider using smoothScatter() instead of plot().

For X-Y-Z plotting see contour, persp and image.

Examples

```r
require(stats) # for lowess, rpois, rnorm
require(graphics) # for plot methods
plot(cars)
lines(lowess(cars))
plot(sin, -pi, 2*pi) # see ?plot.function
## Discrete Distribution Plot:
plot(table(rpois(100, 5)), type = "h", col = "red", lwd = 10,
     main = "rpois(100, lambda = 5)")
## Simple quantiles/ECDF, see ecdf() {library(stats)} for a better one:
pplot(x <- sort(rnorm(47)), type = "s", main = "plot(x, type = \"s\")")
points(x, cex = .5, col = "dark red")
```
**pmatch**

**Partial String Matching**

**Description**

`pmatch` seeks matches for the elements of its first argument among those of its second.

**Usage**

```r
pmatch(x, table, nomatch = NA_integer_, duplicates.ok = FALSE)
```

**Arguments**

- `x`: the values to be matched: converted to a character vector by `as.character`. Long vectors are supported.
- `table`: the values to be matched against: converted to a character vector. Long vectors are not supported.
- `nomatch`: the value to be returned at non-matching or multiply partially matching positions. Note that it is coerced to integer.
- `duplicates.ok`: should elements in `table` be used more than once?

**Details**

The behaviour differs by the value of `duplicates.ok`. Consider first the case if this is true. First exact matches are considered, and the positions of the first exact matches are recorded. Then unique partial matches are considered, and if found recorded. (A partial match occurs if the whole of the element of `x` matches the beginning of the element of `table`.) Finally, all remaining elements of `x` are regarded as unmatched. In addition, an empty string can match nothing, not even an exact match to an empty string. This is the appropriate behaviour for partial matching of character indices, for example.

If `duplicates.ok` is `FALSE`, values of `table` once matched are excluded from the search for subsequent matches. This behaviour is equivalent to the R algorithm for argument matching, except for the consideration of empty strings (which in argument matching are matched after exact and partial matching to any remaining arguments).

`charmatch` is similar to `pmatch` with `duplicates.ok` true, the differences being that it differentiates between no match and an ambiguous partial match, it does match empty strings, and it does not allow multiple exact matches.

NA values are treated as if they were the string constant "NA".

**Value**

An integer vector (possibly including NA if `nomatch = NA`) of the same length as `x`, giving the indices of the elements in `table` which matched, or `nomatch`.

**References**


polyroot

See Also

match, charmatch and match.arg, match.fun, match.call, for function argument matching etc.,
startsWith for particular checking of initial matches; grep etc for more general (regexp) matching
of strings.

Examples

```r
pmatch("", ") # returns NA
pmatch("m", c("mean", "median", "mode")) # returns NA
pmatch("med", c("mean", "median", "mode")) # returns 2

pmatch(c("", "ab", "ab"), c("abc", "ab"), duplicates.ok = FALSE)
pmatch(c("", "ab", "ab"), c("abc", "ab"), duplicates.ok = TRUE)
## compare
ccharmatch(c("", "ab", "ab"), c("abc", "ab"))
```

polyroot

Find Zeros of a Real or Complex Polynomial

Description

Find zeros of a real or complex polynomial.

Usage

polyroot(z)

Arguments

z the vector of polynomial coefficients in increasing order.

Details

A polynomial of degree \( n - 1 \),

\[
p(x) = z_1 + z_2 x + \cdots + z_n x^{n-1}
\]

is given by its coefficient vector \( z[1:n] \). polyroot returns the \( n - 1 \) complex zeros of \( p(x) \) using
the Jenkins-Traub algorithm.

If the coefficient vector \( z \) has zeroes for the highest powers, these are discarded.

There is no maximum degree, but numerical stability may be an issue for all but low-degree poly-
nomials.

Value

A complex vector of length \( n - 1 \), where \( n \) is the position of the largest non-zero element of \( z \).

Source

C translation by Ross Ihaka of Fortran code in the reference, with modifications by the R Core
Team.
References


See Also

`uniroot` for numerical root finding of arbitrary functions; `complex` and the zero example in the demos directory.

Examples

```r
polyroot(c(1, 2, 1))
round(polyroot(choose(8, 0:8)), 11) # guess what!
for (n1 in 1:4) print(polyroot(1:n1), digits = 4)
polyroot(c(1, 2, 1, 0, 0)) # same as the first
```

### pos.to.env

*Convert Positions in the Search Path to Environments*

**Description**

Returns the environment at a specified position in the search path.

**Usage**

```r
pos.to.env(x)
```

**Arguments**

- `x` an integer between 1 and `length(search())`, the length of the search path, or -1.

**Details**

Several R functions for manipulating objects in environments (such as `get` and `ls`) allow specifying environments via corresponding positions in the search path. `pos.to.env` is a convenience function for programmers which converts these positions to corresponding environments; users will typically have no need for it. It is primitive.

-1 is interpreted as the environment the function is called from.

This is a primitive function.

**Examples**

```r
pos.to.env(1) # R_GlobalEnv
# the next returns the base environment
pos.to.env(length(search()))
```
pretty

Pretty Breakpoints

Description

Compute a sequence of about \( n+1 \) equally spaced ‘round’ values which cover the range of the values in \( x \). The values are chosen so that they are 1, 2 or 5 times a power of 10.

Usage

```r
pretty(x, ...)
```

## Default S3 method:
```r
pretty(x, n = 5, min.n = n %/% 3, shrink.sml = 0.75,
      high.u.bias = 1.5, u5.bias = .5 + 1.5*high.u.bias,
      eps.correct = 0, f.min = 2^-20, ...)
```

```r
.pretty(x, n = 5L, min.n = n %/% 3, shrink.sml = 0.75,
       high.u.bias = 1.5, u5.bias = .5 + 1.5*high.u.bias,
       eps.correct = 0L, f.min = 2^-20, bounds = TRUE)
```

Arguments

- `x`: an object coercible to numeric by `as.numeric`.
- `n`: integer giving the desired number of intervals. Non-integer values are rounded down.
- `min.n`: nonnegative integer giving the minimal number of intervals. If \( \text{min.n} == 0 \), `pretty(.)` may return a single value.
- `shrink.sml`: positive number, a factor (smaller than one) by which a default scale is shrunk in the case when \( \text{range}(x) \) is very small (usually 0).
- `high.u.bias`: non-negative numeric, typically \( \geq 1 \). The interval unit is determined as \{1,2,5,10\} times \( b \), a power of 10. Larger `high.u.bias` values favor larger units.
- `u5.bias`: non-negative numeric multiplier favoring factor 5 over 2. Default and ‘optimal’: \( u5.bias = .5 + 1.5*\text{high.u.bias} \).
- `eps.correct`: integer code, one of \{0,1,2\}. If non-0, an epsilon correction is made at the boundaries such that the result boundaries will be outside \( \text{range}(x) \); in the small case, the correction is only done if `eps.correct >= 2`.
- `f.min`: positive factor multiplied by `.Machine$\text{double.xmin}` to get the smallest “acceptable” cell \( c_m \) which determines the unit of the algorithm. Smaller cell values are set to \( c_m \), signalling a warning about being “corrected”. New from R 4.2.0, previously `f.min = 20` was hardcoded in the algorithm.
- `bounds`: a logical indicating if the resulting vector should cover the full range(\( x \)), i.e., strictly include the bounds of \( x \). New from R 4.2.0, allowing `bound=FALSE` to reproduce how R’s graphics engine computes axis tick locations (in `GEPretty()`).
- `...`: further arguments for methods.
Details

pretty ignores non-finite values in x.

Let \(d <= \max(x) - \min(x) \geq 0\). If \(d\) is not (very close) to 0, we let \(c <= d/n\), otherwise more or less \(c <= \max(\text{abs}(\text{range}(x)))\times \text{shrink.sml} / \min.n\). Then, the 10 base \(b\) is \(10^{\left\lfloor \log_{10}(c) \right\rfloor}\) such that \(b \leq c < 10b\).

Now determine the basic unit \(u\) as one of \(\{1, 2, 5, 10\}\) \(b\), depending on \(c/b \in [1, 10)\) and the two 'bias' coefficients, \(h = \text{high.u.bias}\) and \(f = \text{u5.bias}\).

Value

pretty() returns an numeric vector of approximately \(n\) increasing numbers which are "pretty" in decimal notation. (in extreme range cases, the numbers can no longer be "pretty" given the other constraints; e.g., for pretty(...)

For ease of investigating the underlying C R_pretty() function, .pretty() returns a named list.

By default, when bounds=TRUE, the entries are 1, u, and n, whereas for bounds=FALSE, they are ns, nu, n, and (a "pretty") unit where the \(n*\)'s are integer valued (but only \(n\) is of class integer). Programmers may use this to create pretty sequence (iterator) objects.

References


See Also

axTicks for the computation of pretty axis tick locations in plots, particularly on the log scale.

Examples

```r
pretty(1:15) # 0 2 4 6 8 10 12 14 16
pretty(1:15, high.u.bias = 2) # 0 5 10 15
pretty(1:15, n = 4) # 0 5 10 15
pretty(1:15 * 2) # 0 5 10 15 20 25 30
pretty(1:20) # 0 5 10 15 20
pretty(1:20, n = 2) # 0 10 20
pretty(1:20, n = 10) # 0 2 4 ... 20

for(k in 5:11) {
  cat("k="", k, ": "); print(diff(range(pretty(100 + c(0, pi*10^-k)))))
}
##-- more bizarre, when min(x) == max(x):
pretty(pi)
```

add.names <- function(v) { names(v) <- paste(v); v}
utils::str(lapply(add.names(-10:20), pretty))
## min.n = 0 returns a length-1 vector "if pretty":
utils::str(lapply(add.names(0:20), pretty, min.n = 0))
sapply( add.names(0:20), pretty, min.n = 4)

pretty(1.234e100)
pretty(1001.1001)
pretty(1001.1001, shrink.sml = 0.2)
for(k in -7:3)
cat("shrink=", formatC(2^k, width = 9), ":",
    formatC(pretty(1001.1001, shrink.sml = 2^k), width = 6), "\n")

### Primitive

#### Look Up a Primitive Function

**Description**

.Primitive looks up by name a ‘primitive’ (internally implemented) function.

**Usage**

.Primitive(name)

**Arguments**

*name* name of the R function.

**Details**

The advantage of .Primitive over .Internal functions is the potential efficiency of argument passing, and that positional matching can be used where desirable, e.g. in `switch`. For more details, see the ‘R Internals’ manual.

All primitive functions are in the base namespace.

This function is almost never used: `name` or, more carefully, `get(name, envir = baseenv())` work equally well and do not depend on knowing which functions are primitive (which does change as R evolves).

**See Also**

`is.primitive` showing that primitive functions come in two types (`typeof`), .Internal.

**Examples**

```r
mysqrt <- .Primitive("sqrt")
c
.Internal # this one *must* be primitive!
`if` # need backticks
```
print

Print Values

Description

print prints its argument and returns it invisibly (via invisible(x)). It is a generic function which means that new printing methods can be easily added for new classes.

Usage

print(x, ...)

## S3 method for class 'factor'
print(x, quote = FALSE, max.levels = NULL,
       width = getOption("width"), ...)

## S3 method for class 'table'
print(x, digits = getOption("digits"), quote = FALSE,
       na.print = ",", zero.print = "0",
       right = is.numeric(x) || is.complex(x),
       justify = "none", ...)

## S3 method for class 'function'
print(x, useSource = TRUE, ...)

Arguments

x
... future arguments passed to or from other methods.
quote
logical, indicating whether or not strings should be printed with surrounding quotes.
max.levels
integer, indicating how many levels should be printed for a factor; if 0, no extra "Levels" line will be printed. The default, NULL, entails choosing max.levels such that the levels print on one line of width width.
width
only used when max.levels is NULL, see above.
digits
minimal number of significant digits, see print.default.
na.print
character string (or NULL) indicating NA values in printed output, see print.default.
zero.print
character specifying how zeros (0) should be printed; for sparse tables, using "." can produce more readable results, similar to printing sparse matrices in Matrix.
right
logical, indicating whether or not strings should be right aligned.
justify
character indicating if strings should left- or right-justified or left alone, passed to format.
useSource
logical indicating if internally stored source should be used for printing when present, e.g., if options(keep.source = TRUE) has been in use.
Details

The default method, `print.default` has its own help page. Use `methods("print")` to get all the methods for the print generic.

`print.factor` allows some customization and is used for printing `ordered` factors as well.

`print.table` for printing tables allows other customization. As of R 3.0.0, it only prints a description in case of a table with 0-extents (this can happen if a classifier has no valid data).

See `noquote` as an example of a class whose main purpose is a specific print method.

References


See Also

The default method `print.default`, and help for the methods above; further `options`, `noquote`.

For more customizable (but cumbersome) printing, see `cat`, `format` or also `write`. For a simple prototypical print method, see `.print.via.format` in package `tools`.

Examples

```r
require(stats)

ts(1:20) #-- print is the "Default function" --> print.ts(.) is called
for(i in 1:3) print(1:i)

## Printing of factors
attenu$station # 117 levels -> 'max.levels' depending on width

## ordered factors: levels "l1 < l2 < .."
esoph$agegp[1:12]
esoph$alcgp[1:12]

## Printing of sparse (contingency) tables
set.seed(521)
t1 <- round(abs(rt(200, df = 1.8)))
t2 <- round(abs(rt(200, df = 1.4)))
table(t1, t2) # simple
print(table(t1, t2), zero.print = ".") # nicer to read

## same for non-integer "table":
T <- table(t2,t1)
T <- T * (1+round(rlnorm(length(T)))/4)
print(T, zero.print = ".") # quite nicer,
print.table(T[,2:8] * 1e9, digits=3, zero.print = ".")

## still slightly inferior to Matrix::Matrix(T) for larger T

## Corner cases with empty extents:
table(1, NA) # < table of extent 1 x 0 >
```
print.data.frame  Printing Data Frames

Description
Print a data frame.

Usage
## S3 method for class 'data.frame'
print(x, ..., digits = NULL,
quote = FALSE, right = TRUE, row.names = TRUE, max = NULL)

Arguments
x
object of class data.frame.

... optional arguments to print methods.
digits
the minimum number of significant digits to be used: see print.default.
quote
logical, indicating whether or not entries should be printed with surrounding quotes.
right
logical, indicating whether or not strings should be right-aligned. The default is right-alignment.
row.names
logical (or character vector), indicating whether (or what) row names should be printed.
max numeric or NULL, specifying the maximal number of entries to be printed. By default, when NULL,getOption("max.print") used.

Details
This calls format which formats the data frame column-by-column, then converts to a character matrix and dispatches to the print method for matrices.

When quote = TRUE only the entries are quoted not the row names nor the column names.

See Also
data.frame.

Examples
(dd <- data.frame(x = 1:8, f = gl(2,4), ch = I(letters[1:8])))
# print() with defaults
print(dd, quote = TRUE, row.names = FALSE)
# suppresses row.names and quotes all entries
print.default  Default Printing

Description

print.default is the default method of the generic print function which prints its argument.

Usage

## Default S3 method:
print(x, digits = NULL, quote = TRUE,
  na.print = NULL, print.gap = NULL, right = FALSE,
  max = NULL, width = NULL, useSource = TRUE, ...)

Arguments

x
the object to be printed.
digits
a non-null value for digits specifies the minimum number of significant digits to be printed in values. The default, NULL, uses getOption("digits"). (For the interpretation for complex numbers see signif.) Non-integer values will be rounded down, and only values greater than or equal to 1 and no greater than 22 are accepted.
quote
logical, indicating whether or not strings (characters) should be printed with surrounding quotes.
na.print
a character string which is used to indicate NA values in printed output, or NULL (see 'Details').
print.gap
a non-negative integer \( \leq 1024 \), or NULL (meaning 1), giving the spacing between adjacent columns in printed vectors, matrices and arrays.
right
logical, indicating whether or not strings should be right aligned. The default is left alignment.
max
a non-null value for max specifies the approximate maximum number of entries to be printed. The default, NULL, uses getOption("max.print"): see that help page for more details.
width
controls the maximum number of columns on a line used in printing vectors, matrices, etc. The default, NULL, uses getOption("width"): see that help page for more details including allowed values.
useSource
logical, indicating whether to use source references or copies rather than deparsing language objects. The default is to use the original source if it is available.
...

Arguments to be passed to or from other methods. They are ignored in this function.

Details

The default for printing NAs is to print NA (without quotes) unless this is a character NA and quote = FALSE, when ‘<NA>’ is printed.

The same number of decimal places is used throughout a vector. This means that digits specifies the minimum number of significant digits to be used, and that at least one entry will be encoded with that minimum number. However, if all the encoded elements then have trailing zeroes, the
number of decimal places is reduced until at least one element has a non-zero final digit. Decimal
dots are only included if at least one decimal place is selected.

Attributes are printed respecting their class(es), using the values of digits to print.default, but
using the default values (for the methods called) of the other arguments.

Option width controls the printing of vectors, matrices and arrays, and option deparse.cutoff controls the printing of language objects such as calls and formulae.

When the methods package is attached, print will call show for R objects with formal classes
(‘S4’) if called with no optional arguments.

**Large number of digits**

Note that for large values of digits, currently for digits ≥ 16, the calculation of the number of
significant digits will depend on the platform’s internal (C library) implementation of ‘sprintf()’
functionality.

**Single-byte locales**

If a non-printable character is encountered during output, it is represented as one of the ANSI escape
sequences (‘\a’, ‘\b’, ‘\f’, ‘\n’, ‘\r’, ‘\t’, ‘\v’, ‘\ ’, and ‘\0’: see Quotes), or failing that as a 3-
digit octal code: for example the UK currency pound sign in the C locale (if implemented correctly)
is printed as ‘\243’. Which characters are non-printable depends on the locale. (Because some
versions of Windows get this wrong, all bytes with the upper bit set are regarded as printable on
Windows in a single-byte locale.)

**Unicode and other multi-byte locales**

In all locales, the characters in the ASCII range (‘0x00’ to ‘0x7f’) are printed in the same way, as-is
if printable, otherwise via ANSI escape sequences or 3-digit octal escapes as described for single-
byte locales. Whether a character is printable depends on the current locale and the operating system
(C library).

Multi-byte non-printing characters are printed as an escape sequence of the form ‘\uxxxx’ or
‘\Uxxxxxxxx’ (in hexadecimal). This is the internal code for the wide-character representation of
the character. If this is not known to be Unicode code points, a warning is issued. The only known
exceptions are certain Japanese ISO 2022 locales on commercial Unixes, which use a concatenation
of the bytes: it is unlikely that R compiles on such a system.

It is possible to have a character string in a character vector that is not valid in the current locale. If
a byte is encountered that is not part of a valid character it is printed in hex in the form ‘\xab’ and
this is repeated until the start of a valid character. (This will rapidly recover from minor errors in
UTF-8.)

**See Also**

The generic print, options. The "noquote" class and print method.
encodeString, which encodes a character vector the way it would be printed.

**Examples**

```r
pi
print(pi, digits = 16)
LETTERS[1:16]
print(LETTERS, quote = FALSE)
```
M <- cbind(I = 1, matrix(1:10000, ncol = 10, 
dimnames = list(NULL, LETTERS[1:10])))
utils::head(M) # makes more sense than
print(M, max = 1000) # prints 90 rows and a message about omitting 910

prmatrix

Print Matrices, Old-style

Description
An earlier method for printing matrices, provided for S compatibility.

Usage
prmatrix(x, rowlab = , collab =,
quote = TRUE, right = FALSE, na.print = NULL, ...)

Arguments
x numeric or character matrix.
rowlab, collab (optional) character vectors giving row or column names respectively. By def-
dault, these are taken from dimnames(x).
quote logical; if TRUE and x is of mode "character", quotes (""") are used.
right if TRUE and x is of mode "character", the output columns are right-justified.
na.print how NAs are printed. If this is non-null, its value is used to represent NA.
...
arguments for print methods.

Details
prmatrix is an earlier form of print.matrix, and is very similar to the S function of the same
name.

Value
Invisibly returns its argument, x.

References
Brooks/Cole.

See Also
print.default, and other print methods.

Examples
prmatrix(m6 <- diag(6), rowlab = rep("", 6), collab = rep("", 6))

chm <- matrix(scan(system.file("help", "AnIndex", package = "splines"),
what = ""), , 2, byrow = TRUE)
chm # uses print.matrix()
prmatrix(chm, collab = paste("Column", 1:3), right = TRUE, quote = FALSE)
Description

`proc.time` determines how much real and CPU time (in seconds) the currently running R process has already taken.

Usage

```
proc.time()
```

Details

`proc.time` returns five elements for backwards compatibility, but its `print` method prints a named vector of length 3. The first two entries are the total user and system CPU times of the current R process and any child processes on which it has waited, and the third entry is the ‘real’ elapsed time since the process was started.

Value

An object of class "proc_time" which is a numeric vector of length 5, containing the user, system, and total elapsed times for the currently running R process, and the cumulative sum of user and system times of any child processes spawned by it on which it has waited. (The `print` method uses the `summary` method to combine the child times with those of the main process.)

The definition of ‘user’ and ‘system’ times is from your OS. Typically it is something like

The ‘user time’ is the CPU time charged for the execution of user instructions of the calling process.
The ‘system time’ is the CPU time charged for execution by the system on behalf of the calling process.

Times of child processes are not available on Windows and will always be given as NA.

The resolution of the times will be system-specific and on Unix-alikes times are rounded down to milliseconds. On modern systems they will be that accurate, but on older systems they might be accurate to 1/100 or 1/60 sec. They are typically available to 10ms on Windows.

This is a primitive function.

References


See Also

`system.time` for timing an R expression, `gc.time` for how much of the time was spent in garbage collection.

`setTimeLimit` to limit the CPU or elapsed time for the session or an expression.
**Examples**

```r
## a way to time an R expression: system.time is preferred
ptm <- proc.time()
for (i in 1:50) mad(stats::runif(500))
proc.time() - ptm
```

---

**prod**  
*Product of Vector Elements*

**Description**

`prod` returns the product of all the values present in its arguments.

**Usage**

```r
prod(..., na.rm = FALSE)
```

**Arguments**

- `...`: numeric or complex or logical vectors.
- `na.rm`: logical. Should missing values be removed?

**Details**

If `na.rm` is FALSE an NA value in any of the arguments will cause a value of NA to be returned, otherwise NA values are ignored.

This is a generic function: methods can be defined for it directly or via the `Summary` group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

Logical true values are regarded as one, false values as zero. For historical reasons, NULL is accepted and treated as if it were `numeric(0)`.

**Value**

The product, a numeric (of type "double") or complex vector of length one. **NB:** the product of an empty set is one, by definition.

**S4 methods**

This is part of the S4 `Summary` group generic. Methods for it must use the signature `x, ..., na.rm`.

**References**


**See Also**

`sum`, `cumprod`, `cumsum`.

`plotmath` for the use of `prod` in plot annotation.
Examples

\[
\text{print(prod(1:7)) == print(gamma(8))}
\]

---

**proportions**

*Express Table Entries as Fraction of Marginal Table*

**Description**

Returns conditional proportions given margins, i.e. entries of \( x \), divided by the appropriate marginal sums.

**Usage**

\[
\text{proportions}(x, \text{margin} = \text{NULL}) \\
\text{prop.table}(x, \text{margin} = \text{NULL})
\]

**Arguments**

- **\( x \)**: table
- **\( \text{margin} \)**: a vector giving the margins to split by. E.g., for a matrix 1 indicates rows, 2 indicates columns, \( c(1, 2) \) indicates rows and columns. When \( x \) has named dimnames, it can be a character vector selecting dimension names.

**Value**

Table like \( x \) expressed relative to \( \text{margin} \)

**Note**

\text{prop.table} is an earlier name, retained for back-compatibility.

**Author(s)**

Peter Dalgaard

**See Also**

\text{marginSums, apply, sweep} are a more general mechanism for sweeping out marginal statistics.

**Examples**

\[
\begin{align*}
\text{m <- matrix(1:4, 2)} \\
\text{m} \\
\text{proportions(m, 1)}
\end{align*}
\]

\[
\begin{align*}
\text{DF <- as.data.frame(UCBAdmissions)} \\
\text{tbl <- xtabs(Freq ~ Gender + Admit, DF)}
\end{align*}
\]

\[
\text{proportions(tbl, "Gender")}
\]
pushBack

Push Text Back on to a Connection

Description

Functions to push back text lines onto a connection, and to enquire how many lines are currently pushed back.

Usage

pushBack(data, connection, newLine = TRUE,
        encoding = c("", "bytes", "UTF-8"))
pushBackLength(connection)
clearPushBack(connection)

Arguments

data                  a character vector.
connection             A connection.
newLine                logical. If true, a newline is appended to each string pushed back.
encoding               character string, partially matched. See details.

Details

Several character strings can be pushed back on one or more occasions. The occasions form a stack, so the first line to be retrieved will be the first string from the last call to pushBack. Lines which are pushed back are read prior to the normal input from the connection, by the normal text-reading functions such as `readLines` and `scan`.

Pushback is only allowed for readable connections in text mode.

Not all uses of connections respect pushbacks, in particular the input connection is still wired directly, so for example parsing commands from the console and `scan("")` ignore pushbacks on stdin.

When character strings with a marked encoding (see Encoding) are pushed back they are converted to the current encoding if encoding = ". This may involve representing characters as ‘<U+xxxx>’ if they cannot be converted. They will be converted to UTF-8 if encoding = "UTF-8" or left as-is if encoding = "bytes".

Value

pushBack and clearPushBack() return nothing, invisibly.
pushBackLength returns the number of lines currently pushed back.

See Also

connections, readLines.
Examples

```
zz <- textConnection(LETTERS)
readLines(zz, 2)
pushBack(c("aa", "bb"), zz)
pushBackLength(zz)
readLines(zz, 1)
pushBackLength(zz)
readLines(zz, 1)
readLines(zz, 1)
close(zz)
```

qr
The QR Decomposition of a Matrix

Description

qr computes the QR decomposition of a matrix.

Usage

```
qr(x, 
## Default S3 method:
qr(x, tol = 1e-07 , LAPACK = FALSE, ...)

qr.coef(qr, y)
qr.qy(qr, y)
qr.qty(qr, y)
qr.resid(qr, y)
qr.fitted(qr, y, k = qr$rank)
qr.solve(a, b, tol = 1e-7)
## S3 method for class 'qr'
solve(a, b, ...)

is.qr(x)
as.qr(x)
```

Arguments

- **x**: a numeric or complex matrix whose QR decomposition is to be computed. Logical matrices are coerced to numeric.
- **tol**: the tolerance for detecting linear dependencies in the columns of x. Only used if LAPACK is false and x is real.
- **qr**: a QR decomposition of the type computed by qr.
- **y, b**: a vector or matrix of right-hand sides of equations.
- **a**: a QR decomposition or (qr.solve only) a rectangular matrix.
- **k**: effective rank.
- **LAPACK**: logical. For real x, if true use LAPACK otherwise use LINPACK (the default).
- **...**: further arguments passed to or from other methods.
Details

The QR decomposition plays an important role in many statistical techniques. In particular it can be used to solve the equation $Ax = b$ for given matrix $A$, and vector $b$. It is useful for computing regression coefficients and in applying the Newton-Raphson algorithm.

The functions `qr.coef`, `qr.resid`, and `qr.fitted` return the coefficients, residuals and fitted values obtained when fitting $y$ to the matrix with QR decomposition $q$. (If pivoting is used, some of the coefficients will be `NA`.) `qr.qy` and `qr.qty` return $Q^*y$ and $t(Q) y$, where $Q$ is the (complete) $Q$ matrix.

All the above functions keep dimnames (and names) of $x$ and $y$ if there are any.

`solve.qr` is the method for `solve` for `qr` objects. `qr.solve` solves systems of equations via the QR decomposition: if $a$ is a QR decomposition it is the same as `solve.qr`, but if $a$ is a rectangular matrix the QR decomposition is computed first. Either will handle over- and under-determined systems, providing a least-squares fit if appropriate.

`is.qr` returns `TRUE` if $x$ is a list and inherits from "qr".

It is not possible to coerce objects to mode "qr". Objects either are QR decompositions or they are not.

The LINPACK interface is restricted to matrices $x$ with less than $2^{31}$ elements.

`qr.fitted` and `qr.resid` only support the LINPACK interface.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

Value

The QR decomposition of the matrix as computed by LINPACK(*) or LAPACK. The components in the returned value correspond directly to the values returned by DQRDC(2)/DGEQP3/ZGEQP3.

- **qr**: a matrix with the same dimensions as $x$. The upper triangle contains the $R$ of the decomposition and the lower triangle contains information on the $Q$ of the decomposition (stored in compact form). Note that the storage used by DQRDC and DGEQP3 differs.
- **qraux**: a vector of length $ncol(x)$ which contains additional information on $Q$.
- **rank**: the rank of $x$ as computed by the decomposition(*): always full rank in the LAPACK case.
- **pivot**: information on the pivoting strategy used during the decomposition.

Non-complex QR objects computed by LAPACK have the attribute "useLAPACK" with value `TRUE`.

*) `dqrdc2` instead of LINPACK’s DQRDC

In the (default) LINPACK case (LAPACK = FALSE), `qr()` uses a modified version of LINPACK’s DQRDC, called ‘dqrdc2’. It differs by using the tolerance `tol` for a pivoting strategy which moves columns with near-zero 2-norm to the right-hand edge of the $x$ matrix. This strategy means that sequential one degree-of-freedom effects can be computed in a natural way.

Note

To compute the determinant of a matrix (do you really need it?), the QR decomposition is much more efficient than using Eigen values (`eigen`). See `det`.

Using LAPACK (including in the complex case) uses column pivoting and does not attempt to detect rank-deficient matrices.
For qr, the LINPACK routine DQRDC (but modified to dqrdc2(*)) and the LAPACK routines DGEQP3 and ZGEPQ3. Further LINPACK and LAPACK routines are used for qr.coef, qr.qy and qr.aty.

LAPACK and LINPACK are from https://netlib.org/lapack/ and https://netlib.org/linpack/ and their guides are listed in the references.

References


See Also


det (using qr) to compute the determinant of a matrix.

Examples

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
h9 <- hilbert(9); h9
qr(h9)$rank #--> only 7
qrh9 <- qr(h9, tol = 1e-10)
qrh9$rank #--> 9
###-- Solve linear equation system H %*% x = y :
y <- 1:9/10
x <- qr.solve(h9, y, tol = 1e-10) # or equivalently :
x <- qr.coef(qrh9, y) #-- is == but much better than
    #-- solve(h9) %*% y
h9 %*% x # = y

### overdetermined system
A <- matrix(runif(12), 4)
b <- 1:4
qr.solve(A, b) # or solve(qr(A), b)
solve(qr(A, LAPACK = TRUE), b)
# this is a least-squares solution, cf. lm(b ~ 0 + A)

### underdetermined system
A <- matrix(runif(12), 3)
b <- 1:3
qr.solve(A, b)
solve(qr(A, LAPACK = TRUE), b)
# solutions will have one zero, not necessarily the same one
Description

Returns the original matrix from which the object was constructed or the components of the decomposition.

Usage

qr.X(qr, complete = FALSE, ncol =)
qr.Q(qr, complete = FALSE, Dvec =)
qr.R(qr, complete = FALSE)

Arguments

qr object representing a QR decomposition. This will typically have come from a previous call to qr or lsfit.

complete logical expression of length 1. Indicates whether an arbitrary orthogonal completion of the Q or X matrices is to be made, or whether the R matrix is to be completed by binding zero-value rows beneath the square upper triangle.

ncol integer in the range 1:nrow(qr$qr). The number of columns to be in the reconstructed X. The default when complete is FALSE is the first min(ncol(X), nrow(X)) columns of the original X from which the qr object was constructed. The default when complete is TRUE is a square matrix with the original X in the first ncol(X) columns and an arbitrary orthogonal completion (unitary completion in the complex case) in the remaining columns.

Dvec vector (not matrix) of diagonal values. Each column of the returned Q will be multiplied by the corresponding diagonal value. Defaults to all 1s.

Value

qr.X returns X, the original matrix from which the qr object was constructed, provided ncol(X) <= nrow(X). If complete is TRUE or the argument ncol is greater than ncol(X), additional columns from an arbitrary orthogonal (unitary) completion of X are returned.

qr.Q returns part or all of Q, the order-nrow(X) orthogonal (unitary) transformation represented by qr. If complete is TRUE, Q has nrow(X) columns. If complete is FALSE, Q has ncol(X) columns. When Dvec is specified, each column of Q is multiplied by the corresponding value in Dvec.

Note that qr.Q(qr, *) is a special case of qr.qy(qr, y) (with a “diagonal” y), and qr.X(qr, *) is basically qr.qy(qr, R) (apart from pivoting and dimnames setting).

qr.R returns R. This may be pivoted, e.g., if a <- qr(x) then x[, a$pivot] = QR. The number of rows of R is either nrow(X) or ncol(X) (and may depend on whether complete is TRUE or FALSE).

See Also

qr, qr.qy.
Examples

```r
p <- ncol(x <- LifeCycleSavings[, -1]) # not the 'sr'
qrstr <- qr(x) # dim(x) == c(n,p)
qrstr $ rank # = 4 = p
Q <- qr.Q(qrstr) # dim(Q) == dim(x)
R <- qr.R(qrstr) # dim(R) == ncol(x)
X <- qr.X(qrstr) # X == x
range(X - as.matrix(x)) # ~ < 6e-12
## X == Q %*% R if there has been no pivoting, as here:
all.equal(unname(X),
          unname(Q %*% R))

# example of pivoting
x <- cbind(int = 1,
           b1 = rep(1:0, each = 3), b2 = rep(0:1, each = 3),
           c1 = rep(c(1,0,0), 2), c2 = rep(c(0,1,0), 2), c3 = rep(c(0,0,1),2))
x # is singular, columns "b2" and "c3" are "extra"
a <- qr(x)
zapsmall(qr.R(a)) # columns are int b1 c1 c2 b2 c3
a$pivot
pivI <- sort.list(a$pivot) # the inverse permutation
all.equal(x,
          qr.Q(a) %*% qr.R(a)) # no, no
stopifnot(
  all.equal(x[, a$pivot], qr.Q(a) %*% qr.R(a)),
  all.equal(x[, pivI], qr.Q(a) %*% qr.R(a)[, pivI])) # TRUE too!
```

Description

The function `quit` or its alias `q` terminate the current R session.

Usage

```r
quit(save = "default", status = 0, runLast = TRUE)
q(save = "default", status = 0, runLast = TRUE)
```

Arguments

- `save` a character string indicating whether the environment (workspace) should be saved, one of "no", "yes", "ask" or "default".
- `status` the (numerical) error status to be returned to the operating system, where relevant. Conventionally 0 indicates successful completion.
- `runLast` should `.Last()` be executed?

Details

`save` must be one of "no", "yes", "ask" or "default". In the first case the workspace is not saved, in the second it is saved and in the third the user is prompted and can also decide not to quit. The default is to ask in interactive use but may be overridden by command-line arguments (which must be supplied in non-interactive use).
Immediately *before* normal termination, `.Last()` is executed if the function `.Last` exists and `runLast` is true. If in interactive use there are errors in the `.Last` function, control will be returned to the command prompt, so do test the function thoroughly. There is a system analogue, `.Last.sys()`, which is run after `.Last()` if `runLast` is true.

Exactly what happens at termination of an R session depends on the platform and GUI interface in use. A typical sequence is to run `.Last()` and `.Last.sys()` (unless `runLast` is false), to save the workspace if requested (and in most cases also to save the session history: see `savehistory`), then run any finalizers (see `reg.finalizer`) that have been set to be run on exit, close all open graphics devices, remove the session temporary directory and print any remaining warnings (e.g., from `.Last()` and device closure).

Some error status values are used by R itself. The default error handler for non-interactive use effectively calls `q("no", 1, FALSE)` and returns error status 1. Error status 2 is used for R ‘suicide’, that is a catastrophic failure, and other small numbers are used by specific ports for initialization failures. It is recommended that users choose statuses of 10 or more.

Valid values of status are system-dependent, but 0:255 are normally valid. (Many OSes will report the last byte of the value, that is report the value modulo 256. But not all.)

**Warning**

The value of `.Last` is for the end user to control: as it can be replaced later in the session, it cannot safely be used programmatically, e.g. by a package. The other way to set code to be run at the end of the session is to use a finalizer: see `reg.finalizer`.

**Note**

The R.app GUI on macOS has its own version of these functions with slightly different behaviour for the `save` argument (the GUI’s ‘Startup’ preferences for this action are taken into account).

**References**


**See Also**

`.First` for setting things on startup.

**Examples**

```r
## Not run: ## Unix-flavour example
.Last <- function() {
  graphics.off() # close devices before printing
  cat("Now sending PDF graphics to the printer:\n")
  system("lpr Rplots.pdf")
  cat("bye bye...\n")
}
quit("yes")
## End(Not run)
```
Description

Descriptions of the various uses of quoting in R.

Details

Three types of quotes are part of the syntax of R: single and double quotation marks and the backtick (or back quote, ``). In addition, backslash is used to escape the following character inside character constants.

Character constants

Single and double quotes delimit character constants. They can be used interchangeably but double quotes are preferred (and character constants are printed using double quotes), so single quotes are normally only used to delimit character constants containing double quotes.

Backslash is used to start an escape sequence inside character constants. Escaping a character not in the following table is an error.

Single quotes need to be escaped by backslash in single-quoted strings, and double quotes in double-quoted strings.

```
'\n'    newline (aka ‘line feed’)
'\r'    carriage return
'\t'    tab
'\b'    backspace
'\a'    alert (bell)
'\f'    form feed
'\v'    vertical tab
'\'     backslash ‘
'\''    ASCII apostrophe ‘’
'\"'    ASCII quotation mark ‘”
'\'     ASCII grave accent (backtick) ‘’
'\u0000'    character with given octal code (1, 2 or 3 digits)
'\x0000'    character with given hex code (1 or 2 hex digits)
'\u{00000000}'    Unicode character with given code (1–4 hex digits)
'\U{00000000}'    Unicode character with given code (1–8 hex digits)
```

Alternative forms for the last two are ‘\u{nnn}’ and ‘\U{nnnnnnnn}’. All except the Unicode escape sequences are also supported when reading character strings by `scan` and `read.table` if `allowEscapes = TRUE`. Unicode escapes can be used to enter Unicode characters not in the current locale’s charset (when the string will be stored internally in UTF-8). The maximum allowed value for ‘\nnn’ is ‘\377’ (the same character as ‘\xff’).

As from R 4.1.0 the largest allowed ‘\U’ value is ‘\U{10FFFF}’, the maximum Unicode point.

The parser does not allow the use of both octal/hex and Unicode escapes in a single string.

These forms will also be used by `print.default` when outputting non-printable characters (including backslash).
Embedded nuls are not allowed in character strings, so using escapes (such as `\0`) for a nul will result in the string being truncated at that point (usually with a warning).

Raw character constants are also available using a syntax similar to the one used in C++: `r"(...)"` with ... any character sequence, except that it must not contain the closing sequence `")"`. The delimiter pairs `[]` and `{}` can also be used, and `R` can be used in place of `r`. For additional flexibility, a number of dashes can be placed between the opening quote and the opening delimiter, as long as the same number of dashes appear between the closing delimiter and the closing quote.

Names and Identifiers

Identifiers consist of a sequence of letters, digits, the period (.) and the underscore. They must not start with a digit nor underscore, nor with a period followed by a digit. **Reserved** words are not valid identifiers.

The definition of a **letter** depends on the current locale, but only ASCII digits are considered to be digits.

Such identifiers are also known as **syntactic names** and may be used directly in R code. Almost always, other names can be used provided they are quoted. The preferred quote is the backtick (``), and `deparse` will normally use it, but under many circumstances single or double quotes can be used (as a character constant will often be converted to a name). One place where backticks may be essential is to delimit variable names in formulae: see **formula**.

Note

UTF-16 surrogate pairs in `\unnnn\uoooo` form will be converted to a single Unicode point, so for example `\u0834\u001E` gives the single character `\U1D11E`. However, unpaired values in the surrogate range such as in the string “abc\u834de” will be converted to a non-standard-conformant UTF-8 string (as is done by most other software): this may change in future.

See Also

Syntax for other aspects of the syntax.

sQuote for quoting English text.

shQuote for quoting OS commands.

The 'R Language Definition' manual.

Examples

'\'single quotes can be used more-or-less interchangeably\'
"with double quotes to create character vectors"

```r
## Single quotes inside single-quoted strings need backslash-escaping.
## Ditto double quotes inside double-quoted strings.
## identical("It\'s alive!", he screamed.
##   "\"It\'s alive!\", he screamed.") # same
```

```r
## Backslashes need doubling, or they have a special meaning.
x <- "In ALGOL, you could do logical AND with /\."
print(x) # shows it as above ("input-like")
writeLines(x) # shows it as you like it ;-)  
```

```r
## Single backslashes followed by a letter are used to denote
## special characters like tab(ulator)s and newlines:
```
x <- "long\lines can be\broken with newlines"
writeLines(x) # see also ?strwrap

## Backticks are used for non-standard variable names.
## (See make.names and ?Reserved for what counts as
## non-standard.)
`x y` <- 1:5
`x y`
d <- data.frame(`1st column` = rchisq(5, 2), check.names = FALSE)
d$`1st column`

## Backslashes followed by up to three numbers are interpreted as
## octal notation for ASCII characters.
"\110\145\154\154\157\40\127\157\162\154\144\41"

## \x followed by up to two numbers is interpreted as
## hexadecimal notation for ASCII characters.
(hw1 <- "\x48\65\6c\6c\6f\20\57\6f\72\6c\64\21")

## Mixing octal and hexadecimal in the same string is OK
(hw2 <- "\110\x65\154\x6c\157\x20\127\x6c\162\144\x21")

## \u is also hexadecimal, but supports up to 4 digits,
## using Unicode specification. In the previous example,
## you can simply replace \x with \u.
(hw3 <- "\u0126\u0119\u1114\u022d\u2001\u03e2\u0954\u0f3f\u13d3\u147b\u203c")

## The last three are all identical to
hw <- "Hello World!"
stopifnot(identical(hw, hw1), identical(hw1, hw2), identical(hw2, hw3))

## Using Unicode makes more sense for non-latin characters.
(nn <- "\u0126\u0119\u1114\u022d\u2001\u03e2\u0954\u0f3f\u13d3\u147b\u203c")

## Mixing \x and \u throws a _parse_ error (which is not catchable!)
## Not run:
"\x48\u65\6c\6c\6f\20\57\6f\72\6c\64\21"

## End(Not run)
## --> Error: mixing Unicode and octal/hex escapes ......

## \U works like \u, but supports up to six hex digits.
## So we can replace \u with \U in the previous example.
n2 <- "\U0126\U0119\U1114\U022d\U2001\U03e2\U0954\U0f3f\U13d3\U147b\U203c"
stopifnot(identical(nn, n2))

## Under systems supporting multi-byte locales (and not Windows),
## \U also supports the rarer characters outside the usual 16^4 range.
## See the R language manual,
## https://cran.r-project.org/doc/manuals/r-release/R-lang.html#Literal-constants
## and bug 16098 https://bugs.r-project.org/show_bug.cgi?id=16098
## This character may or not be printable (the platform decides)
## and if it is, may not have a glyph in the font used.
"\U1d4d7" # On Windows this used to give the incorrect value of "\Ud4d7"

## nul characters (for terminating strings in C) are not allowed (parse errors)
## Not run:
"foo\0bar" # Error: nul character not allowed (line 1)
"foo\u0000bar" # same error

## End(Not run)

## A Windows path written as a raw string constant:
r"(c:\Program files\R)"

## More raw strings:
r"{"1\2}"  
r"use both "double" and 'single' quotes"

---(\1--)-)---

### R.Version

#### Version Information

#### Description

R.Version() provides detailed information about the version of R running.

R.version is a variable (a list) holding this information (and version is a copy of it for S compatibility).

#### Usage

R.Version()
R.version
R.version.string
version
Rcompiled_by()

#### Details

This gives details of the OS under which R was built, not the one under which it is currently running (for which see Sys.info).

Note that OS names might not be what you expect: for example macOS Mavericks 10.9.4 identifies itself as ‘darwin13.3.0’, Linux usually as ‘linux-gnu’, Solaris 10 as ‘solaris2.10’ and Windows as ‘mingw32’.

R.version$crt is supported on Windows since R 4.2.0 and returns "ucrt" to denote the Universal C Runtime. It would return "msvcrt" for the older Microsoft Visual C++ Runtime (but R does not use that runtime since 4.2.0).

#### Value

R.Version returns a list with character-string components

platform the platform for which R was built. A triplet of the form CPU-VENDOR-OS, as determined by the configure script. E.g. "i686-unknown-linux-gnu" or "i386-pc-mingw32".

arch the architecture (CPU) R was built on/for.

os the underlying operating system.
crt the C runtime on Windows.

system CPU and OS, separated by a comma.

status the status of the version (e.g., "alpha")

major the major version number

minor the minor version number, including the patchlevel

year the year the version was released

month the month the version was released

day the day the version was released

svn rev the Subversion revision number, which should be either "unknown" or a single number. (A range of numbers or a number with ‘M’ or ‘S’ appended indicates inconsistencies in the sources used to build this version of R.)

language always "R".

version.string a character string concatenating some of the info above, useful for plotting, etc.

R.version and version are lists of class "simple.list" which has a print method.

R_compiled_by returns a two-element character vector giving details of the C and Fortran compilers used to build R. (Empty strings if no information is available.)

Note

Do not use R.version$os to test the platform the code is running on: use .Platform$OS.type instead. Slightly different versions of the OS may report different values of R.version$os, as may different versions of R. Alternatively, osVersion typically contains more details about the platform R is running on.

R.version.string is a copy of R.version$version.string for simplicity and backwards compatibility.

See Also

sessionInfo which provides additional information; getRversion typically used inside R code, osVersion, .Platform, Sys.info.

Examples

require(graphics)

R.version$os # to check how lucky you are ...
plot(0) # any plot
mtext(R.version.string, side = 1, line = 4, adj = 1) # a useful bottom-right note

## a good way to detect macOS:
if(grepl("^darwin", R.version$os)) message("running on macOS")

## Short R version string, ("space free", useful in file/directory names; 
## also fine for unreleased versions of R):
shortRversion <- function() {
  rvs <- R.version.string
  if(grepl("devel", (st <- R.version$status)))
    rvs <- sub(paste0(" ",st," "), "-devel_", rvs, fixed=TRUE)
  gsub("([()])", ",", gsub(" ", ",", sub(" version ", ",", rvs)))}
Random Number Generation

Description

.Random.seed is an integer vector, containing the random number generator (RNG) state for random number generation in R. It can be saved and restored, but should not be altered by the user. 

RNGkind is a more friendly interface to query or set the kind of RNG in use.

RNGversion can be used to set the random generators as they were in an earlier R version (for reproducibility).

set.seed is the recommended way to specify seeds.

Usage

Random.seed <- c(rng.kind, n1, n2, ...)

RNGkind(kind = NULL, normal.kind = NULL, sample.kind = NULL)
RNGversion(vstr)
set.seed(seed, kind = NULL, normal.kind = NULL, sample.kind = NULL)

Arguments

kind character or NULL. If kind is a character string, set R’s RNG to the kind desired. Use "default" to return to the R default. See ‘Details’ for the interpretation of NULL.

normal.kind character string or NULL. If it is a character string, set the method of Normal generation. Use "default" to return to the R default. NULL makes no change.

sample.kind character string or NULL. If it is a character string, set the method of discrete uniform generation (used in sample, for instance). Use "default" to return to the R default. NULL makes no change.

seed a single value, interpreted as an integer, or NULL (see ‘Details’).

vstr a character string containing a version number, e.g., "1.6.2". The default RNG configuration of the current R version is used if vstr is greater than the current version.

rng.kind integer code in 0:k for the above kind.

n1, n2, ... integers. See the details for how many are required (which depends on rng.kind).

Details

The currently available RNG kinds are given below. kind is partially matched to this list. The default is "Mersenne-Twister".
"Wichmann–Hill" The seed, `.Random.seed[-1] == r[1:3]` is an integer vector of length 3, where each `r[i]` is in `1:(p[i] - 1)`, where `p` is the length 3 vector of primes, `p = (30269, 30307, 30323)`. The Wichmann–Hill generator has a cycle length of $6.9536 \times 10^{12} = \text{prod}(p-1)/4$, see *Applied Statistics* (1984) 33, 123 which corrects the original article. It exhibits 12 clear failures in the TestU01 Crush suite and 22 in the BigCrush suite (*L’Ecuyer*, 2007).

"Marsaglia–Multicarry": A *multiply-with-carry* RNG is used, as recommended by George Marsaglia in his post to the mailing list ‘sci.stat.math’. It has a period of more than $2^{60}$. It exhibits 40 clear failures in L’Ecuyer’s TestU01 Crush suite. Combined with Ahrens-Dieter or Kinderman-Ramage it exhibits deviations from normality even for univariate distribution generation. See PR#18168 for a discussion.

The seed is two integers (all values allowed).

"Super-Duper": Marsaglia’s famous Super-Duper from the 70’s. This is the original version which does not pass the MTUPLE test of the Diehard battery. It has a period of $\approx 4.6 \times 10^{18}$ for most initial seeds. The seed is two integers (all values allowed for the first seed: the second must be odd).

We use the implementation by Reeds et al (1982–84).

The two seeds are the Tausworthe and congruence long integers, respectively. A one-to-one mapping to S’s `.Random.seed[1:12]` is possible but we will not publish one, not least as this generator is not exactly the same as that in recent versions of S-PLUS.


"Mersenne-Twister": From Matsumoto and Nishimura (1998); code updated in 2002. A twisted GFSR with period $2^{19937} - 1$ and equidistribution in 623 consecutive dimensions (over the whole period). The ‘seed’ is a 624-dimensional set of 32-bit integers plus a current position in that set.

R uses its own initialization method due to B. D. Ripley and is not affected by the initialization issue in the 1998 code of Matsumoto and Nishimura addressed in a 2002 update.

It exhibits 2 clear failures in each of the TestU01 Crush and the BigCrush suite (*L’Ecuyer*, 2007).

"Knuth-TAOCP-2002": A 32-bit integer GFSR using lagged Fibonacci sequences with subtraction. That is, the recurrence used is

$$X_j = (X_{j-100} - X_{j-37}) \mod 2^{30}$$

and the ‘seed’ is the set of the 100 last numbers (actually recorded as 101 numbers, the last being a cyclic shift of the buffer). The period is around $2^{129}$.


The 2002 version was not backwards compatible with the earlier version: the initialization of the GFSR from the seed was altered. R did not allow you to choose consecutive seeds, the reported ‘weakness’, and already scrambled the seeds. Otherwise, the algorithm is identical to Knuth-TAOCP-2002, with the same lagged Fibonacci recurrence formula.

Initialization of this generator is done in interpreted R code and so takes a short but noticeable time.

It exhibits 3 clear failure in the TestU01 Crush suite and 4 clear failures in the BigCrush suite (*L’Ecuyer*, 2007).

"L’Ecuyer-CMRG": A ‘combined multiple-recursive generator’ from L’Ecuyer (1999), each element of which is a feedback multipliciative generator with three integer elements: thus the seed is a (signed) integer vector of length 6. The period is around $2^{191}$.

The 6 elements of the seed are internally regarded as 32-bit unsigned integers. Neither the first three nor the last three should be all zero, and they are limited to less than 4294967087 and 4294944443 respectively.
This is not particularly interesting of itself, but provides the basis for the multiple streams used in package `parallel`.

It exhibits 6 clear failures in each of the TestU01 Crush and the BigCrush suite (L’Ecuyer, 2007).

"user-supplied": Use a user-supplied generator. See `Random.user` for details.

`normal.kind` can be "Kinderman-Ramage", "Buggy Kinderman-Ramage" (not for `set.seed`), "Ahrens-Dieter", "Box-Muller", "Inversion" (the default), or "user-supplied". (For inversion, see the reference in `qnorm`.) The Kinderman-Ramage generator used in versions prior to 1.7.0 (now called "Buggy") had several approximation errors and should only be used for reproduction of old results. The "Box-Muller" generator is stateful as pairs of normals are generated and returned sequentially. The state is reset whenever it is selected (even if it is the current normal generator) and when `kind` is changed.

`sample.kind` can be "Rounding" or "Rejection", or partial matches to these. The former was the default in versions prior to 3.6.0: it made `sample` noticeably non-uniform on large populations, and should only be used for reproduction of old results. See PR#17494 for a discussion.

`set.seed` uses a single integer argument to set as many seeds as are required. It is intended as a simple way to get quite different seeds by specifying small integer arguments, and also as a way to get valid seed sets for the more complicated methods (especially "Mersenne-Twister" and "Knuth-TAOCP"). There is no guarantee that different values of `seed` will seed the RNG differently, although any exceptions would be extremely rare. If called with `seed = NULL` it re-initializes (see ‘Note’) as if no seed had yet been set.

The use of `kind = NULL, normal.kind = NULL` or `sample.kind = NULL` in `RNGkind` or `set.seed` selects the currently-used generator (including that used in the previous session if the workspace has been restored): if no generator has been used it selects "default".

**Value**

`.Random.seed` is an `integer` vector whose first element `codes` the kind of RNG and normal generator. The lowest two decimal digits are in $0:(k-1)$ where $k$ is the number of available RNGs. The hundreds represent the type of normal generator (starting at 0), and the ten thousands represent the type of discrete uniform sampler.

In the underlying C, `.Random.seed[-1]` is unsigned; therefore in R `.Random.seed[-1]` can be negative, due to the representation of an unsigned integer by a signed integer.

`RNGkind` returns a three-element character vector of the RNG, normal and sample kinds selected before the call, invisibly if either argument is not NULL. A type starts a session as the default, and is selected either by a call to `RNGkind` or by setting `.Random.seed` in the workspace. (NB: prior to R 3.6.0 the first two kinds were returned in a two-element character vector.)

`RNGversion` returns the same information as `RNGkind` about the defaults in a specific R version.

`set.seed` returns NULL, invisibly.

**Note**

Initially, there is no seed; a new one is created from the current time and the process ID when one is required. Hence different sessions will give different simulation results, by default. However, the seed might be restored from a previous session if a previously saved workspace is restored.

`.Random.seed` saves the seed set for the uniform random-number generator, at least for the system generators. It does not necessarily save the state of other generators, and in particular does not save the state of the Box–Muller normal generator. If you want to reproduce work later, call `set.seed` (preferably with explicit values for `kind` and `normal.kind`) rather than set `.Random.seed`. 
The object `.Random.seed` is only looked for in the user’s workspace. Do not rely on randomness of low-order bits from RNGs. Most of the supplied uniform generators return 32-bit integer values that are converted to doubles, so they take at most \(2^{32}\) distinct values and long runs will return duplicated values (Wichmann-Hill is the exception, and all give at least 30 varying bits.)

**Author(s)**


**References**


The TestU01 C library is available from http://simul.iro.umontreal.ca/testu01/tu01.html or also https://github.com/umontreal-simul/TestU01-2009.


See Also

sample for random sampling with and without replacement.

Distributions for functions for random-variate generation from standard distributions.

Examples

```r
require(stats)

## Seed the current RNG, i.e., set the RNG status
set.seed(42); u1 <- runif(30)
set.seed(42); u2 <- runif(30) # the same because of identical RNG status:
stopifnot(identical(u1, u2))

## the default random seed is 626 integers, so only print a few
runif(1); .Random.seed[1:6]; runif(1); .Random.seed[1:6]
## If there is no seed, a "random" new one is created:
rm(.Random.seed); runif(1); .Random.seed[1:6]

ok <- RNGkind()
RNGkind("Wich") # (partial string matching on 'kind')

## This shows how 'runif(.)' works for Wichmann-Hill,
## using only R functions:

p.WH <- c(30269, 30307, 30323)
a.WH <- c( 171, 172, 170)
next.WHseed <- function(i.seed = .Random.seed[-1]){
  (a.WH * i.seed) %% p.WH }
my.runif1 <- function(i.seed = .Random.seed)
  { ns <- next.WHseed(i.seed[-1]); sum(ns / p.WH) %% 1 }
set.seed(1998-12-04)# (when the next lines were added to the souRce)
rs <- .Random.seed
(WHs <- next.WHseed(rs[-1]))
u <- runif(1)
stopifnot(
  next.WHseed(rs[-1]) == .Random.seed[-1],
  all.equal(u, my.runif1(rs))
)

## ----
.Random.seed
RNGkind("Super") # matches "Super-Duper"
RNGkind()
.Random.seed # new, corresponding to Super-Duper

## Reset:
RNGkind(ok[1])

RNGversion(getRversion()) # the default version for this R version

## ----
sum(duplicated(runif(1e6))) # around 110 for default generator
## and we would expect about almost sure duplicates beyond about
qbirthday(1 - 1e-6, classes = 2e9) # 235,000
```
Description

Function **RNGkind** allows user-coded uniform and normal random number generators to be supplied. The details are given here.

Details

A user-specified uniform RNG is called from entry points in dynamically-loaded compiled code. The user must supply the entry point **user_unif_rand**, which takes no arguments and returns a pointer to a double. The example below will show the general pattern. The generator should have at least 25 bits of precision.

Optionally, the user can supply the entry point **user_unif_init**, which is called with an unsigned int argument when **RNGkind** (or **set.seed**) is called, and is intended to be used to initialize the user’s RNG code. The argument is intended to be used to set the ‘seeds’; it is the seed argument to **set.seed** or an essentially random seed if **RNGkind** is called.

If only these functions are supplied, no information about the generator’s state is recorded in .Random.seed. Optionally, functions **user_unif_nseed** and **user_unif_seedloc** can be supplied which are called with no arguments and should return pointers to the number of seeds and to an integer (specifically, ‘Int32’) array of seeds. Calls to **GetRNGstate** and **PutRNGstate** will then copy this array to and from .Random.seed.

A user-specified normal RNG is specified by a single entry point **user_norm_rand**, which takes no arguments and returns a pointer to a double.

Warning

As with all compiled code, mis-specifying these functions can crash R. Do include the ‘R_ext/Random.h’ header file for type checking.

Examples

```c
#include <R_ext/Random.h>

static Int32 seed;
static double res;
static int nseed = 1;

double * user_unif_rand(void)
{
    seed = 69069 * seed + 1;
    res = seed * 2.32830643653869e-10;
    return &res;
}

void user_unif_init(Int32 seed_in) { seed = seed_in; }
int * user_unif_nseed(void) { return &nseed; }
int * user_unif_seedloc(void) { return (int *) &seed; }
```
/* ratio-of-uniforms for normal */
#include <math.h>
static double x;

double * user_norm_rand(void)
{
    double u, v, z;
    do {
        u = unif_rand();
        v = 0.857764 * (2. * unif_rand() - 1);
        x = v/u; z = 0.25 * x * x;
        if (z < 1. - u) break;
        if (z > 0.259/u + 0.35) continue;
    } while (z > -log(u));
    return &x;
}

## Use under Unix:
R CMD SHLIB urand.c
R
> dyn.load("urand.so")
> RNGkind("user")
> runif(10)
> .Random.seed
> RNGkind(), "user")
> rnorm(10)
> RNGkind()
[1] "user-supplied" "user-supplied"

## End(Not run)

---

### range

**Range of Values**

range returns a vector containing the minimum and maximum of all the given arguments.

**Usage**

range(..., na.rm = FALSE)

#### Default S3 method:
range(..., na.rm = FALSE, finite = FALSE)

**Arguments**

... any numeric or character objects.

na.rm logical, indicating if NA’s should be omitted.

finite logical, indicating if all non-finite elements should be omitted.
Details

range is a generic function: methods can be defined for it directly or via the Summary group generic. For this to work properly, the arguments . . . should be unnamed, and dispatch is on the first argument.

If na.rm is FALSE, NA and NaN values in any of the arguments will cause NA values to be returned, otherwise NA values are ignored.

If finite is TRUE, the minimum and maximum of all finite values is computed, i.e., finite = TRUE includes na.rm = TRUE.

A special situation occurs when there is no (after omission of NAs) nonempty argument left, see min.

S4 methods

This is part of the S4 Summary group generic. Methods for it must use the signature x, . . . , na.rm.

References


See Also

min, max.

The extendrange() utility in package grDevices.

Examples

(r.x <- range(stats::rnorm(100)))

diff(r.x) # the SAMPLE range

x <- c(NA, 1:3, -1:1/0); x

range(x)

range(x, na.rm = TRUE)

range(x, finite = TRUE)

---------

rank       Sample Ranks
---------

Description

Returns the sample ranks of the values in a vector. Ties (i.e., equal values) and missing values can be handled in several ways.

Usage

rank(x, na.last = TRUE,
     ties.method = c("average", "first", "last", "random", "max", "min"))
Arguments

x  a numeric, complex, character or logical vector.
na.last  a logical or character string controlling the treatment of NAs. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed; if "keep" they are kept with rank NA.
ties.method  a character string specifying how ties are treated, see ‘Details’; can be abbreviated.

Details

If all components are different (and no NAs), the ranks are well defined, with values in seq_along(x). With some values equal (called ‘ties’), the argument ties.method determines the result at the corresponding indices. The "first" method results in a permutation with increasing values at each index set of ties, and analogously "last" with decreasing values. The "random" method puts these in random order whereas the default, "average", replaces them by their mean, and "max" and "min" replaces them by their maximum and minimum respectively, the latter being the typical sports ranking.

NA values are never considered to be equal: for na.last = TRUE and na.last = FALSE they are given distinct ranks in the order in which they occur in x.

NB: rank is not itself generic but xtfrm is, and rank(xtfrm(x), ...) will have the desired result if there is a xtfrm method. Otherwise, rank will make use of ==, >, is.na and extraction methods for classed objects, possibly rather slowly.

Value

A numeric vector of the same length as x with names copied from x (unless na.last = NA, when missing values are removed). The vector is of integer type unless x is a long vector or ties.method = "average" when it is of double type (whether or not there are any ties).

References


See Also

order and sort: xtfrm, see above.

Examples

(r1 <- rank(x1 <- c(3, 1, 4, 15, 92)))
x2 <- c(3, 1, 4, 1, 5, 9, 2, 6, 5, 3, 5)
names(x2) <- letters[1:11]
(r2 <- rank(x2))  # ties are averaged

## rank() is "idempotent": rank(rank(x)) == rank(x):
stopifnot(rank(r1) == r1, rank(r2) == r2)

## ranks without averaging
rank(x2, ties.method= "first")  # first occurrence wins
rank(x2, ties.method= "last")   # last occurrence wins
rank(x2, ties.method= "random") # ties broken at random
rank(x2, ties.method= "random") # and again
## keep ties ties, no average
(rma <- rank(x2, ties.method= "max")) # as used classically
(rmi <- rank(x2, ties.method= "min")) # as in Sports
stopifnot(rma + rmi == round(r2 + r2))

## Comparing all tie.methods:
tMeth <- eval(formals(rank)$ties.method)
rx2 <- sapply(tMeth, function(M) rank(x2, ties.method=M))
cbind(x2, rx2)

## ties.method's does not matter w/o ties:
x <- sample(47)
rx <- sapply(tMeth, function(MM) rank(x, ties.method=MM))
stopifnot(all(rx[,1] == rx))

---

### rapport

**Recursively Apply a Function to a List**

#### Description

rapport is a recursive version of *lapply* with flexibility in how the result is structured (how = "..”).

#### Usage

`rapport(object, f, classes = "ANY", deflt = NULL, how = c("unlist", "replace", "list"), ...)`

#### Arguments

- **object**: a list or expression, i.e., “list-like”.
- **f**: a function of one “principal” argument, passing further arguments via ....
- **classes**: character vector of class names, or "ANY" to match any class.
- **deflt**: The default result (not used if how = "replace").
- **how**: character string partially matching the three possibilities given: see ‘Details’.
- **...**: additional arguments passed to the call to f.

#### Details

This function has two basic modes. If how = "replace", each element of object which is not itself list-like and has a class included in classes is replaced by the result of applying f to the element. Otherwise, with mode how = "list" or how = "unlist", conceptually object is copied, all non-list elements which have a class included in classes are replaced by the result of applying f to the element and all others are replaced by deflt. Finally, if how = "unlist", unlist(recursive = TRUE) is called on the result.

The semantics differ in detail from *lapply*: in particular the arguments are evaluated before calling the C code.

In R 3.5.x and earlier, object was required to be a list, which was not the case for its list-like components.
Value

If how = "unlist", a vector, otherwise “list-like” of similar structure as object.

References

(rapply is only described briefly there.)

See Also

lapply, dendrapply.

Examples

X <- list(list(a = pi, b = list(c = 1L)), d = "a test")
# the "identity operation":
rapply(X, function(x) x, how = "replace") -> X.; stopifnot(identical(X, X.))
rapply(X, sqrt, classes = "numeric", how = "replace")
rapply(X, deparse, control = "all") # passing extras. argument of deparse()
rapply(X, nchar, classes = "character", deflt = NA_integer_, how = "list")
rapply(X, nchar, classes = "character", deflt = NA_integer_, how = "unlist")
rapply(X, log, classes = "numeric", how = "unlist")

## with expression() / list():
E <- expression(list(a = pi, b = expression(c = C1 * C2)), d = "a test")
LE <- list(expression(a = pi, b = expression(c = C1 * C2)), d = "a test")
rapply(E, nchar, how="replace") # "expression(c = C1 * C2)" are 23 chars
rapply(E, nchar, classes = "character", deflt = NA_integer_, how = "unlist")
rapply(LE, as.character) # a "pi" | b1 "expression" | b2 "C1 * C2" ..
rapply(LE, nchar) # (see above)
stopifnot(exprs = {
  identical(E , rapply(E , identity, how = "replace"))
  identical(LE, rapply(LE, identity, how = "replace"))
})

Description

Creates or tests for objects of type "raw".

Usage

raw(length = 0)
as.raw(x)
is.raw(x)

Arguments

length desired length.

x object to be coerced.
Details

The raw type is intended to hold raw bytes. It is possible to extract subsequences of bytes, and to replace elements (but only by elements of a raw vector). The relational operators (see Comparison, using the numerical order of the byte representation) work, as do the logical operators (see Logic) with a bitwise interpretation.

A raw vector is printed with each byte separately represented as a pair of hex digits. If you want to see a character representation (with escape sequences for non-printing characters) use rawToChar.

Coercion to raw treats the input values as representing small (decimal) integers, so the input is first coerced to integer, and then values which are outside the range [0 . . . 255] or are NA are set to 0 (the nul byte).

as.raw and is.raw are primitive functions.

Value

raw creates a raw vector of the specified length. Each element of the vector is equal to 0. Raw vectors are used to store fixed-length sequences of bytes.

as.raw attempts to coerce its argument to be of raw type. The (elementwise) answer will be 0 unless the coercion succeeds (or if the original value successfully coerces to 0).

is.raw returns true if and only if typeof(x) == "raw".

See Also

charToRaw, rawShift, etc.

& for bitwise operations on raw vectors.

Examples

xx <- raw(2)
xx[1] <- as.raw(40) # NB, not just 40.
xx[2] <- charToRaw("A")
xx ## 28 41 -- raw prints hexadecimals
dput(xx) ## as.raw(c(0x28, 0x41))
as.integer(xx) ## 40 65

x <- "A test string"
y <- charToRaw(x))
is.vector(y) # TRUE
rawToChar(y)
is.raw(x)
is.raw(y)
isnot( charToRaw("\xa3") == as.raw(0xa3) )

isASCII <- function(txt) all(charToRaw(txt) <= as.raw(127))
isASCII(x) # true
isASCII("\xa325.63") # false (in Latin-1, this is an amount in UK pounds)
**rawConnection**

*Raw Connections*

**Description**

Input and output raw connections.

**Usage**

```r
rawConnection(object, open = "r")
```

```r
rawConnectionValue(con)
```

**Arguments**

- **object**: character or raw vector. A description of the connection. For an input this is an R raw vector object, and for an output connection the name for the connection.
- **open**: character. Any of the standard connection open modes.
- **con**: An output raw connection.

**Details**

An input raw connection is opened and the raw vector is copied at the time the connection object is created, and `close` destroys the copy.

An output raw connection is opened and creates an R raw vector internally. The raw vector can be retrieved via `rawConnectionValue`.

If a connection is open for both input and output the initial raw vector supplied is copied when the connections is open.

**Value**

For `rawConnection`, a connection object of class "rawConnection" which inherits from class "connection".

For `rawConnectionValue`, a raw vector.

**Note**

As output raw connections keep the internal raw vector up to date call-by-call, they are relatively expensive to use (although over-allocation is used), and it may be better to use an anonymous `file()` connection to collect output.

On (rare) platforms where `vsnprintf` does not return the needed length of output there is a 100,000 character limit on the length of line for output connections: longer lines will be truncated with a warning.

**See Also**

`connections`, `showConnections`.
Examples

```
zz <- rawConnection(raw(0), "r")  # start with empty raw vector
writeBin(LETTERS, zz)
seek(zz, 0)
readLines(zz)  # raw vector has embedded nuls
seek(zz, 0)
writeBin(letters[1:3], zz)
rawConnectionValue(zz)
close(zz)
```

---

**rawConversion**

*Convert to or from (Bit/Packed) Raw Vectors*

**Description**

Conversion to and from and manipulation of objects of type "raw", both used as bits or "packed" 8 bits.

**Usage**

```
charToRaw(x)
rawToChar(x, multiple = FALSE)
rawShift(x, n)
rawToBits(x)
intToBits(x)
packBits(x, type = c("raw", "integer", "double"))
numToInts(x)
numToBits(x)
```

**Arguments**

- `x` object to be converted or shifted.
- `multiple` logical: should the conversion be to a single character string or multiple individual characters?
- `n` the number of bits to shift. Positive numbers shift right and negative numbers shift left: allowed values are -8 ... 8.
- `type` the result type, partially matched.

**Details**

- `packBits` accepts raw, integer or logical inputs, the last two without any NAs.
- `numToBits(.)` and `packBits(. , type="double")` are *inverse* functions of each other, see also the examples.
- Note that ‘bytes’ are not necessarily the same as characters, e.g. in UTF-8 locales.
Value

charToRaw converts a length-one character string to raw bytes. It does so without taking into account any declared encoding (see Encoding).

rawToChar converts raw bytes either to a single character string or a character vector of single bytes (with "\n" for \0). (Note that a single character string could contain embedded nuls; only trailing nulls are allowed and will be removed.) In either case it is possible to create a result which is invalid in a multibyte locale, e.g. one using UTF-8. Long vectors are allowed if multiple is true.

rawShift(x, n) shift the bits in x by n positions to the right, see the argument n, above.

rawToBits returns a raw vector of 8 times the length of a raw vector with entries 0 or 1. intToBits returns a raw vector of 32 times the length of an integer vector with entries 0 or 1. (Non-integral numeric values are truncated to integers.) In both cases the unpacking is least-significant bit first.

packBits packs its input (using only the lowest bit for raw or integer vectors) least-significant bit first to a raw, integer or double ("numeric") vector.

numToInts() and numToBits() split double precision numeric vectors either into to two integers each or into 64 bits each, stored as raw. In both cases the unpacking is least-significant element first.

Examples

```
x <- "A test string"
y <- charToRaw(x)
is.vector(y) # TRUE

rawToChar(y)
rawToChar(y, multiple = TRUE)
(xx <- c(y, charToRaw("&"), charToRaw(" more")))
rawToChar(xx)

rawShift(y, 1)
rawShift(y,-2)

rawToBits(y)

showBits <- function(r) stats::symnum(as.logical(rawToBits(r)))

z <- as.raw(5)
z ; showBits(z)
showBits(rawShift(z, 1)) # shift to right
showBits(rawShift(z, 2))
showBits(z)
showBits(rawShift(z, -1)) # shift to left
showBits(rawShift(z, -2)) # .
showBits(rawShift(z, -3)) # shifted off entirely

packBits(as.raw(0:31))
i <- -2:3
stopifnot(exprs = {
    identical(i, packBits(intToBits(i), "integer"))
    identical(packBits( 0:31) ,
               packBits(as.raw(0:31)))
})

str(pBi <- packBits(intToBits(i)))
data.frame(B = matrix(pBi, nrow=6, byrow=TRUE),
          hex = format(as.hexmode(i)), i
```
## Look at internal bit representation of ...

```r
bitI <- function(x) vapply(as.integer(x), function(x) {
  b <- substr(as.character(rev(intToBits(x))), 2L, 2L)
  paste0(c(b[1L], " ", b[2:32]), collapse = "")
}, "")
print(bitI(-8:8), width = 35, quote = FALSE)
```

## ... of double precision numbers in format 'sign exp | mantissa'
where 1 bit sign 1 <==> "-";
11 bit exp is the base-2 exponent biased by $2^{10} - 1$ (1023)
52 bit mantissa is without the implicit leading '1'

```r
bitC <- function(x) noquote(vapply(as.double(x), function(x) {
  # split one double
  b <- substr(as.character(rev(numToBits(x))), 2L, 2L)
  paste0(c(b[1L], " ", b[2:12], " | ", b[13:64]), collapse = "")
}, ""))
bitC(17)
bitC(c(-1,0,1))
bitC(2^(-2:5))
bitC(1+2^(-1:53)) # from 0.5 converge to 1
```

```r
d2bI <- function(x) vapply(as.double(x), function(x) intToBits(numToInts(x)), raw(64L))
d2b <- function(x) vapply(as.double(x), function(x) numToBits(x) , raw(64L))
set.seed(1)
x <- c(sort(rt(2048, df=1.5)), 2^(-10:10), 1+2^(-1:53))
str(bx <- d2b(x)) # a 64 x 2122 raw matrix
stopifnot( identical(bx, d2bI(x)) )
```

```r
packBits(numToBits(pi), type="double")
```

```r
pbx <- apply(bx, 2, packBits, type="double")
```

```r
stopifnot( identical(pbx, x))
```

---

### Utilities for Processing Rd Files

#### Description

Utilities for converting files in R documentation (Rd) format to other formats or create indices from them, and for converting documentation in other formats to Rd format.

#### Usage

```
R CMD Rdconv [options] file
R CMD Rd2pdf [options] files
```
**readBin**

**Arguments**
- **file**
  - the path to a file to be processed.
- **files**
  - a list of file names specifying the R documentation sources to use, by either giving the paths to the files, or the path to a directory with the sources of a package.
- **options**
  - further options to control the processing, or for obtaining information about usage and version of the utility.

**Details**

`R CMD Rdconv` converts Rd format to plain text, HTML or LaTeX formats: it can also extract the examples.

`R CMD Rd2pdf` is the user-level program for producing PDF output from Rd sources. It will make use of the environment variables `R_PAPERSIZE` (set by `R CMD`, with a default set when `R` was installed: values for `R_PAPERSIZE` are `a4`, `letter`, `legal` and `executive`) and `R_PDFVIEWER` (the PDF pre-viewer). Also, `Rd2pdf_INPUTENC` can be set to `inputenx` to make use of the LaTeX package of that name rather than `inputenc`; this might be needed for better support of the UTF-8 encoding.

`R CMD Rd2pdf` calls `tools::texi2pdf` to produce its PDF file: see its help for the possibilities for the `texi2dvi` command which that function uses (and which can be overridden by setting environment variable `R_TEXI2DVICMD`).

Use `R CMD foo --help` to obtain usage information on utility `foo`.

**See Also**
The chapter ‘Processing Rd format’ in the ‘Writing R Extensions’ manual.

---

**readBin**  
*Transfer Binary Data To and From Connections*

**Description**

Read binary data from or write binary data to a connection or raw vector.

**Usage**

```r
readBin(con, what, n = 1L, size = NA_integer_, signed = TRUE, endian = .Platform$endian)
writeBin(object, con, size = NA_integer_, endian = .Platform$endian, useBytes = FALSE)
```

**Arguments**

- **con**  
  - A connection object or a character string naming a file or a raw vector.
- **what**  
  - Either an object whose mode will give the mode of the vector to be read, or a character vector of length one describing the mode: one of "numeric", "double", "integer", "int", "logical", "complex", "character", "raw".
- **n**  
  - numeric. The (maximal) number of records to be read. You can use an over-estimate here, but not too large as storage is reserved for `n` items.
size integer. The number of bytes per element in the byte stream. The default, NA_integer_, uses the natural size. Size changing is not supported for raw and complex vectors.

signed logical. Only used for integers of sizes 1 and 2, when it determines if the quantity on file should be regarded as a signed or unsigned integer.

 endian The endian-ness ("big" or "little") of the target system for the file. Using "swap" will force swapping endian-ness.

object An R object to be written to the connection.

useBytes See writeLines.

Details

These functions can only be used with binary-mode connections. If con is a character string, the functions call file to obtain a binary-mode file connection which is opened for the duration of the function call.

If the connection is open it is read/written from its current position. If it is not open, it is opened for the duration of the call in an appropriate mode (binary read or write) and then closed again. An open connection must be in binary mode.

If readBin is called with con a raw vector, the data in the vector is used as input. If writeBin is called with con a raw vector, it is just an indication that a raw vector should be returned.

If size is specified and not the natural size of the object, each element of the vector is coerced to an appropriate type before being written or as it is read. Possible sizes are 1, 2, 4 and possibly 8 for integer or logical vectors, and 4, 8 and possibly 12/16 for numeric vectors. (Note that coercion occurs as signed types except if signed = FALSE when reading integers of sizes 1 and 2.) Changing sizes is unlikely to preserve NA_s, and the extended precision sizes are unlikely to be portable across platforms.

readBin and writeBin read and write C-style zero-terminated character strings. Input strings are limited to 10000 characters. readChar and writeChar can be used to read and write fixed-length strings. No check is made that the string is valid in the current locale’s encoding.

Handling R’s missing and special (Inf, -Inf and NaN) values is discussed in the ‘R Data Import/Export’ manual.

Only $2^{31} - 1$ bytes can be written in a single call (and that is the maximum capacity of a raw vector on 32-bit platforms).

‘Endian-ness’ is relevant for size > 1, and should always be set for portable code (the default is only appropriate when writing and then reading files on the same platform).

Value

For readBin, a vector of appropriate mode and length the number of items read (which might be less than n).

For writeBin, a raw vector (if con is a raw vector) or invisibly NULL.

Note

Integer read/writes of size 8 will be available if either C type long is of size 8 bytes or C type long long exists and is of size 8 bytes.

Real read/writes of size sizeof(long double) (usually 12 or 16 bytes) will be available only if that type is available and different from double.
readBin

If `readBin(what = character())` is used incorrectly on a file which does not contain C-style character strings, warnings (usually many) are given. From a file or connection, the input will be broken into pieces of length 10000 with any final part being discarded.

See Also

The ‘R Data Import/Export’ manual.

`readChar` to read/write fixed-length strings.

`connections`, `readLines`, `writeLines`.

`.Machine` for the sizes of long, long long and long double.

Examples

```R
zzfil <- tempfile("testbin")
zz <- file(zzfil, "wb")
writeBin(1:10, zz)
writeBin(pi, zz, endian = "swap")
writeBin(pi^2, zz, size = 4, endian = "swap")
writeBin(pi+3i, zz)
writeBin("A test of a connection", zz)
z <- paste("A very long string", 1:100, collapse = " + ")
writeBin(z, zz)
if(.Machine$sizeof.long == 8 || .Machine$sizeof.longlong == 8)
  writeBin(as.integer(5^(1:10)), zz, size = 8)
if((s <- .Machine$sizeof.longdouble) > 8)
  writeBin((pi/3)^(1:10), zz, size = s)
close(zz)

zz <- file(zzfil, "rb")
readBin(zz, integer(), 4)
readBin(zz, integer(), 6)
readBin(zz, numeric(), 1, endian = "swap")
readBin(zz, numeric(), size = 4)
readBin(zz, character(), 1)
z2 <- readBin(zz, character(), 1)
if(.Machine$sizeof.long == 8 || .Machine$sizeof.longlong == 8)
  readBin(zz, integer(), 10, size = 8)
if((s <- .Machine$sizeof.longdouble) > 8)
  readBin(zz, numeric(), 10, size = s)
close(zz)
unlink(zzfil)
stopifnot(z2 == z)
```

## signed vs unsigned ints

```R
zzfil <- tempfile("testbin")
zz <- file(zzfil, "wb")
x <- as.integer(seq(0, 255, 32))
writeBin(x, zz, size = 1)
writeBin(x, zz, size = 1)
x <- as.integer(seq(0, 60000, 10000))
writeBin(x, zz, size = 2)
writeBin(x, zz, size = 2)
close(zz)
```
zz <- file(zzfil, "rb")
readBin(zz, integer(), 8, size = 1)
readBin(zz, integer(), 8, size = 1, signed = FALSE)
readBin(zz, integer(), 7, size = 2)
readBin(zz, integer(), 7, size = 2, signed = FALSE)
close(zz)
unlink(zzfil)

## use of raw
z <- writeBin(pi^{1:5}, raw(), size = 4)
readBin(z, numeric(), 5, size = 4)
z <- writeBin(c("a", "test", "of", "character"), raw())
readBin(z, character(), 4)

---

**readChar**  
Transfer Character Strings To and From Connections

**Description**
Transfer character strings to and from connections, without assuming they are null-terminated on the connection.

**Usage**

```r
readChar(con, nchars, useBytes = FALSE)
writeChar(object, con, nchars = nchar(object, type = "chars"),
          eos = "", useBytes = FALSE)
```

**Arguments**

- `con` A connection object, or a character string naming a file, or a raw vector.
- `nchars` integer vector, giving the lengths in characters of (unterminated) character strings to be read or written. Elements must be >= 0 and not NA.
- `useBytes` logical: For readChar, should nchars be regarded as a number of bytes not characters in a multi-byte locale? For writeChar, see `writeLines`.
- `object` A character vector to be written to the connection, at least as long as nchars.
- `eos` "end of string": character string. The terminator to be written after each string, followed by an ASCII nul; use NULL for no terminator at all.

**Details**
These functions complement `readBin` and `writeBin` which read and write C-style zero-terminated character strings. They are for strings of known length, and can optionally write an end-of-string mark. They are intended only for character strings valid in the current locale.

These functions are intended to be used with binary-mode connections. If `con` is a character string, the functions call `file` to obtain a binary-mode file connection which is opened for the duration of the function call.

If the connection is open it is read/written from its current position. If it is not open, it is opened for the duration of the call in an appropriate mode (binary read or write) and then closed again. An open connection must be in binary mode.
readChar

If `readChar` is called with `con` a raw vector, the data in the vector is used as input. If `writeChar` is called with `con` a raw vector, it is just an indication that a raw vector should be returned.

Character strings containing ASCII `nul` will be read correctly by `readChar` but truncated at the first `nul` with a warning.

If the character length requested for `readChar` is longer than the data available on the connection, what is available is returned. For `writeChar` if too many characters are requested the output is zero-padded, with a warning.

Missing strings are written as `NA`.

Value

For `readChar`, a character vector of length the number of items read (which might be less than `length(nchars)`).

For `writeChar`, a raw vector (if `con` is a raw vector) or invisibly `NULL`.

Note

Earlier versions of R allowed embedded nul bytes within character strings, but not R >= 2.8.0. `readChar` was commonly used to read fixed-size zero-padded byte fields for which `readBin` was unsuitable. `readChar` can still be used for such fields if there are no embedded nulls: otherwise `readBin(what = "raw")` provides an alternative.

`nchars` will be interpreted in bytes not characters in a non-UTF-8 multi-byte locale, with a warning.

There is little validity checking of UTF-8 reads.

Using these functions on a text-mode connection may work but should not be mixed with text-mode access to the connection, especially if the connection was opened with an encoding argument.

See Also

The ‘R Data Import/Export’ manual.

`connections, readLines, writeLines, readBin`

Examples

```r
## test fixed-length strings
zzfil <- tempfile("testchar")
zz <- file(zzfil, "wb")
x <- c("a", "this will be truncated", "abc")
nc <- c(3, 10, 3)
writeChar(x, zz, nc, eos = NULL)
writeChar(x, zz, eos = \"\r\n\")
close(zz)

zz <- file(zzfil, "rb")
readChar(zz, nc)
readChar(zz, nchar(x)+3) # need to read the terminator explicitly
close(zz)
unlink(zzfil)
```
**Description**

`readline` reads a line from the terminal (in interactive use).

**Usage**

```r
readline(prompt = "")
```

**Arguments**

- `prompt` the string printed when prompting the user for input. Should usually end with a space " ".

**Details**

The prompt string will be truncated to a maximum allowed length, normally 256 chars (but can be changed in the source code).

This can only be used in an interactive session.

**Value**

A character vector of length one. Both leading and trailing spaces and tabs are stripped from the result.

In non-interactive use the result is as if the response was RETURN and the value is " ".

**See Also**

`readLines` for reading text lines from connections, including files.

**Examples**

```r
fun <- function() {
  ANSWER <- readline("Are you a satisfied R user? ")
  ## a better version would check the answer less cursorily, and
  ## perhaps re-prompt
  if (substr(ANSWER, 1, 1) == "n")
    cat("This is impossible. YOU LIED!
"
  else
    cat("I knew it.
"
}
if(interactive()) fun()
```
readLines

**Description**

Read some or all text lines from a connection.

**Usage**

```r
readLines(con = stdin(), n = -1L, ok = TRUE, warn = TRUE,
           encoding = "unknown", skipNul = FALSE)
```

**Arguments**

- `con`: a connection object or a character string.
- `n`: integer. The (maximal) number of lines to read. Negative values indicate that one should read up to the end of input on the connection.
- `ok`: logical. Is it OK to reach the end of the connection before `n > 0` lines are read? If not, an error will be generated.
- `warn`: logical. Warn if a text file is missing a final EOL or if there are embedded nuls in the file.
- `encoding`: encoding to be assumed for input strings. It is used to mark character strings as known to be in Latin-1, UTF-8 or to be bytes: it is not used to re-encode the input. To do the latter, specify the encoding as part of the connection `con` or via `options(encoding=)`: see the examples and 'Details'.
- `skipNul`: logical: should nuls be skipped?

**Details**

If the `con` is a character string, the function calls `file` to obtain a file connection which is opened for the duration of the function call. This can be a compressed file. (tilde expansion of the file path is done by `file`.)

If the connection is open it is read from its current position. If it is not open, it is opened in "rt" mode for the duration of the call and then closed (but not destroyed; one must call `close` to do that).

If the final line is incomplete (no final EOL marker) the behaviour depends on whether the connection is blocking or not. For a non-blocking text-mode connection the incomplete line is pushed back, silently. For all other connections the line will be accepted, with a warning. Whatever mode the connection is opened in, any of LF, CRLF or CR will be accepted as the EOL marker for a line.

Embedded nuls in the input stream will terminate the line currently being read, with a warning (unless `skipNul = TRUE` or `warn = FALSE`).

If `con` is a not-already-open `connection` with a non-default encoding argument, the text is converted to UTF-8 and declared as such (and the encoding argument to `readLines` is ignored). See the examples.

**Value**

A character vector of length the number of lines read.

The elements of the result have a declared encoding if `encoding` is "latin1" or "UTF-8".
Note

The default connection, stdin, may be different from con = "stdin": see file.

See Also

connections, writeLines, readBin, scan

Examples

```r
fil <- tempfile(fileext = ".data")
cat("TITLE extra line", "2 3 5 7", ",", "11 13 17", file = fil,
    sep = "\n")
readlines(fil, n = -1)
unlink(fil) # tidy up

## difference in blocking
fil <- tempfile("test")
cat("123\nabc", file = fil)
readlines(fil) # line with a warning

con <- file(fil, "r", blocking = FALSE)
readlines(con) # "123"
cat(" def\n", file = fil, append = TRUE)
readlines(con) # gets both
close(con)

unlink(fil) # tidy up

## Not run:
# read a 'Windows Unicode' file
A <- readLines(con <- file("Unicode.txt", encoding = "UCS-2LE"))
close()
unique(Encoding(A)) # will most likely be UTF-8

## End(Not run)
```

readRDS

Serialization Interface for Single Objects

Description

Functions to write a single R object to a file, and to restore it.

Usage

```r
saveRDS(object, file = "", ascii = FALSE, version = NULL,
    compress = TRUE, refhook = NULL)
readRDS(file, refhook = NULL)
infoRDS(file)
```
Arguments

object \( \mathbb{R} \) object to serialize.

file a connection or the name of the file where the \( \mathbb{R} \) object is saved to or read from.

ascii a logical. If TRUE or NA, an ASCII representation is written; otherwise (default), a binary one is used. See the comments in the help for \texttt{save}.

version the workspace format version to use. NULL specifies the current default version (3). The only other supported value is 2, the default from \texttt{R 1.4.0} to \texttt{R 3.5.0}.

compress a logical specifying whether saving to a named file is to use "gzip" compression, or one of "gzip", "bzip2" or "xz" to indicate the type of compression to be used. Ignored if \texttt{file} is a connection.

refhook a hook function for handling reference objects.

Details

\texttt{saveRDS} and \texttt{readRDS} provide the means to save a single \( \mathbb{R} \) object to a connection (typically a file) and to restore the object, quite possibly under a different name. This differs from \texttt{save} and \texttt{load}, which save and restore one or more named objects into an environment. They are widely used by \texttt{R} itself, for example to store metadata for a package and to store the \texttt{help.search} databases: the ".rds" file extension is most often used.

Functions \texttt{serialize} and \texttt{unserialize} provide a slightly lower-level interface to serialization: objects serialized to a connection by \texttt{serialize} can be read back by \texttt{readRDS} and conversely.

Function \texttt{infoRDS} retrieves meta-data about serialization produced by \texttt{saveRDS} or \texttt{serialize}. \texttt{infoRDS} cannot be used to detect whether a file is a serialization nor whether it is valid.

All of these interfaces use the same serialization format, but \texttt{save} writes a single line header (typically "RDXs\n") before the serialization of a single object (a pairlist of all the objects to be saved).

If \texttt{file} is a file name, it is opened by \texttt{gzfile} except for \texttt{save(compress = FALSE)} which uses \texttt{file}. Only for the exception are marked encodings of \texttt{file} which cannot be translated to the native encoding handled on Windows.

Compression is handled by the connection opened when \texttt{file} is a file name, so is only possible when \texttt{file} is a connection if handled by the connection. So e.g. \texttt{url} connections will need to be wrapped in a call to \texttt{gzcon}.

If a connection is supplied it will be opened (in binary mode) for the duration of the function if not already open: if it is already open it must be in binary mode for \texttt{saveRDS(ascii = FALSE)} or to read non-ASCII saves.

Value

For \texttt{readRDS}, an \( \mathbb{R} \) object.

For \texttt{saveRDS}, NULL invisibly.

For \texttt{infoRDS}, an \( \mathbb{R} \) list with elements \texttt{version} (version number, currently 2 or 3), \texttt{writer_version} (version of \( \mathbb{R} \) that produced the serialization), \texttt{min_reader_version} (minimum version of \( \mathbb{R} \) that can read the serialization), \texttt{format} (data representation) and \texttt{native_encoding} (native encoding of the session that produced the serialization, available since version 3). The data representation is given as "xdr" for big-endian binary representation, "ascii" for ASCII representation (produced via ascii = TRUE or ascii = NA) or "binary" (binary representation with native ‘endian-ness’ which can be produced by \texttt{serialize}).
Warning

Files produced by saveRDS (or serialize to a file connection) are not suitable as an interchange format between machines, for example to download from a website. The files produced by save have a header identifying the file type and so are better protected against erroneous use.

See Also

serialize, save and load.

The 'R Internals' manual for details of the format used.

Examples

```r
fil <- tempfile("women", fileext = ".rds")
## save a single object to file
saveRDS(women, fil)
## restore it under a different name
women2 <- readRDS(fil)
identical(women, women2)
## or examine the object via a connection, which will be opened as needed.
con <- gzfile(fil)
readRDS(con)
close(con)

## Less convenient ways to restore the object
## which demonstrate compatibility with unserialize()
con <- gzfile(fil, "rb")
identical(unserialize(con), women)
close(con)
con <- gzfile(fil, "rb")
wm <- readBin(con, "raw", n = 1e4) # size is a guess
close(con)
identical(unserialize(wm), women)

## Format compatibility with serialize():
fil2 <- tempfile("women")
con <- file(fil2, "w")
serialize(women, con) # ASCII, uncompressed
close(con)
identical(women, readRDS(fil2))
fil3 <- tempfile("women")
con <- bzfile(fil3, "w")
serialize(women, con) # binary, bzip2-compressed
close(con)
identical(women, readRDS(fil3))

unlink(c(fil, fil2, fil3))
```

readRenviron

Set Environment Variables from a File

Description

Read as file such as ‘.Renviron’ or ‘Renviron.site’ in the format described in the help for Startup, and set environment variables as defined in the file.
Recall

Usage

readRenviron(path)

Arguments

path A length-one character vector giving the path to the file. Tilde-expansion is performed where supported.

Value

Scalar logical indicating if the file was read successfully. Returned invisibly. If the file cannot be opened for reading, a warning is given.

See Also

Startup for the file format.

Examples

## Not run:
## re-read a startup file (or read it in a vanilla session)
readRenviron("~/.Renviron")

## End(Not run)

Recall

Recursive Calling

Description

Recall is used as a placeholder for the name of the function in which it is called. It allows the definition of recursive functions which still work after being renamed, see example below.

Usage

Recall(...) 

Arguments

... all the arguments to be passed.

Note

Recall will not work correctly when passed as a function argument, e.g. to the apply family of functions.

See Also

do.call and call.
local for another way to write anonymous recursive functions.
Examples

```r
data <- function(n)
  if(n<=2) { if(n>=0) 1 else 0 } else Recall(n-1) + Recall(n-2)
data <- function(n)
## renaming wouldn't work without Recall
fibo(10) # 55
```

reg.finalizer

Finalization of Objects

Description

Registers an R function to be called upon garbage collection of object or (optionally) at the end of an R session.

Usage

```r
reg.finalizer(e, f, onexit = FALSE)
```

Arguments

- `e`: Object to finalize. Must be an environment or an external pointer.
- `f`: Function to call on finalization. Must accept a single argument, which will be the object to finalize.
- `onexit`: logical: should the finalizer be run if the object is still uncollected at the end of the R session?

Details

The main purpose of this function is to allow objects that refer to external items (a temporary file, say) to perform cleanup actions when they are no longer referenced from within R. This only makes sense for objects that are never copied on assignment, hence the restriction to environments and external pointers. *Inter alia*, it provides a way to program code to be run at the end of an R session without manipulating `.Last`. For use in a package, it is often a good idea to set a finalizer on an object in the namespace: then it will be called at the end of the session, or soon after the namespace is unloaded if that is done during the session.

Value

NULL.

Note

R's interpreter is not re-entrant and the finalizer could be run in the middle of a computation. So there are many functions which it is potentially unsafe to call from `f`: one example which caused trouble is `options`. Finalizers are scheduled at garbage collection but only run at a relatively safe time thereafter.
See Also
gc and Memory for garbage collection and memory management.

Examples

f <- function(e) print("cleaning....")
g <- function(x){ e <- environment(); reg.finalizer(e, f) }
g()
invisible(gc()) # trigger cleanup

regex

Regular Expressions as used in R

Description

This help page documents the regular expression patterns supported by grep and related functions grepl, regexpr, gregexpr, sub and gsub, as well as by strsplit and optionally by agrep and agrepl.

Details

A ‘regular expression’ is a pattern that describes a set of strings. Two types of regular expressions are used in R, extended regular expressions (the default) and Perl-like regular expressions used by perl = TRUE. There is also fixed = TRUE which can be considered to use a literal regular expression.

Other functions which use regular expressions (often via the use of grep) include apropos, browseEnv, help.search, list.files and ls. These will all use extended regular expressions.

Patterns are described here as they would be printed by cat: (do remember that backslashes need to be doubled when entering R character strings, e.g. from the keyboard).

Long regular expression patterns may or may not be accepted: the POSIX standard only requires up to 256 bytes.

Extended Regular Expressions

This section covers the regular expressions allowed in the default mode of grep, grepl, regexpr, gregexpr, sub, gsub, regexec and strsplit. They use an implementation of the POSIX 1003.2 standard: that allows some scope for interpretation and the interpretations here are those currently used by R. The implementation supports some extensions to the standard.

Regular expressions are constructed analogously to arithmetic expressions, by using various operators to combine smaller expressions. The whole expression matches zero or more characters (read ‘character’ as ‘byte’ if useBytes = TRUE).

The fundamental building blocks are the regular expressions that match a single character. Most characters, including all letters and digits, are regular expressions that match themselves. Any metacharacter with special meaning may be quoted by preceding it with a backslash. The metacharacters in extended regular expressions are ‘\’, ‘\|’, ‘\(’, ‘\)’, ‘\{’, ‘\[’, ‘\^’, ‘\$', ‘\*’, ‘\+’, ‘\?’, ‘\’’, ‘\’’, ‘\$’ and ‘\?’.

Escaping non-metacharacters with a backslash is implementation-dependent. The current implementation interprets ‘\a’ as ‘BEL’, ‘\b’ as ‘ESC’, ‘\f’ as ‘FF’, ‘\n’ as ‘LF’, ‘\r’ as ‘CR’ and ‘\t’ as ‘TAB’. (Note that these will be interpreted by R’s parser in literal character strings.)
A character class is a list of characters enclosed between `['` and `']` which matches any single character in that list; unless the first character of the list is the caret `^`, when it matches any character not in the list. For example, the regular expression `['0123456789']` matches any single digit, and `['abc']` matches anything except the characters `a`, `b` or `c`. A range of characters may be specified by giving the first and last characters, separated by a hyphen. (Because their interpretation is locale- and implementation-dependent, character ranges are best avoided. Some but not all implementations include both cases in ranges when doing caseless matching.) The only portable way to specify all ASCII letters is to list them all as the character class `['ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz']`. (The current implementation uses numerical order of the encoding, normally a single-byte encoding or Unicode points.)

Certain named classes of characters are predefined. Their interpretation depends on the locale (see locales); the interpretation below is that of the POSIX locale.

`\[:alnum:\]` Alphanumeric characters: `[:alpha:]` and `[:digit:]`.

`\[:alpha:\]` Alphabetic characters: `[:lower:]` and `[:upper:]`.

`\[:blank:\]` Blank characters: space and tab, and possibly other locale-dependent characters, but on most platforms not including non-breaking space.

`\[:cntrl:\]` Control characters. In ASCII, these characters have octal codes 000 through 037, and 177 (DEL). In another character set, these are the equivalent characters, if any.

`\[:digit:\]` Digits: `0 1 2 3 4 5 6 7 8 9`.

`\[:graph:\]` Graphical characters: `[:alnum:]` and `[:punct:]`.

`\[:lower:\]` Lower-case letters in the current locale.

`\[:print:\]` Printable characters: `[:alnum:]`, `[:punct:]` and space.

`\[:punct:\]` Punctuation characters:

`\[:space:\]` Space characters: tab, newline, vertical tab, form feed, carriage return, space and possibly other locale-dependent characters – on most platforms this does not include non-breaking spaces.

`\[:upper:\]` Upper-case letters in the current locale.

`\[:xdigit:\]` Hexadecimal digits:

For example, `\[:alnum:]` means `['0-9A-Za-z]`, except the latter depends upon the locale and the character encoding, whereas the former is independent of locale and character set. (Note that the brackets in these class names are part of the symbolic names, and must be included in addition to the brackets delimiting the bracket list.) Most metacharacters lose their special meaning inside a character class. To include a literal `']`, place it first in the list. Similarly, to include a literal `'^'`, place it anywhere but first. Finally, to include a literal `'^'`, place it first or last (or, for perl = TRUE only, precede it by a backslash). (Only `'^'` and `']'` are special inside character classes.)

The period `.' matches any single character. The symbol `\^w` matches a ‘word’ character (a synonym for `\[:alnum:]`, an extension) and `\W` is its negation (`\[^\[:alnum:]\]`). Symbols `\d`, `\s`, `\D` and `\S` denote the digit and space classes and their negations (these are all extensions).

The caret `\^` and the dollar sign `\$` are metacharacters that respectively match the empty string at the beginning and end of a line. The symbols `\<` and `\>` match the empty string at the beginning and end of a word. The symbol `\b` matches the empty string at either edge of a word, and `\B` matches the empty string provided it is not at an edge of a word. (The interpretation of ‘word’ depends on the locale and implementation: these are all extensions.)

A regular expression may be followed by one of several repetition quantifiers:
‘?’ The preceding item is optional and will be matched at most once.

‘*’ The preceding item will be matched zero or more times.

‘+’ The preceding item will be matched one or more times.

‘(n)’ The preceding item is matched exactly n times.

‘{n,}’ The preceding item is matched n or more times.

‘{n,m}’ The preceding item is matched at least n times, but not more than m times.

By default repetition is greedy, so the maximal possible number of repeats is used. This can be changed to ‘minimal’ by appending ? to the quantifier. (There are further quantifiers that allow approximate matching: see the TRE documentation.)

Regular expressions may be concatenated; the resulting regular expression matches any string formed by concatenating the substrings that match the concatenated subexpressions.

Two regular expressions may be joined by the infix operator ‘|’; the resulting regular expression matches any string matching either subexpression. For example, ‘abba|cde’ matches either the string abba or the string cde. Note that alternation does not work inside character classes, where ‘|’ has its literal meaning.

Repetition takes precedence over concatenation, which in turn takes precedence over alternation. A whole subexpression may be enclosed in parentheses to override these precedence rules.

The backreference ‘\N’, where ‘N = 1 ... 9’, matches the substring previously matched by the Nth parenthesized subexpression of the regular expression. (This is an extension for extended regular expressions: POSIX defines them only for basic ones.)

Perl-like Regular Expressions

The perl = TRUE argument to grep, regexpr, gregexpr, sub, gsub and strsplit switches to the PCRE library that implements regular expression pattern matching using the same syntax and semantics as Perl 5.x, with just a few differences.

For complete details please consult the man pages for PCRE, especially man pcrepattern and man pcreapi, on your system or from the sources at https://www.pcre.org. (The version in use can be found by calling extSoftVersion. It need not be the version described in the system’s man page. PCRE1 (reported as version < 10.00 by extSoftVersion) has been feature-frozen for some time (essentially 2012), the man pages at https://www.pcre.org/original/doc/html/ should be a good match. PCRE2 (PCRE version >= 10.00) has man pages at https://www.pcre.org/current/doc/html/).

Perl regular expressions can be computed byte-by-byte or (UTF-8) character-by-character: the latter is used in all multibyte locales and if any of the inputs are marked as UTF-8 (see Encoding, or as Latin-1 except in a Latin-1 locale.

All the regular expressions described for extended regular expressions are accepted except ‘\<’ and ‘\>’: in Perl all backslashed metacharacters are alphanumeric and backslashed symbols always are interpreted as a literal character. ‘{’ is not special if it would be the start of an invalid interval specification. There can be more than 9 backreferences (but the replacement in sub can only refer to the first 9).

Character ranges are interpreted in the numerical order of the characters, either as bytes in a single-byte locale or as Unicode code points in UTF-8 mode. So in either case ‘[A-Za-z]’ specifies the set of ASCII letters.

In UTF-8 mode the named character classes only match ASCII characters: see ‘\p’ below for an alternative.

The construct ‘{...}’ is used for Perl extensions in a variety of ways depending on what immediately follows the ‘?’.
Perl-like matching can work in several modes, set by the options `(?i)` (caseless, equivalent to Perl’s `/i`), `(?m)` (multiline, equivalent to Perl’s `/m`), `(?s)` (single line, so a dot matches all characters, even new lines: equivalent to Perl’s `/s`) and `(?x)` (extended, whitespace data characters are ignored unless escaped and comments are allowed: equivalent to Perl’s `/x`). These can be concatenated, so for example, `(?1m)` sets caseless multiline matching. It is also possible to unset these options by preceding the letter with a hyphen, and to combine setting and unsetting such as `(?1m-sx)`. These settings can be applied within patterns, and then apply to the remainder of the pattern. Additional options not in Perl include `(?u)` to set ‘ungreedy’ mode (so matching is minimal unless `?` is used as part of the repetition quantifier, when it is greedy). Initially none of these options are set.

If you want to remove the special meaning from a sequence of characters, you can do so by putting them between `\Q` and `\E`. This is different from Perl in that `$` and `@` are handled as literals in `\Q...\E` sequences in PCRE, whereas in Perl, `$` and `@` cause variable interpolation.

The escape sequences `\d`, `\s` and `\w` represent any decimal digit, space character and ‘word’ character (letter, digit or underscore in the current locale: in UTF-8 mode only ASCII letters and digits are considered) respectively, and their upper-case versions represent their negation. Vertical tab was not regarded as a space character in a C locale before PCRE 8.34. Sequences `\h`, `\v`, `\H` and `\V` match horizontal and vertical space or the negation. (In UTF-8 mode, these do match non-ASCII Unicode code points.)

There are additional escape sequences: `\cx` is ‘cntr1-1-x’ for any ‘x’, ‘\ddd’ is the octal character (for up to three digits unless interpretable as a backreference, as ‘\1’ to ‘\7’ always are), and ‘\xhh’ specifies a character by two hex digits. In a UTF-8 locale, ‘\x{h...}’ specifies a Unicode code point by one or more hex digits. (Note that some of these will be interpreted by R’s parser in literal character strings.)

Outside a character class, ‘\A’ matches at the start of a subject (even in multiline mode, unlike ‘^’), ‘\Z’ matches at the end of a subject or before a newline at the end, ‘\z’ matches only at end of a subject, and ‘\G’ matches at first matching position in a subject (which is subtly different from Perl’s end of the previous match). ‘\C’ matches a single byte, including a newline, but its use is warned against. In UTF-8 mode, ‘\R’ matches any Unicode newline character (not just CR), and ‘\X’ matches any number of Unicode characters that form an extended Unicode sequence. ‘\X’, ‘\R’ and ‘\B’ cannot be used inside a character class (with PCRE1, they are treated as characters ‘X’, ‘R’ and ‘B’; with PCRE2 they cause an error).

A hyphen (minus) inside a character class is treated as a range, unless it is first or last character in the class definition. It can be quoted to represent the hyphen literal (`\-`). PCRE1 allows an unquoted hyphen at some other locations inside a character class where it cannot represent a valid range, but PCRE2 reports an error in such cases.

In UTF-8 mode, some Unicode properties may be supported via `\p{xx}` and `\P{xx}` which match characters with and without property ‘xx’ respectively. For a list of supported properties see the PCRE documentation, but for example ‘Lu’ is ‘upper case letter’ and ‘Sc’ is ‘currency symbol’. (This support depends on the PCRE library being compiled with ‘Unicode property support’ which can be checked via `pcre_config`. PCRE2 when compiled with Unicode support always supports also Unicode properties.)

The sequence `(?#` marks the start of a comment which continues up to the next closing parenthesis. Nested parentheses are not permitted. The characters that make up a comment play no part at all in the pattern matching.

If the extended option is set, an unescaped ‘#’ character outside a character class introduces a comment that continues up to the next newline character in the pattern.

The pattern `(?:...)` groups characters just as parentheses do but does not make a backreference. Patterns `(?!...)` and `(?!...)` are zero-width positive and negative lookahead assertions: they match if an attempt to match the . . . forward from the current position would succeed (or not), but
use up no characters in the string being processed. Patterns ‘(?<=...)’ and ‘(?<!...)’ are the
lookbehind equivalents: they do not allow repetition quantifiers nor ‘\C’ in . . . .

regexp and gregexpr support ‘named capture’. If groups are named, e.g.,
“(?<first>[A-Z][a-z]+)” then the positions of the matches are also returned by name.
(Named backreferences are not supported by sub.)

Atomic grouping, possessive qualifiers and conditional and recursive patterns are not covered here.

Author(s)

This help page is based on the TRE documentation and the POSIX standard, and the pcre2pattern
man page from PCRE2 10.35.

See Also

grep, apropos, browseEnv, glob2rx, help.search, list.files, ls, strsplit and agrep.

The TRE regexpr syntax.

The POSIX 1003.2 standard at https://pubs.opengroup.org/onlinepubs/9699919799/
basedefs/V1_chap09.html.

The pcre2pattern or pcrepattern man page (found as part of https://www.pcre.org/
original/pcre.txt), and details of Perl’s own implementation at https://perldoc.perl.org/
perlre.

__regmatches__

__Extract or Replace Matched Substrings__

### Description

Extract or replace matched substrings from match data obtained by regexpr, gregexpr, Regexexec
or gregexec.

### Usage

```r
regmatches(x, m, invert = FALSE)
```

```r
regmatches(x, m, invert = FALSE) <- value
```

### Arguments

- `x`  
a character vector
- `m`  
an object with match data
- `invert`  
a logical: if TRUE, extract or replace the non-matched substrings.
- `value`  
an object with suitable replacement values for the matched or non-matched sub-
strings (see Details).
Details

If `invert` is `FALSE` (default), `regmatches` extracts the matched substrings as specified by the match data. For vector match data (as obtained from `regexpr`), empty matches are dropped; for list match data, empty matches give empty components (zero-length character vectors).

If `invert` is `TRUE`, `regmatches` extracts the non-matched substrings, i.e., the strings are split according to the matches similar to `strsplit` (for vector match data, at most a single split is performed).

If `invert` is `NA`, `regmatches` extracts both non-matched and matched substrings, always starting and ending with a non-match (empty if the match occurred at the beginning or the end, respectively).

Note that the match data can be obtained from regular expression matching on a modified version of `x` with the same numbers of characters.

The replacement function can be used for replacing the matched or non-matched substrings. For vector match data, if `invert` is `FALSE`, `value` should be a character vector with length the number of matched elements in `m`. Otherwise, it should be a list of character vectors with the same length as `m`, each as long as the number of replacements needed. Replacement coerces values to character or list and generously recycles values as needed. Missing replacement values are not allowed.

Value

For `regmatches`, a character vector with the matched substrings if `m` is a vector and `invert` is `FALSE`. Otherwise, a list with the matched or/and non-matched substrings.

For `regmatches<-`, the updated character vector.

Examples

```r
x <- c("A and B", "A, B and C", "A, B, C and D", "foobar")
pattern <- "[[:space:]]*\[(,|and)\[[:space:]]\]
## Match data from regexpr()
m <- regexpr(pattern, x)
regmatches(x, m)
regmatches(x, m, invert = TRUE)
## Match data from gregexpr()
m <- gregexpr(pattern, x)
regmatches(x, m)
regmatches(x, m, invert = TRUE)

## Consider
x <- "John (fishing, hunting), Paul (hiking, biking)"
## Suppose we want to split at the comma (plus spaces) between the
## persons, but not at the commas in the parenthesized hobby lists.
## One idea is to "blank out" the parenthesized parts to match the
## parts to be used for splitting, and extract the persons as the
## non-matched parts.
## First, match the parenthesized hobby lists.
m <- gregexpr("\([[:space:]]\)\", x)
## Create blank strings with given numbers of characters.
blanks <- function(n) strrep(" ", n)
## Create a copy of x with the parenthesized parts blanked out.
s <- x
regmatches(s, m) <- Map(blanks, lapply(regmatches(s, m), nchar))
s
## Compute the positions of the split matches (note that we cannot call
## strsplit() on x with match data from s).
m <- gregexpr("", " ", s)
```
remove

## And finally extract the non-matched parts.
regmatches(x, m, invert = TRUE)

## regexec() and gregexec() return overlapping ranges because the
## first match is the full match. This conflicts with regmatches().
## and regmatches(..., invert=TRUE). We can work-around by dropping
## the first match.
drop_first <- function(x) {
  if(!anyNA(x) && all(x > 0)) {
    ml <- attr(x, 'match.length')
    if(is.matrix(x)) x <- x[-1,] else x <- x[-1]
    attr(x, 'match.length') <- if(is.matrix(ml)) ml[-1,] else ml[-1]
  }
  x
}
m <- gregexec("(\w+) \(((?:\w+(?:, )?)+)\)", x)
regmatches(x, m)
try(regmatches(x, m, invert=TRUE))
regmatches(x, lapply(m, drop_first))
## invert=TRUE loses matrix structure because we are retrieving what
## is in between every sub-match
regmatches(x, lapply(m, drop_first), invert=TRUE)
y <- z <- x
## Notice *list*(...) on the RHS
regmatches(y, lapply(m, drop_first)) <- list(c("<NAME>"", "<HOBBY-LIST>"))
y
regmatches(z, lapply(m, drop_first), invert=TRUE) <-
  list(sprintf("%d", 1:5))
z

## With `perl = TRUE` and `invert = FALSE` capture group names
## are preserved. Collect functions and arguments in calls:
NEWS <- head(readLines(file.path(R.home(), 'doc', 'NEWS.2')), 100)
m <- gregexec("(?<fun>\w+)\((?<args>[^)]*\))\)", NEWS, perl = TRUE)
y <- regmatches(NEWS, m)
y[[16]]
## Make tabular, adding original line numbers
mdat <- as.data.frame(t(do.call(cbind, y)))
mdat <- cbind(mdat, line=rep(seq_along(y), lengths(y) / ncol(mdat)))
head(mdat)
NEWS[head(mdat[['line']])]

---

### Description

`remove` and `rm` can be used to remove objects. These can be specified successively as character
strings, or in the character vector `list`, or through a combination of both. All objects thus specified
will be removed.

If `envir` is `NULL` then the currently active environment is searched first.

If `inherits` is `TRUE` then parents of the supplied directory are searched until a variable with the
given name is encountered. A warning is printed for each variable that is not found.
Usage

```r
remove(..., list = character(), pos = -1,
       envir = as.environment(pos), inherits = FALSE)
```

```r
rm (..., list = character(), pos = -1,
     envir = as.environment(pos), inherits = FALSE)
```

Arguments

- `...`: the objects to be removed, as names (unquoted) or character strings (quoted).
- `list`: a character vector (or `NULL`) naming objects to be removed.
- `pos`: where to do the removal. By default, uses the current environment. See ‘details’ for other possibilities.
- `envir`: the environment to use. See ‘details’.
- `inherits`: should the enclosing frames of the environment be inspected?

Details

The `pos` argument can specify the environment from which to remove the objects in any of several ways: as an integer (the position in the search list); as the character string name of an element in the search list; or as an environment (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily there for back compatibility.

It is not allowed to remove variables from the base environment and base namespace, nor from any environment which is locked (see `lockEnvironment`).

Earlier versions of R incorrectly claimed that supplying a character vector in `...` removed the objects named in the character vector, but it removed the character vector. Use the `list` argument to specify objects via a character vector.

References


See Also

`ls`, `objects`

Examples

```r
tmp <- 1:4
## work with tmp and cleanup
rm(tmp)

## Not run:
## remove (almost) everything in the working environment.
## You will get no warning, so don't do this unless you are really sure.
rm(list = ls())

## End(Not run)
```
rep

Replicate Elements of Vectors and Lists

Description

rep replicates the values in x. It is a generic function, and the (internal) default method is described here.

rep.int and rep_len are faster simplified versions for two common cases. Internally, they are generic, so methods can be defined for them (see InternalMethods).

Usage

rep(x, ...)
rep.int(x, times)
rep_len(x, length.out)

Arguments

x a vector (of any mode including a list) or a factor or (for rep only) a POSIXct or POSIXlt or Date object; or an S4 object containing such an object.
...

further arguments to be passed to or from other methods. For the internal default method these can include:
times an integer-valued vector giving the (non-negative) number of times to repeat each element if of length length(x), or to repeat the whole vector if of length 1. Negative or NA values are an error. A double vector is accepted, other inputs being coerced to an integer or double vector.
length.out non-negative integer. The desired length of the output vector. Other inputs will be coerced to a double vector and the first element taken. Ignored if NA or invalid.
each non-negative integer. Each element of x is repeated each times. Other inputs will be coerced to an integer or double vector and the first element taken. Treated as 1 if NA or invalid.
times, length.out

see ... above.

Details

The default behaviour is as if the call was

rep(x, times = 1, length.out = NA, each = 1)

. Normally just one of the additional arguments is specified, but if each is specified with either of the other two, its replication is performed first, and then that implied by times or length.out.

If times consists of a single integer, the result consists of the whole input repeated this many times. If times is a vector of the same length as x (after replication by each), the result consists of x[1] repeated times[1] times, x[2] repeated times[2] times and so on.
length.out may be given in place of times, in which case x is repeated as many times as is necessary to create a vector of this length. If both are given, length.out takes priority and times is ignored.

Non-integer values of times will be truncated towards zero. If times is a computed quantity it is prudent to add a small fuzz or use round. And analogously for each.

If x has length zero and length.out is supplied and is positive, the values are filled in using the extraction rules, that is by an NA of the appropriate class for an atomic vector (0 for raw vectors) and NULL for a list.

Value
An object of the same type as x.

rep.int and rep_len return no attributes (except the class if returning a factor).

The default method of rep gives the result names (which will almost always contain duplicates) if x had names, but retains no other attributes.

Note
Function rep.int is a simple case which was provided as a separate function partly for S compatibility and partly for speed (especially when names can be dropped). The performance of rep has been improved since, but rep.int is still at least twice as fast when x has names.

The name rep.int long precedes making rep generic.

Function rep is a primitive, but (partial) matching of argument names is performed as for normal functions.

For historical reasons rep (only) works on NULL: the result is always NULL even when length.out is positive.

Although it has never been documented, these functions have always worked on expression vectors.

References

See Also
seq, sequence, replicate.

Examples

rep(1:4, 2)
rep(1:4, each = 2)       # not the same.
rep(1:4, c(2,2,2,2))    # same as second.
rep(1:4, c(2,1,2,1))
rep(1:4, each = 2, length.out = 4)  # first 4 only.
rep(1:4, each = 2, length.out = 10)  # 8 integers plus two recycled 1's.
rep(1:4, each = 2, times = 3)       # length 24, 3 complete replications

rep(1, 40*(1-.8))  # length 7 on most platforms
rep(1, 40*(1-.8)+1e-7)  # better

## replicate a list
fred <- list(happy = 1:10, name = "squash")
replace

### Replace Values in a Vector

**Description**

`replace` replaces the values in `x` with indices given in `list` by those given in `values`. If necessary, the values in `values` are recycled.

**Usage**

`replace(x, list, values)`

**Arguments**

- `x`: vector
- `list`: an index vector
- `values`: replacement values

**Value**

A vector with the values replaced.

**Note**

`x` is unchanged: remember to assign the result.

**References**

Reserved Words in R

Description

The reserved words in R’s parser are

if else repeat while function for in next break
TRUE FALSE NULL Inf NaN NA_integer_ NA_real_ NA_complex_ NA_character_

... and .1, .2 etc, which are used to refer to arguments passed down from a calling function, see ....

Details

Reserved words outside quotes are always parsed to be references to the objects linked to in the ‘Description’, and hence they are not allowed as syntactic names (see make.names). They are allowed as non-syntactic names, e.g. inside backtick quotes.

rev

Reverse Elements

Description

rev provides a reversed version of its argument. It is generic function with a default method for vectors and one for dendrograms.

Note that this is no longer needed (nor efficient) for obtaining vectors sorted into descending order, since that is now rather more directly achievable by sort(x, decreasing = TRUE).

Usage

rev(x)

Arguments

x a vector or another object for which reversal is defined.

References


See Also

seq, sort.

Examples

x <- c(1:5, 5:3)
## sort into descending order; first more efficiently:
stopifnot(sort(x, decreasing = TRUE) == rev(sort(x)))
stopifnot(rev(1:7) == 7:1) # don’t need ’rev’ here
Return the R Home Directory

Description

Return the R home directory, or the full path to a component of the R installation.

Usage

R.home(component = "home")

Arguments

component As well as "home" which gives the R home directory, other known values are "bin", "doc", "etc", "include", "modules" and "share" giving the paths to the corresponding parts of an R installation.

Details

The R home directory is the top-level directory of the R installation being run.

The R home directory is often referred to as R_HOME, and is the value of an environment variable of that name in an R session. It can be found outside an R session by R RHOME.

The paths to components often are subdirectories of R_HOME but need not be: "doc", "include" and "share" are not for some Linux binary installations of R.

Value

A character string giving the R home directory or path to a particular component. Normally the components are all subdirectories of the R home directory, but this need not be the case in a Unix-like installation.

The value for "modules" and on Windows "bin" is a sub-architecture-specific location. (This is not so for "etc", which may have sub-architecture-specific files as well as common ones.)

On a Unix-alike, the constructed paths are based on the current values of the environment variables R_HOME and where set R_SHARE_DIR, R_DOC_DIR and R_INCLUDE_DIR (these are set on startup and should not be altered).

On Windows the values of R.home() and R_HOME are switched to the 8.3 short form of path elements if required and if the Windows service to do that is enabled. The value of R_HOME is set to use forward slashes (since many package maintainers pass it unquoted to shells, for example in Makefile's).

See Also

commandArgs()[1] may provide related information.

Examples

## These result quite platform-dependently :
rbind(home = R.home(),
       bin = R.home("bin")) # often the 'bin' sub directory of 'home'
       # but not always ...
list.files(R.home("bin"))
Run Length Encoding

Description

Compute the lengths and values of runs of equal values in a vector – or the reverse operation.

Usage

```r
rle(x)
inverse.rle(x, ...)
```

Arguments

- `x`: a vector (atomic, not a list) for `rle()`; an object of class "rle" for `inverse.rle()`.
- `...`: further arguments; ignored here.
- `digits`: number of significant digits for printing, see `print.default`.
- `prefix`: character string, prepended to each printed line.

Details

'vector' is used in the sense of `is.vector`.

Missing values are regarded as unequal to the previous value, even if that is also missing.

`inverse.rle()` is the inverse function of `rle()`, reconstructing `x` from the runs.

Value

`rle()` returns an object of class "rle" which is a list with components:

- `lengths`: an integer vector containing the length of each run.
- `values`: a vector of the same length as `lengths` with the corresponding values.

`inverse.rle()` returns an atomic vector.

Examples

```r
x <- rev(rep(6:10, 1:5))
rle(x)
## lengths [1:5] 5 4 3 2 1
## values [1:5] 10 9 8 7 6

z <- c(TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE)
rle(z)
rle(as.character(z))
print(rle(z), prefix = "..| ")

N <- integer(0)
```
### Round

**Description**

- **ceiling** takes a single numeric argument `x` and returns a numeric vector containing the smallest integers not less than the corresponding elements of `x`.
- **floor** takes a single numeric argument `x` and returns a numeric vector containing the largest integers not greater than the corresponding elements of `x`.
- **trunc** takes a single numeric argument `x` and returns a numeric vector containing the integers formed by truncating the values in `x` toward 0.
- **round** rounds the values in its first argument to the specified number of decimal places (default 0). See 'Details' about "round to even" when rounding off a 5.
- **signif** rounds the values in its first argument to the specified number of significant digits. Hence, for numeric `x`, `signif(x, dig)` is the same as `round(x, dig - ceiling(log10(abs(x))))`. For complex `x`, this is not the case, see the 'Details'.

**Usage**

```r
ceiling(x)
floor(x)
trunc(x, ...)
round(x, digits = 0)
signif(x, digits = 6)
```

**Arguments**

- `x` a numeric vector. Or, for `round` and `signif`, a complex vector.
- `digits` integer indicating the number of decimal places (round) or significant digits (signif) to be used. For round, negative values are allowed (see `Details`).
- `...` arguments to be passed to methods.

**Details**

These are generic functions: methods can be defined for them individually or via the `Math` group generic.

Note that for rounding off a 5, the IEC 60559 standard (see also 'IEEE 754') is expected to be used, 'go to the even digit'. Therefore `round(0.5)` is 0 and `round(-1.5)` is -2. However, this is dependent on OS services and on representation error (since e.g. 0.15 is not represented exactly, the rounding rule applies to the represented number and not to the printed number, and so `round(0.15, 1)` could be either 0.1 or 0.2).

Rounding to a negative number of digits means rounding to a power of ten, so for example `round(x, digits = -2)` rounds to the nearest hundred.
For `signif` the recognized values of digits are 1...22, and non-missing values are rounded to the nearest integer in that range. Complex numbers are rounded to retain the specified number of digits in the larger of the components. Each element of the vector is rounded individually, unlike printing.

These are all primitive functions.

**S4 methods**

These are all (internally) S4 generic.

`ceiling`, `floor` and `trunc` are members of the `Math` group generic. As an S4 generic, `trunc` has only one argument.

`round` and `signif` are members of the `Math2` group generic.

**Warning**

The realities of computer arithmetic can cause unexpected results, especially with `floor` and `ceiling`. For example, we ‘know’ that `floor(log(x, base = 8))` for `x = 8` is 1, but 0 has been seen on an R platform. It is normally necessary to use a tolerance.

Rounding to decimal digits in binary arithmetic is non-trivial (when `digits != 0`) and may be surprising. Be aware that most decimal fractions are not exactly representable in binary double precision. In R 4.0.0, the algorithm for `round(x, d)`, for `d > 0`, has been improved to `measure` and round “to nearest even”, contrary to earlier versions of R (or also to `sprintf()` or `format()` based rounding).

**References**


**See Also**

`as.integer`. Package `round`’s `roundX()` for several versions or implementations of rounding, including some previous and the current R version (as `version = "3d.C"`).

**Examples**

```r
round(.5 + -2:4) # IEEE / IEC rounding: -2 0 0 2 2 4 4
## (this is *good* behaviour -- do *NOT* report it as bug !)

( x1 <- seq(-2, 4, by = .5) )
round(x1) #-- IEEE / IEC rounding !
x1[trunc(x1) != floor(x1)]
x1[round(x1) != floor(x1 + .5)]
(non.int <- ceiling(x1) != floor(x1))

x2 <- pi * 100^(-1:3)
round(x2, 3)
signif(x2, 3)
```
**Description**

Round or truncate date-time objects.

**Usage**

```r
## S3 method for class 'POSIXt'
round(x,
       units = c("secs", "mins", "hours", "days", "months", "years"))

## S3 method for class 'POSIXt'
trunc(x,
      units = c("secs", "mins", "hours", "days", "months", "years"),
      ...)  
```

```r
## S3 method for class 'Date'
round(x, ...)
## S3 method for class 'Date'
trunc(x,
      units = c("secs", "mins", "hours", "days", "months", "years"),
      ...)
```

**Arguments**

- `x` an object inheriting from "POSIXt" or "Date".
- `units` one of the units listed, a string. Can be abbreviated.
- `...` arguments to be passed to or from other methods, notably digits for round.

**Details**

The time is rounded or truncated to the second, minute, hour, day, month or year. Time zones are only relevant to days or more, when midnight in the current time zone is used.

For units arguments besides "months" and "years", the methods for class "Date" are of little use except to remove fractional days.

**Value**

An object of class "POSIXt" or "Date".

**See Also**

- `round` for the generic function and default methods.
- `DateTimeClasses`, `Date`
Examples

```r
round(.leap.seconds + 1000, "hour")
## IGNORE_RDIFF_BEGIN
trunc(Sys.time(), "day")
(timM <- trunc(Sys.time() -> St, "months")) # shows timezone
(datM <- trunc(Sys.Date() -> Sd, "months"))
(timY <- trunc(St, "years")) # + timezone
(datY <- trunc(Sd, "years"))
## IGNORE_RDIFF_END
stopifnot(inherits(datM, "Date"), inherits(timM, "POSIXt"),
substring(format(datM), 9,10) == "01", # first of month
substring(format(datY), 6,10) == "01-01", # Jan 1
identical(format(datM), format(timM)),
identical(format(datY), format(timY)))
```

Description

Returns a matrix of integers indicating their row number in a matrix-like object, or a factor indicating the row labels.

Usage

```r
row(x, as.factor = FALSE)
.row(dim)
```

Arguments

- `x`: a matrix-like object, that is one with a two-dimensional `dim`.
- `dim`: a matrix dimension, i.e., an integer valued numeric vector of length two (with non-negative entries).
- `as.factor`: a logical value indicating whether the value should be returned as a factor of row labels (created if necessary) rather than as numbers.

Value

An integer (or factor) matrix with the same dimensions as `x` and whose \( i j \)-th element is equal to \( i \) (or the \( i \)-th row label).

References


See Also

- `col` to get columns; `slice.index` for a general way to get slice indices in an array.
Examples

x <- matrix(1:12, 3, 4)
# extract the diagonal of a matrix - more slowly than diag(x)
dx <- x[row(x) == col(x)]
dx

# create an identity 5-by-5 matrix more slowly than diag(n = 5):
x <- matrix(0, nrow = 5, ncol = 5)
x[row(x) == col(x)] <- 1
x

(i34 <- .row(3:4))
stopifnot(identical(i34, .row(c(3,4)))) # 'dim' maybe "double"

---

row+colnames

Row and Column Names

Description

Retrieve or set the row or column names of a matrix-like object.

Usage

rownames(x, do.NULL = TRUE, prefix = "row")
rownames(x) <- value

colnames(x, do.NULL = TRUE, prefix = "col")
colnames(x) <- value

Arguments

x a matrix-like R object, with at least two dimensions for colnames.
do.NULL logical. If FALSE and names are NULL, names are created.
prefix for created names.
value a valid value for that component of dimnames(x). For a matrix or array this is either NULL or a character vector of non-zero length equal to the appropriate dimension.

Details

The extractor functions try to do something sensible for any matrix-like object x. If the object has dimnames the first component is used as the row names, and the second component (if any) is used for the column names. For a data frame, rownames and colnames eventually call row.names and names respectively, but the latter are preferred.

If do.NULL is FALSE, a character vector (of length NROW(x) or NCOL(x)) is returned in any case, prepending prefix to simple numbers, if there are no dimnames or the corresponding component of the dimnames is NULL.

The replacement methods for arrays/matrices coerce vector and factor values of value to character, but do not dispatch methods for as.character.
For a data frame, value for rownames should be a character vector of non-duplicated and non-missing names (this is enforced), and for colnames a character vector of (preferably) unique syntactically-valid names. In both cases, value will be coerced by `as.character`, and setting colnames will convert the row names to character.

**Note**

If the replacement versions are called on a matrix without any existing dimnames, they will add suitable dimnames. But constructions such as

```r
rownames(x)[3] <- "c"
```

may not work unless x already has dimnames, since this will create a length-3 value from the NULL value of rownames(x).

**See Also**

`dimnames, case.names, variable.names`.

**Examples**

```r
m0 <- matrix(NA, 4, 0)
rownames(m0)

m2 <- cbind(1, 1:4)
colnames(m2, do.NULL = FALSE)
colnames(m2) <- c("x", "y")
rownames(m2) <- rownames(m2, do.NULL = FALSE, prefix = "Obs.")
m2
```

---

**row.names**

Get and Set Row Names for Data Frames

**Description**

All data frames have row names, a character vector of length the number of rows with no duplicates nor missing values.

There are generic functions for getting and setting row names, with default methods for arrays. The description here is for the `data.frame` method.

`.rowNamesDF<-` is a (non-generic replacement) function to set row names for data frames, with extra argument `make.names`. This function only exists as workaround as we cannot easily change the `rownames<-` generic without breaking legacy code in existing packages.

**Usage**

```r
row.names(x)
rownames(x) <- value
.rowNamesDF(x, make.names=FALSE) <- value
```
Arguments

- **x**: object of class "data.frame", or any other class for which a method has been defined.

- **make.names**: logical, i.e., one of FALSE, NA, TRUE, indicating what should happen if the specified row names, i.e., `value`, are invalid, e.g., duplicated or NA. The default (is back compatible), FALSE, will signal an error, where NA will “automatic” row names and TRUE will call `make.names(value, unique=TRUE)` for constructing valid names.

- **value**: an object to be coerced to character unless an integer vector. It should have (after coercion) the same length as the number of rows of `x` with no duplicated nor missing values. NULL is also allowed: see ‘Details’.

Details

A data frame has (by definition) a vector of **row names** which has length the number of rows in the data frame, and contains neither missing nor duplicated values. Where a row names sequence has been added by the software to meet this requirement, they are regarded as ‘automatic’.

Row names are currently allowed to be integer or character, but for backwards compatibility (with \( R \leq 2.4.0 \)) `row.names` will always return a character vector. (Use `attr(x, "row.names")` if you need to retrieve an integer-valued set of row names.)

Using NULL for the value resets the row names to `seq_len(nrow(x))`, regarded as ‘automatic’.

Value

- `row.names` returns a character vector.
- `row.names<-` returns a data frame with the row names changed.

Note

`row.names` is similar to `rownames` for arrays, and it has a method that calls `rownames` for an array argument.

Row names of the form `1:n` for \( n > 2 \) are stored internally in a compact form, which might be seen from C code or by deparsing but never via `row.names` or `attr(x, "row.names")`. Additionally, some names of this sort are marked as ‘automatic’ and handled differently by `as.matrix` and `data.matrix` (and potentially other functions). (All zero-row data frames are regarded as having automatic row names.)

References


See Also

`data.frame`, `rownames`, `names`, `.row_names_info` for the internal representations.
Examples

```r
def <- data.frame(x = c(TRUE, FALSE, NA, NA), y = c(12, 34, 56, 78))
row.names(df) <- 1:4
attr(df, "row.names") #> 1:4
deparse(df) # or dput(df)
##--> c(NA, 4L) : Compact storage, *not* regarded as automatic.

row.names(df) <- NULL
attr(df, "row.names") #> 1:4
deparse(df) # or dput(df) -- shows
##--> c(NA, -4L) : Compact storage, regarded as automatic.
```

---

### rowsum

Give Column Sums of a Matrix or Data Frame, Based on a Grouping Variable

#### Description

Compute column sums across rows of a numeric matrix-like object for each level of a grouping variable. rowsum is generic, with a method for data frames and a default method for vectors and matrices.

#### Usage

```r
rowsum(x, group, reorder = TRUE, ...)  
```  
```r  
## S3 method for class 'data.frame'  
rowsum(x, group, reorder = TRUE, na.rm = FALSE, ...)  
## Default S3 method:  
rowsum(x, group, reorder = TRUE, na.rm = FALSE, ...)  
```

#### Arguments

- `x` a matrix, data frame or vector of numeric data. Missing values are allowed. A numeric vector will be treated as a column vector.
- `group` a vector or factor giving the grouping, with one element per row of `x`. Missing values will be treated as another group and a warning will be given.
- `reorder` if TRUE, then the result will be in order of `sort(unique(group))`, if FALSE, it will be in the order that groups were encountered.
- `na.rm` logical (TRUE or FALSE). Should NA (including NaN) values be discarded?
- `...` other arguments to be passed to or from methods

#### Details

The default is to reorder the rows to agree with `tapply` as in the example below. Reordering should not add noticeably to the time except when there are very many distinct values of `group` and `x` has few columns.

The original function was written by Terry Therneau, but this is a new implementation using hashing that is much faster for large matrices.
To sum over all the rows of a matrix (i.e., a single group) use `colSums`, which should be even faster. For integer arguments, over/underflow in forming the sum results in `NA`.

**Value**

A matrix or data frame containing the sums. There will be one row per unique value of `group`.

**See Also**

`tapply, aggregate, rowSums`

**Examples**

```r
require(stats)
x <- matrix(runif(100), ncol = 5)
group <- sample(1:8, 20, TRUE)
(xsum <- rowsum(x, group))
## Slower versions
tapply(x, list(group[row(x)], col(x)), sum)
t(t(sapply(split(as.data.frame(x), group), colSums))
aggregate(x, list(group), sum)[-1]
```

---

**S3method**

Register S3 Methods

**Description**

Register S3 methods in R scripts.

**Usage**

`.S3method(generic, class, method)`

**Arguments**

- `generic` a character string naming an S3 generic function.
- `class` a character string naming an S3 class.
- `method` a character string or function giving the S3 method to be registered. If not given, the function named `generic .class` is used.

**Details**

This function should only be used in R scripts: for package code, one should use the corresponding `‘S3method’ ‘NAMESPACE’` directive.
Examples

```r
## Create a generic function and register a method for objects
## inheriting from class 'cls':
gen <- function(x) UseMethod("gen")
met <- function(x) writeLines("Hello world.")
.S3method("gen", "cls", met)
## Create an object inheriting from class 'cls', and call the
## generic on it:
x <- structure(123, class = "cls")
gen(x)
```

Description

`sample` takes a sample of the specified size from the elements of `x` using either with or without replacement.

Usage

```r
sample(x, size, replace = FALSE, prob = NULL)
sample.int(n, size = n, replace = FALSE, prob = NULL,
          useHash = (n > 1e+07 && !replace && is.null(prob) && size <= n/2))
```

Arguments

- `x` either a vector of one or more elements from which to choose, or a positive integer. See ‘Details.’
- `n` a positive number, the number of items to choose from. See ‘Details.’
- `size` a non-negative integer giving the number of items to choose.
- `replace` should sampling be with replacement?
- `prob` a vector of probability weights for obtaining the elements of the vector being sampled.
- `useHash` logical indicating if the hash-version of the algorithm should be used. Can only be used for `replace = FALSE`, `prob = NULL`, and `size <= n/2`, and really should be used for large `n`, as `useHash=FALSE` will use memory proportional to `n`.

Details

If `x` has length 1, is numeric (in the sense of `is.numeric`) and `x >= 1`, sampling via `sample` takes place from `1:x`. *Note* that this convenience feature may lead to undesired behaviour when `x` is of varying length in calls such as `sample(x)`. See the examples.

Otherwise `x` can be any R object for which `length` and subsetting by integers make sense: S3 or S4 methods for these operations will be dispatched as appropriate.

For `sample` the default for `size` is the number of items inferred from the first argument, so that `sample(x)` generates a random permutation of the elements of `x` (or `1:x`).
It is allowed to ask for size = 0 samples with n = 0 or a length-zero x, but otherwise n > 0 or positive length(x) is required.

Non-integer positive numerical values of n or x will be truncated to the next smallest integer, which has to be no larger than .Machine$integer.max.

The optional prob argument can be used to give a vector of weights for obtaining the elements of the vector being sampled. They need not sum to one, but they should be non-negative and not all zero. If replace is true, Walker’s alias method (Ripley, 1987) is used when there are more than 200 reasonably probable values: this gives results incompatible with those from R < 2.2.0.

If replace is false, these probabilities are applied sequentially, that is the probability of choosing the next item is proportional to the weights amongst the remaining items. The number of nonzero weights must be at least size in this case.

sample.int is a bare interface in which both n and size must be supplied as integers.

Argument n can be larger than the largest integer of type integer, up to the largest representable integer in type double. Only uniform sampling is supported. Two random numbers are used to ensure uniform sampling of large integers.

Value

For sample a vector of length size with elements drawn from either x or from the integers 1:x.

For sample.int, an integer vector of length size with elements from 1:n, or a double vector if n ≥ 2^31.

References


See Also

RNGkind(sample.kind = ..) about random number generation, notably the change of sample() results with R version 3.6.0.

CRAN package sampling for other methods of weighted sampling without replacement.

Examples

```r
x <- 1:12
# a random permutation
sample(x)
# bootstrap resampling -- only if length(x) > 1 !
sample(x, replace = TRUE)

# 100 Bernoulli trials
sample(c(0,1), 100, replace = TRUE)

## More careful bootstrapping -- Consider this when using sample()
## programmatically (i.e., in your function or simulation)!
# sample()’s surprise -- example
x <- 1:10
sample(x[x > 8]) # length 2
sample(x[x > 9]) # oops -- length 10!
```
```r
sample(x[x > 10]) # length 0

## safer version:
resample <- function(x, ...) x[sample.int(length(x), ...)]
resample(x[x > 8]) # length 2
resample(x[x > 9]) # length 1
resample(x[x > 10]) # length 0

## R 3.0.0 and later
sample.int(1e10, 12, replace = TRUE)
sample.int(1e10, 12) # not that there is much chance of duplicates
```

---

**save**

**Save R Objects**

**Description**

`save` writes an external representation of R objects to the specified file. The objects can be read back from the file at a later date by using the function `load` or `attach` (or `data` in some cases).

`save.image()` is just a short-cut for 'save my current workspace', i.e., `save(list = ls(all.names = TRUE), file = ".RData", envir = .GlobalEnv)`. It is also what happens with `q("yes")`.

**Usage**

```r
save(..., list = character(),
     file = stop("'file' must be specified"),
     ascii = FALSE, version = NULL, envir = parent.frame(),
     compress = isTRUE(!ascii), compression_level,
     eval.promises = TRUE, precheck = TRUE)

save.image(file = ".RData", version = NULL, ascii = FALSE,
           compress = !ascii, safe = TRUE)
```

**Arguments**

- `...` the names of the objects to be saved (as symbols or character strings).
- `list` a character vector (or `NULL`) containing the names of objects to be saved.
- `file` a (writable binary-mode) connection or the name of the file where the data will be saved (when tilde expansion is done). Must be a file name for `save.image` or `version = 1`.
- `ascii` if TRUE, an ASCII representation of the data is written. The default value of `ascii` is FALSE which leads to a binary file being written. If NA and `version >= 2`, a different ASCII representation is used which writes double/complex numbers as binary fractions.
- `version` the workspace format version to use. NULL specifies the current default format (3). Version 1 was the default from R 0.99.0 to R 1.3.1 and version 2 from R 1.4.0 to 3.5.0. Version 3 is supported from R 3.5.0.
- `envir` environment to search for objects to be saved.
compress

 logical or character string specifying whether saving to a named file is to use compression. TRUE corresponds to gzip compression, and character strings "gzip", "bzip2" or "xz" specify the type of compression. Ignored when file is a connection and for workspace format version 1.

compression_level

 integer: the level of compression to be used. Defaults to 6 for gzip compression and to 9 for bzip2 or xz compression. See the help for file for possible values and their merits.

eval.promises

 logical: should objects which are promises be forced before saving?

precheck

 logical: should the existence of the objects be checked before starting to save (and in particular before opening the file/connection)? Does not apply to version 1 saves.

safe

 logical. If TRUE, a temporary file is used for creating the saved workspace. The temporary file is renamed to file if the save succeeds. This preserves an existing workspace file if the save fails, but at the cost of using extra disk space during the save.

Details

The names of the objects specified either as symbols (or character strings) in ... or as a character vector in list are used to look up the objects from environment envir. By default promises are evaluated, but if eval.promises = FALSE promises are saved (together with their evaluation environments). (Promises embedded in objects are always saved unevaluated.)

All R platforms use the XDR (bigendian) representation of C ints and doubles in binary save-d files, and these are portable across all R platforms.

ASCII saves used to be useful for moving data between platforms but are now mainly of historical interest. They can be more compact than binary saves where compression is not used, but are almost always slower to both read and write: binary saves compress much better than ASCII ones. Further, decimal ASCII saves may not restore double/complex values exactly, and what value is restored may depend on the R platform.

Default values for the ascii, compress, safe and version arguments can be modified with the "save.defaults" option (used both by save and save.image), see also the 'Examples' section. If a "save.image.defaults" option is set it is used in preference to "save.defaults" for function save.image (which allows this to have different defaults). In addition, compression_level can be part of the "save.defaults" option.

A connection that is not already open will be opened in mode "wb". Supplying a connection which is open and not in binary mode gives an error.

Compression

Large files can be reduced considerably in size by compression. A particular 46MB R object was saved as 35MB without compression in 2 seconds, 22MB with gzip compression in 8 secs, 19MB with bzip2 compression in 13 secs and 9.4MB with xz compression in 40 secs. The load times were 1.3, 2.8, 5.5 and 5.7 seconds respectively. These results are indicative, but the relative performances do depend on the actual file: xz compressed unusually well here.

It is possible to compress later (with gzip, bzip2 or xz) a file saved with compress = FALSE: the effect is the same as saving with compression. Also, a saved file can be uncompressed and recompressed under a different compression scheme (and see resaveRdaFiles for a way to do so from within R).
Parallel compression

That file can be a connection can be exploited to make use of an external parallel compression utility such as pigz (https://zlib.net/pigz/) or pbzip2 (https://launchpad.net/pbzip2) via a pipe connection. For example, using 8 threads,

```r
con <- pipe("pigz -p8 > fname.gz", "wb")
save(myObj, file = con); close(con)
```

```r
con <- pipe("pbzip2 -p8 -9 > fname.bz2", "wb")
save(myObj, file = con); close(con)
```

```r
con <- pipe("xz -T8 -6 -e > fname.xz", "wb")
save(myObj, file = con); close(con)
```

where the last requires xz 5.1.1 or later built with support for multiple threads (and parallel compression is only effective for large objects: at level 6 it will compress in serialized chunks of 12MB).

Warnings

The ... arguments only give the names of the objects to be saved: they are searched for in the environment given by the envir argument, and the actual objects given as arguments need not be those found.

Saved R objects are binary files, even those saved with ascii = TRUE, so ensure that they are transferred without conversion of end-of-line markers and of 8-bit characters. The lines are delimited by LF on all platforms.

Although the default version was not changed between R 1.4.0 and R 3.4.4 nor since R 3.5.0, this does not mean that saved files are necessarily backwards compatible. You will be able to load a saved image into an earlier version of R which supports its version unless use is made of later additions (for example for version 2, raw vectors, external pointers and some S4 objects).

One such 'later addition' was long vectors, introduced in R 3.0.0 and loadable only on 64-bit platforms.

Loading files saved with ASCII = NA requires a C99-compliant C function sscanf: this is a problem on Windows, first worked around in R 3.1.2: version-2 files in that format should be readable in earlier versions of R on all other platforms.

Note

For saving single R objects, saveRDS() is mostly preferable to save(), notably because of the functional nature of readRDS(), as opposed to load().

The most common reason for failure is lack of write permission in the current directory. For save.image and for saving at the end of a session this will shown by messages like

```r
Error in gzfile(file, "wb") : unable to open connection
In addition: Warning message:
In gzfile(file, "wb"):
cannot open compressed file '.RDataTmp',
probable reason 'Permission denied'
```

See Also

dput, dump, load, data.

For other interfaces to the underlying serialization format, see serialize and saveRDS.
scale

Scaling and Centering of Matrix-like Objects

Description

scale is a generic function whose default method centers and/or scales the columns of a numeric matrix.

Usage

scale(x, center = TRUE, scale = TRUE)

Arguments

x a numeric matrix(like object).

center either a logical value or numeric-alike vector of length equal to the number of columns of x, where ‘numeric-alike’ means that as.numeric(.) will be applied successfully if is.numeric(.) is not true.

scale either a logical value or a numeric-alike vector of length equal to the number of columns of x.

Details

The value of center determines how column centering is performed. If center is a numeric-alike vector with length equal to the number of columns of x, then each column of x has the corresponding value from center subtracted from it. If center is TRUE then centering is done by subtracting the column means (omitting NAs) of x from their corresponding columns, and if center is FALSE, no centering is done.

The value of scale determines how column scaling is performed (after centering). If scale is a numeric-alike vector with length equal to the number of columns of x, then each column of x is divided by the corresponding value from scale. If scale is TRUE then scaling is done by dividing the (centered) columns of x by their standard deviations if center is TRUE, and the root mean square otherwise. If scale is FALSE, no scaling is done.
The root-mean-square for a (possibly centered) column is defined as \( \sqrt{\frac{\sum(x^2)}{(n-1)}} \), where \( x \) is a vector of the non-missing values and \( n \) is the number of non-missing values. In the case center = TRUE, this is the same as the standard deviation, but in general it is not. (To scale by the standard deviations without centering, use scale(x, center = FALSE, scale = apply(x, 2, sd, na.rm = TRUE)).)

Value

For scale.default, the centered, scaled matrix. The numeric centering and scalings used (if any) are returned as attributes "scaled:center" and "scaled:scale"

References


See Also

sweep which allows centering (and scaling) with arbitrary statistics.

For working with the scale of a plot, see par.

Examples

require(stats)
x <- matrix(1:10, ncol = 2)
(centered.x <- scale(x, scale = FALSE))
cov(centered.scaled.x <- scale(x)) # all 1

Description

Read data into a vector or list from the console or file.

Usage

\[
\text{scan(file = "", what = double(), nmax = -1, n = -1, sep = "", quote = if(identical(sep, \"\n\") \"" else \"\"\", dec = \"\"\", skip = 0, nlines = 0, na.strings = \"NA\", flush = FALSE, fill = FALSE, strip.white = FALSE, quiet = FALSE, blank.lines.skip = TRUE, multi.line = TRUE, comment.char = \"\", allowEscapes = FALSE, fileEncoding = \"\", encoding = "unknown", text, skipNul = FALSE)}
\]

Arguments

file the name of a file to read data values from. If the specified file is "", then input is taken from the keyboard (or whatever stdin() reads if input is redirected or R is embedded). (In this case input can be terminated by a blank line or an EOF signal, 'Ctrl-D' on Unix and 'Ctrl-Z' on Windows.)
Otherwise, the file name is interpreted relative to the current working directory (given by `getwd()`), unless it specifies an absolute path. Tilde-expansion is performed where supported. When running R from a script, `file = "stdin"` can be used to refer to the process’s stdin file stream.

This can be a compressed file (see `file`). Alternatively, `file` can be a connection, which will be opened if necessary, and if so closed at the end of the function call. Whatever mode the connection is opened in, any of LF, CRLF or CR will be accepted as the EOL marker for a line and so will match `sep = "\n"`.

`file` can also be a complete URL. (For the supported URL schemes, see the ‘URLs’ section of the help for `url`.)

To read a data file not in the current encoding (for example a Latin-1 file in a UTF-8 locale or conversely) use a `file` connection setting its `encoding` argument (or `scan`’s `fileEncoding` argument).

The type of what gives the type of data to be read. (Here ‘type’ is used in the sense of `typeof`.) The supported types are logical, integer, numeric, complex, character, raw and list. If what is a list, it is assumed that the lines of the data file are records each containing `length(what)` items (‘fields’) and the list components should have elements which are one of the first six (atomic) types listed or NULL, see section ‘Details’ below.

The maximum number of data values to be read, or if what is a list, the maximum number of records to be read. If omitted or not positive or an invalid value for an integer (and `nlines` is not set to a positive value), `scan` will read to the end of `file`.

integer: the maximum number of data values to be read, defaulting to no limit. Invalid values will be ignored.

by default, scan expects to read ‘white-space’ delimited input fields. Alternatively, `sep` can be used to specify a character which delimits fields. A field is always delimited by an end-of-line marker unless it is quoted. If specified this should be the empty character string (the default) or NULL or a character string containing just one single-byte character.

the set of quoting characters as a single character string or NULL. In a multibyte locale the quoting characters must be ASCII (single-byte).

decimal point character. This should be a character string containing just one single-byte character. (NULL and a zero-length character vector are also accepted, and taken as the default.)

the number of lines of the input file to skip before beginning to read data values.

if positive, the maximum number of lines of data to be read.

character vector. Elements of this vector are to be interpreted as missing (NA) values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields. Note that the test happens after white space is stripped from the input, so `na.strings` values may need their own white space stripped in advance.

logical: if `TRUE`, `scan` will flush to the end of the line after reading the last of the fields requested. This allows putting comments after the last field, but precludes putting more that one record on a line.

logical: if `TRUE`, `scan` will implicitly add empty fields to any lines with fewer fields than implied by what.
strip.white

vector of logical value(s) corresponding to items in the what argument. It is used only when sep has been specified, and allows the stripping of leading and trailing ‘white space’ from character fields (numeric fields are always stripped). Note: white space inside quoted strings is not stripped.

If strip.white is of length 1, it applies to all fields; otherwise, if strip.white[i] is TRUE and the i-th field is of mode character (because what[i] is) then the leading and trailing unquoted white space from field i is stripped.

quiet

logical: if FALSE (default), scan() will print a line, saying how many items have been read.

blank.lines.skip

logical: if TRUE blank lines in the input are ignored, except when counting skip and nlines.

multi.line

logical. Only used if what is a list. If FALSE, all of a record must appear on one line (but more than one record can appear on a single line). Note that using fill = TRUE implies that a record will be terminated at the end of a line.

comment.char

character: a character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether (the default).

allowEscapes

logical. Should C-style escapes such as ‘\n’ be processed (the default) or read verbatim? Note that if not within quotes these could be interpreted as a delimiter (but not as a comment character).

The escapes which are interpreted are the control characters ‘\a, \b, \f, \n, \r, \t, \v’ and octal and hexadecimal representations like ‘\040’ and ‘\0x2A’.

Any other escaped character is treated as itself, including backslash. Note that Unicode escapes (starting ‘u’ or ‘\U’: see Quotes) are never processed.

fileEncoding

character string: if non-empty declares the encoding used on a file (not a connection nor the keyboard) so the character data can be re-encoded. See the ‘Encoding’ section of the help for file, and the ‘R Data Import/Export Manual’.

encoding

encoding to be assumed for input strings. If the value is "latin1" or "UTF-8" it is used to mark character strings as known to be in Latin-1 or UTF-8: it is not used to re-encode the input (see fileEncoding). See also ‘Details’.

text

character string: if file is not supplied and this is, then data are read from the value of text via a text connection.

skipNul

logical: should nuls be skipped when reading character fields?

Details

The value of what can be a list of types, in which case scan returns a list of vectors with the types given by the types of the elements in what. This provides a way of reading columnar data. If any of the types is NULL, the corresponding field is skipped (but a NULL component appears in the result).

The type of what or its components can be one of the six atomic vector types or NULL (see is.atomic).

‘White space’ is defined for the purposes of this function as one or more contiguous characters from the set space, horizontal tab, carriage return and line feed (aka “newline”, “\n”). It does not include form feed nor vertical tab, but in Latin-1 and Windows 8-bit locales (but not UTF-8) ‘space’ includes the non-breaking space ‘\xa0’.

Empty numeric fields are always regarded as missing values. Empty character fields are scanned as empty character vectors, unless na.strings contains "" when they are regarded as missing values.
The allowed input for a numeric field is optional whitespace followed either NA or an optional sign followed by a decimal or hexadecimal constant (see NumericConstants), or NaN, Inf or infinity (ignoring case). Out-of-range values are recorded as Inf, -Inf or 0.

For an integer field the allowed input is optional whitespace, followed by either NA or an optional sign and one or more digits (’0-9’): all out-of-range values are converted to NA_integer_.

If sep is the default (""), the character ‘\' in a quoted string escapes the following character, so quotes may be included in the string by escaping them.

If sep is non-default, the fields may be quoted in the style of ‘.csv’ files where separators inside quotes (’’ or “”) are ignored and quotes may be put inside strings by doubling them. However, if sep = "\n" it is assumed by default that one wants to read entire lines verbatim.

Quoting is only interpreted in character fields and in NULL fields (which might be skipping character fields).

Note that since sep is a separator and not a terminator, reading a file by scan("foo", sep = "\n", blank.lines.skip = FALSE) will give an empty final line if the file ends in a line feed ("\n") and not if it does not. This might not be what you expected; see also readLines.

If comment.char occurs (except inside a quoted character field), it signals that the rest of the line should be regarded as a comment and be discarded. Lines beginning with a comment character (possibly after white space with the default separator) are treated as blank lines.

There is a line-length limit of 4095 bytes when reading from the console (which may impose a lower limit: see ‘An Introduction to R’).

There is a check for a user interrupt every 1000 lines if what is a list, otherwise every 10000 items.

If file is a character string and fileEncoding is non-default, or if it is a not-already-open connection with a non-default encoding argument, the text is converted to UTF-8 and declared as such (and the encoding argument to scan is ignored). See the examples of readLines.

Embedded nuls in the input stream will terminate the field currently being read, with a warning once per call to scan. Setting skipNul = TRUE causes them to be ignored.

Value

if what is a list, a list of the same length and same names (as any) as what.

Otherwise, a vector of the type of what.

Character strings in the result will have a declared encoding if encoding is "latin1" or "UTF-8".

Note

The default for multi.line differs from S. To read one record per line, use flush = TRUE and multi.line = FALSE. (Note that quoted character strings can still include embedded newlines.)

If number of items is not specified, the internal mechanism re-allocates memory in powers of two and so could use up to three times as much memory as needed. (It needs both old and new copies.)

If you can, specify either n or nmax whenever inputting a large vector, and nmax or nlines when inputting a large list.

Using scan on an open connection to read partial lines can lose chars: use an explicit separator to avoid this.

Having nul bytes in fields (including ‘\0’ if allowEscapes = TRUE) may lead to interpretation of the field being terminated at the nul. They not normally present in text files – see readBin.
References


See Also

`read.table` for more user-friendly reading of data matrices; `readLines` to read a file a line at a time. `write`.

Quotes for the details of C-style escape sequences.

`readChar` and `readBin` to read fixed or variable length character strings or binary representations of numbers a few at a time from a connection.

Examples

```r
cat("TITLE extra line", "2 3 5 7", "11 13 17", file = "ex.data", sep = "\n")
pp <- scan("ex.data", skip = 1, quiet = TRUE)
scan("ex.data", skip = 1)
scan("ex.data", skip = 1, nlines = 1) # only 1 line after the skipped one
scan("ex.data", what = list("","")) # flush is F -> read "7"
scan("ex.data", what = list("",""), flush = TRUE)
unlink("ex.data") # tidy up

## "inline" usage
scan(text = "1 2 3")
```

search

Give Search Path for R Objects

Description

Gives a list of `attached` packages (see `library`), and R objects, usually `data.frames`.

Usage

```r
search()
searchpaths()
```

Value

A character vector, starting with ".GlobalEnv", and ending with "package:base" which is R's `base` package required always.

`searchpaths` gives a similar character vector, with the entries for packages being the path to the package used to load the code.

References


see

See Also
.packages to list just the packages on search path.
.loadedNamespaces to list loaded namespaces.
attach and detach to change the search path, objects to find R objects in there.

Examples

search()
searchpaths()

seek Functions to Reposition Connections

Description
Functions to re-position connections.

Usage

seek(con, 
## S3 method for class 'connection'
seek(con, where = NA, origin = "start", rw = ",", 

isSeekable(con)

truncate(con, 

Arguments

con a connection.
where numeric. A file position (relative to the origin specified by origin), or NA.
rw character string. Empty or "read" or "write", partial matches allowed.
origin character string. One of "start", "current", "end": see 'Details'.
... further arguments passed to or from other methods.

Details

seek with where = NA returns the current byte offset of a connection (from the beginning), and with a non-missing where argument the connection is re-positioned (if possible) to the specified position. isSeekable returns whether the connection in principle supports seek: currently only (possibly gz-compressed) file connections do.

where is stored as a real but should represent an integer: non-integer values are likely to be truncated. Note that the possible values can exceed the largest representable number in an R integer on 64-bit builds, and on some 32-bit builds.

File connections can be open for both writing/appending, in which case R keeps separate positions for reading and writing. Which seek refers to can be set by its rw argument: the default is the last mode (reading or writing) which was used. Most files are only opened for reading or writing and so default to that state. If a file is open for both reading and writing but has not been used, the default is to give the reading position (0).
The initial file position for reading is always at the beginning. The initial position for writing is at the beginning of the file for modes "r+" and "r+b", otherwise at the end of the file. Some platforms only allow writing at the end of the file in the append modes. (The reported write position for a file opened in an append mode will typically be unreliable until the file has been written to.)

gzfile connections support seek with a number of limitations, using the file position of the uncompressed file. They do not support origin = "end". When writing, seeking is only possible forwards: when reading seeking backwards is supported by rewinding the file and re-reading from its start.

If seek is called with a non-NA value of where, any pushback on a text-mode connection is discarded.

truncate truncates a file opened for writing at its current position. It works only for file connections, and is not implemented on all platforms: on others (including Windows) it will not work for large (> 2Gb) files.

None of these should be expected to work on text-mode connections with re-encoding selected.

Value

seek returns the current position (before any move), as a (numeric) byte offset from the origin, if relevant, or 0 if not. Note that the position can exceed the largest representable number in an R integer on 64-bit builds, and on some 32-bit builds.

truncate returns NULL: it stops with an error if it fails (or is not implemented).

isSeekable returns a logical value, whether the connection supports seek.

Warning

Use of seek on Windows is discouraged. We have found so many errors in the Windows implementation of file positioning that users are advised to use it only at their own risk, and asked not to waste the R developers’ time with bug reports on Windows’ deficiencies.

See Also

connections

seq

Sequence Generation

Description

Generate regular sequences. seq is a standard generic with a default method. seq.int is a primitive which can be much faster but has a few restrictions. seq_along and seq_len are very fast primitives for two common cases.

Usage

seq(...)

## Default S3 method:
seq(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
     length.out = NULL, along.with = NULL, ...)

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seq

Sequence Generation

Description

Generate regular sequences. seq is a standard generic with a default method. seq.int is a primitive which can be much faster but has a few restrictions. seq_along and seq_len are very fast primitives for two common cases.

Usage

seq(...)

## Default S3 method:
seq(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
     length.out = NULL, along.with = NULL, ...)

Value

seek returns the current position (before any move), as a (numeric) byte offset from the origin, if relevant, or 0 if not. Note that the position can exceed the largest representable number in an R integer on 64-bit builds, and on some 32-bit builds.

truncate returns NULL: it stops with an error if it fails (or is not implemented).

isSeekable returns a logical value, whether the connection supports seek.

Warning

Use of seek on Windows is discouraged. We have found so many errors in the Windows implementation of file positioning that users are advised to use it only at their own risk, and asked not to waste the R developers’ time with bug reports on Windows’ deficiencies.

See Also

connections

Description

Generate regular sequences. seq is a standard generic with a default method. seq.int is a primitive which can be much faster but has a few restrictions. seq_along and seq_len are very fast primitives for two common cases.

Usage

seq(...)

## Default S3 method:
seq(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
     length.out = NULL, along.with = NULL, ...)
seq

seq.int(from, to, by, length.out, along.with, ...)

seq_along(along.with)
seq_len(length.out)

Arguments

... arguments passed to or from methods.
from, to the starting and (maximal) end values of the sequence. Of length 1 unless just
from is supplied as an unnamed argument.
by number: increment of the sequence.
length.out desired length of the sequence. A non-negative number, which for seq and
seq.int will be rounded up if fractional.
along.with take the length from the length of this argument.

Details

Numerical inputs should all be finite (that is, not infinite, NaN or NA).
The interpretation of the unnamed arguments of seq and seq.int is not standard, and it is recom-
mented always to name the arguments when programming.
seq is generic, and only the default method is described here. Note that it dispatches on the class
of the first argument irrespective of argument names. This can have unintended consequences if it
is called with just one argument intending this to be taken as along.with: it is much better to use
seq_along in that case.
seq.int is an internal generic which dispatches on methods for "seq" based on the class of the
first supplied argument (before argument matching).
Typical usages are

seq(from, to)
seq(from, to, by = )
seq(from, to, length.out = )
seq(along.with = )
seq(from)
seq(length.out = )

The first form generates the sequence from, from+/−1, ..., to (identical to from:to).
The second form generates from, from+by, ..., up to the sequence value less than or equal to to.
Specifying to ~ from and by of opposite signs is an error. Note that the computed final value can go
just beyond to to allow for rounding error, but is truncated to to. (‘Just beyond’ is by up to 10−10
times abs(from − to).)
The third generates a sequence of length.out equally spaced values from from to to. (length.out
is usually abbreviated to length or len, and seq_len is much faster.)
The fourth form generates the integer sequence 1, 2, ..., length(along.with). (along.with is
usually abbreviated to along, and seq_along is much faster.)
The fifth form generates the sequence 1, 2, ..., length(from) (as if argument along.with had
been specified), unless the argument is numeric of length 1 when it is interpreted as 1:from (even
for seq(8) for compatibility with S). Using either seq_along or seq_len is much preferred (unless
strict S compatibility is essential).
The final form generates the integer sequence 1, 2, ..., length.out unless length.out = 0, when it generates integer(0).

Very small sequences (with from - to of the order of $10^{-14}$ times the larger of the ends) will return from.

For seq (only), up to two of from, to and by can be supplied as complex values provided length.out or along.with is specified. More generally, the default method of seq will handle classed objects with methods for the Math, Ops and Summary group generics.

seq.int, seq_along and seq_len are primitive.

Value

seq.int and the default method of seq for numeric arguments return a vector of type "integer" or "double": programmers should not rely on which.

seq_along and seq_len return an integer vector, unless it is a long vector when it will be double.

References


See Also

The methods seq.Date and seq.POSIXt.

See rep, sequence, row, col.

Examples

```
seq(0, 1, length.out = 11)
seq(stats::rnorm(20)) # effectively 'along'
seq(1, 9, by = 2)    # matches 'end'
seq(1, 9, by = pi)   # stays below 'end'
seq(1, 6, by = 3)
seq(1.575, 5.125, by = 0.05)
seq(17) # same as 1:17, or even better seq_len(17)
```

seq.Date

Generate Regular Sequences of Dates

Description

The method for seq for objects of class "Date" representing calendar dates.

Usage

```
## S3 method for class 'Date'
seq(from, to, by, length.out = NULL, along.with = NULL, ...)
```
Arguments

from           starting date. Required
to             end date. Optional.
by             increment of the sequence. Optional. See ‘Details’.
length.out   integer, optional. Desired length of the sequence.
along.with    take the length from the length of this argument.
...            arguments passed to or from other methods.

Details

by can be specified in several ways.

- A number, taken to be in days.
- A object of class difftime
- A character string, containing one of "day", "week", "month", "quarter" or "year". This can optionally be preceded by a (positive or negative) integer and a space, or followed by "s". See seq.POSIXt for the details of "month".

Value

A vector of class "Date".

See Also

Date

Examples

## first days of years
seq(as.Date("1910/1/1"), as.Date("1999/1/1"), "years")
## by month
seq(as.Date("2000/1/1"), by = "month", length.out = 12)
## quarters
seq(as.Date("2000/1/1"), as.Date("2003/1/1"), by = "quarter")

## find all 7th of the month between two dates, the last being a 7th.
st <- as.Date("1998-12-17")
en <- as.Date("2000-1-7")
ll <- seq(en, st, by = "-1 month")
rev(ll[ll > st & ll < en])

seq.POSIXt
Generate Regular Sequences of Times

Description

The method for seq for date-time classes.
Usage

```r
## S3 method for class 'POSIXt'
seq(from, to, by, length.out = NULL, along.with = NULL, ...)
```

Arguments

- **from**: starting date. Required.
- **to**: end date. Optional.
- **by**: increment of the sequence. Optional. See ‘Details’.
- **length.out**: integer, optional. Desired length of the sequence.
- **along.with**: take the length from the length of this argument.
- **...**: arguments passed to or from other methods.

Details

by can be specified in several ways.

- A number, taken to be in seconds.
- A object of class `difftime`
- A character string, containing one of "sec", "min", "hour", "day", "DSTday", "week", "month", "quarter" or "year". This can optionally be preceded by a (positive or negative) integer and a space, or followed by "s".

The difference between "day" and "DSTday" is that the former ignores changes to/from daylight savings time and the latter takes the same clock time each day. "week" ignores DST (it is a period of 144 hours), but "7 DSTdays" can be used as an alternative. "month" and "year" allow for DST.

The **time zone** of the result is taken from `from`: remember that GMT means UTC (and not the time zone of Greenwich, England) and so does not have daylight savings time.

Using "month" first advances the month without changing the day: if this results in an invalid day of the month, it is counted forward into the next month: see the examples.

Value

A vector of class "POSIXct".

See Also

`DateTimeClasses`

Examples

```r
## first days of years
seq(ISOdate(1910,1,1), ISOdate(1999,1,1), "years")
```

```r
## by month
seq(ISOdate(2000,1,1), by = "month", length.out = 12)
seq(ISOdate(2000,1,31), by = "month", length.out = 4)
```

```r
## quarters
seq(ISOdate(1990,1,1), ISOdate(2000,1,1), by = "quarter") # or "3 months"
```

```r
## days vs DSTdays: use c() to lose the time zone.
seq(c(ISOdate(2000,3,20)), by = "day", length.out = 10)
seq(c(ISOdate(2000,3,20)), by = "DSTday", length.out = 10)
seq(c(ISOdate(2000,3,20)), by = "7 DSTdays", length.out = 4)
```
Create A Vector of Sequences

Description

The default method for `sequence` generates the sequence `seq(from[i], by = by[i], length.out = nvec[i])` for each element `i` in the parallel (and recycled) vectors `from`, `by` and `nvec`. It then returns the result of concatenating those sequences.

Usage

```r
sequence(nvec, ...)  
## Default S3 method:  
sequence(nvec, from = 1L, by = 1L, ...)
```

Arguments

- `nvec` coerced to a non-negative integer vector each element of which specifies the length of a sequence.
- `from` coerced to an integer vector each element of which specifies the first element of a sequence.
- `by` coerced to an integer vector each element of which specifies the step size between elements of a sequence.
- `...` additional arguments passed to methods.

Details

Negative values are supported for `from` and `by`. `sequence(nvec, from, by=0L)` is equivalent to `rep(from, each=nvec)`. This function was originally implemented in R with fewer features, but it has since become more flexible, and the default method is implemented in C for speed.

Author(s)

Of the current version, Michael Lawrence based on code from the S4Vectors Bioconductor package

See Also

- `gl`, `seq`, `rep`

Examples

```r
sequence(c(3, 2))  # the concatenated sequences 1:3 and 1:2.
#> [1] 1 2 3 1 2
sequence(c(3, 2), from=2L)
#> [1] 2 3 4 2 3
sequence(c(3, 2), from=2L, by=2L)
#> [1] 2 4 6 2 4
sequence(c(3, 2), by=c(-1L, 1L))
#> [1] 1 0 -1 1 2
```
serialize

Simple Serialization Interface

Description

A simple low-level interface for serializing to connections.

Usage

```r
serialize(object, connection, ascii, xdr = TRUE, version = NULL, refhook = NULL)
unserialize(connection, refhook = NULL)
```

Arguments

- `object` R object to serialize.
- `connection` an open connection or (for `serialize`) NULL or (for `unserialize`) a raw vector (see ‘Details’).
- `ascii` a logical. If TRUE or NA, an ASCII representation is written; otherwise (default) a binary one. See also the comments in the help for `save`.
- `xdr` a logical: if a binary representation is used, should a big-endian one (XDR) be used?
- `version` the workspace format version to use. NULL specifies the current default version (3). The only other supported value is 2, the default from R 1.4.0 to R 3.5.0.
- `refhook` a hook function for handling reference objects.

Details

The function `serialize` serializes `object` to the specified connection. If `connection` is NULL then `object` is serialized to a raw vector, which is returned as the result of `serialize`.

Sharing of reference objects is preserved within the object but not across separate calls to `serialize`.

`unserialize` reads an object (as written by `serialize`) from `connection` or a raw vector.

The `refhook` functions can be used to customize handling of non-system reference objects (all external pointers and weak references, and all environments other than namespace and package environments and `.GlobalEnv`). The hook function for `serialize` should return a character vector for references it wants to handle; otherwise it should return NULL. The hook for `unserialize` will be called with character vectors supplied to `serialize` and should return an appropriate object.

For a text-mode connection, the default value of `ascii` is set to TRUE: only ASCII representations can be written to text-mode connections and attempting to use `ascii = FALSE` will throw an error.

The format consists of a single line followed by the data: the first line contains a single character: `X` for binary serialization and `A` for ASCII serialization, followed by a new line. (The format used is identical to that used by `readRDS`.)

As almost all systems in current use are little-endian, `xdr = FALSE` can be used to avoid byte-shuffling at both ends when transferring data from one little-endian machine to another (or between processes on the same machine). Depending on the system, this can speed up serialization and unserialization by a factor of up to 3x.
Value

For serialize, NULL unless connection = NULL, when the result is returned in a raw vector.
For unserialize an R object.

Warning

These functions have provided a stable interface since R 2.4.0 (when the storage of serialized objects was changed from character to raw vectors). However, the serialization format may change in future versions of R, so this interface should not be used for long-term storage of R objects.

On 32-bit platforms a raw vector is limited to $2^{31} - 1$ bytes, but R objects can exceed this and their serializations will normally be larger than the objects.

See Also

saveRDS for a more convenient interface to serialize an object to a file or connection.
save and load to serialize and restore one or more named objects.
The ‘R Internals’ manual for details of the format used.

Examples

```r
x <- serialize(list(1, 2, 3), NULL)
unserialize(x)
```

## see also the examples for saveRDS

---

sets

Set Operations

Description

Performs set union, intersection, (asymmetric!) difference, equality and membership on two vectors.

Usage

```r
union(x, y)
intersect(x, y)
setdiff(x, y)
setequal(x, y)
is.element(el, set)
```

Arguments

- `x, y, el, set` vectors (of the same mode) containing a sequence of items (conceptually) with no duplicated values.
Details

Each of union, intersect, setdiff and setequal will discard any duplicated values in the arguments, and they apply `as.vector` to their arguments (and so in particular coerce factors to character vectors).

is.element(x, y) is identical to x %in% y.

Value

For union, a vector of a common mode.
For intersect, a vector of a common mode, or NULL if x or y is NULL.
For setdiff, a vector of the same mode as x.
A logical scalar for setequal and a logical of the same length as x for is.element.

See Also

%in%

'plotmath' for the use of union and intersect in plot annotation.

Examples

```r
(x <- c(sort(sample(1:20, 9)), NA))
(y <- c(sort(sample(3:23, 7)), NA))
union(x, y)
intersect(x, y)
setdiff(x, y)
setdiff(y, x)
setequal(x, y)

## True for all possible x & y :
setequal( union(x, y),
         c(setdiff(x, y), intersect(x, y), setdiff(y, x)))

is.element(x, y) # length 10
is.element(y, x) # length 8
```

---

**setTimeLimit**

*Set CPU and/or Elapsed Time Limits*

Description

Functions to set CPU and/or elapsed time limits for top-level computations or the current session.

Usage

```r
setTimeLimit(cpu = Inf, elapsed = Inf, transient = FALSE)

setSessionTimeLimit(cpu = Inf, elapsed = Inf)
```
Arguments
cpu, elapsed double (of length one). Set a limit on the total or elapsed cpu time in seconds, respectively.

transient logical. If TRUE, the limits apply only to the rest of the current computation.

Details

setTimeLimit sets limits which apply to each top-level computation, that is a command line (including any continuation lines) entered at the console or from a file. If it is called from within a computation the limits apply to the rest of the computation and (unless transient = TRUE) to subsequent top-level computations.

setSessionTimeLimit sets limits for the rest of the session. Once a session limit is reached it is reset to Inf.

Setting any limit has a small overhead – well under 1% on the systems measured.

Time limits are checked whenever a user interrupt could occur. This will happen frequently in \texttt{R} code and during \texttt{Sys.sleep}, but only at points in compiled C and Fortran code identified by the code author.

‘Total cpu time’ includes that used by child processes where the latter is reported.

---

\texttt{showConnections} \hspace{1cm} \textit{Display Connections}

Description

Display aspects of \texttt{connections}.

Usage

\begin{verbatim}
showConnections(all = FALSE)
getConnection(what)
closeAllConnections()

stdin()
stdout()
stderr()
nullfile()

isatty(con)

getAllConnections()
\end{verbatim}

Arguments

all logical: if true all connections, including closed ones and the standard ones are displayed. If false only open user-created connections are included.

what integer: a row number of the table given by \texttt{showConnections}.

con a connection.
showConnections

Details

stdin(), stdout() and stderr() are standard connections corresponding to input, output and error on the console respectively (and not necessarily to file streams). They are text-mode connections of class "terminal" which cannot be opened or closed, and are read-only, write-only and write-only respectively. The stdout() and stderr() connections can be re-directed by sink (and in some circumstances the output from stdout() can be split: see the help page).

The encoding for stdin() when redirected can be set by the command-line flag ‘--encoding’.

nullfile() returns filename of the null device (“/dev/null” on Unix, "nul:" on Windows).

showConnections returns a matrix of information. If a connection object has been lost or forgotten, getConnection will take a row number from the table and return a connection object for that connection, which can be used to close the connection, for example. However, if there is no R level object referring to the connection it will be closed automatically at the next garbage collection (except for gzcon connections).

closeAllConnections closes (and destroys) all user connections, restoring all sink diversions as it does so.

isatty returns true if the connection is one of the class "terminal" connections and it is apparently connected to a terminal, otherwise false. This may not be reliable in embedded applications, including GUI consoles.

getAllConnections returns a sequence of integer connection descriptors for use with getConnection, corresponding to the row names of the table returned by showConnections(all = TRUE).

Value

stdin(), stdout() and stderr() return connection objects.

showConnections returns a character matrix of information with a row for each connection, by default only for open non-standard connections.

getConnection returns a connection object, or NULL.

Note

stdin() refers to the ‘console’ and not to the C-level ‘stdin’ of the process. The distinction matters in GUI consoles (which may not have an active ‘stdin’, and if they do it may not be connected to console input), and also in embedded applications. If you want access to the C-level file stream ‘stdin’, use file("stdin").

When R is reading a script from a file, the file is the ‘console’: this is traditional usage to allow in-line data (see ‘An Introduction to R’ for an example).

See Also

closeAllConnections, isatty, nullfile, showConnections, textConnection

Examples

showConnections(all = TRUE)

## Not run:
textConnection(letters)
# oops, I forgot to record that one
showConnections()
#  class   description  mode text isopen can read can write
#3 "letters" "textConnection" "r" "text" "opened" "yes" "no"
mycon <- getConnection(3)
## End(Not run)
c(isatty(stdin()), isatty(stdout()), isatty(stderr()))

shQuote

Quote Strings for Use in OS Shells

Description

Quote a string to be passed to an operating system shell.

Usage

shQuote(string, type = c("sh", "csh", "cmd", "cmd2"))

Arguments

string a character vector, usually of length one.
type character: the type of shell quoting. Partial matching is supported. "cmd" and "cmd2" refer to the Windows shell. "cmd" is the default under Windows.

Details

The default type of quoting supported under Unix-alikes is that for the Bourne shell sh. If the string does not contain single quotes, we can just surround it with single quotes. Otherwise, the string is surrounded in double quotes, which suppresses all special meanings of metacharacters except dollar, backquote and backslash, so these (and of course double quote) are preceded by backslash. This type of quoting is also appropriate for bash, ksh and zsh.

The other type of quoting is for the C-shell (csh and tcsh). Once again, if the string does not contain single quotes, we can just surround it with single quotes. If it does contain single quotes, we can use double quotes provided it does not contain dollar or backquote (and we need to escape backslash, exclamation mark and double quote). As a last resort, we need to split the string into pieces not containing single quotes (some may be empty) and surround each with single quotes, and the single quotes with double quotes.

In Windows, command line interpretation is done by the application as well as the shell. It may depend on the compiler used: Microsoft’s rules for the C run-time are given at https://learn.microsoft.com/en-us/cpp/c-language/parsing-c-command-line-arguments?view=msvc-160. It may depend on the whim of the programmer of the application: check its documentation. The type = "cmd" prepares the string for parsing as an argument by the Microsoft’s rules and makes shQuote safe for use with many applications when used with system or system2. It surrounds the string by double quotes and escapes internal double quotes by a backslash. Any trailing backslashes and backslashes that were originally before double quotes are doubled.

The Windows cmd.exe shell (used by default with shell) uses type = "cmd2" quoting: special characters are prefixed with "^". In some cases, two types of quoting should be used: first for the application, and then type = "cmd2" for cmd.exe. See the examples below.

Value

A character vector of the same length as string.
sign

References
Discussion in PR#16636.

See Also
Quotes for quoting R code.
sQuote for quoting English text.

Examples

```r
test <- "abc$def`gh`i\j"
cat(shQuote(test), "\n")
## Not run: system(paste("echo", shQuote(test)))
test <- "don't do it!"
cat(shQuote(test), "\n")

tryit <- paste("use the", sQuote("-c"), "switch\nlike this")
cat(shQuote(tryit), "\n")
## Not run: system(paste("echo", shQuote(tryit)))
cat(shQuote(tryit, type = "csh"), "\n")

## Windows-only example, assuming cmd.exe:
perlcmd <- 'print "Hello World\n";'
## Not run:
shell(shQuote(paste("perl -e",
     shQuote(perlcmd, type = "cmd")),
     type = "cmd2"))
## End(Not run)
```

Description

sign returns a vector with the signs of the corresponding elements of x (the sign of a real number is 1, 0, or −1 if the number is positive, zero, or negative, respectively).

Note that sign does not operate on complex vectors.

Usage

```r
sign(x)
```

Arguments

- `x` a numeric vector

Details

This is an internal generic primitive function: methods can be defined for it directly or via the Math group generic.
Signals

See Also

abs

Examples

```r
sign(pi) # == 1
sign(-2:3) # -1 -1 0 1 1 1
```

Signals

Interrupting Execution of R

Description

On receiving SIGUSR1 R will save the workspace and quit. SIGUSR2 has the same result except that the `.Last` function and `on.exit` expressions will not be called.

Usage

```r
kill -USR1 pid
kill -USR2 pid
```

Arguments

```r
pid The process ID of the R process.
```

Details

The commands history will also be saved if would be at normal termination.

This is not available on Windows, and possibly on other OSes which do not support these signals.

Warning

It is possible that one or more R objects will be undergoing modification at the time the signal is sent. These objects could be saved in a corrupted form.

See Also

```r
Sys.getpid to report the process ID for future use.
```
sink diverts R output to a connection (and stops such diversions).
sink.number() reports how many diversions are in use.
sink.number(type = "message") reports the number of the connection currently being used for error messages.

Usage

sink(file = NULL, append = FALSE, type = c("output", "message"), split = FALSE)
sink.number(type = c("output", "message"))

Arguments

file a writable connection or a character string naming the file to write to, or NULL to stop sink-ing.
append logical. If TRUE, output will be appended to file; otherwise, it will overwrite the contents of file.
type character string. Either the output stream or the messages stream. The name will be partially matched so can be abbreviated.
split logical: if TRUE, output will be sent to the new sink and to the current output stream, like the Unix program tee.

Details

sink diverts R output to a connection (and must be used again to finish such a diversion, see below!). If file is a character string, a file connection with that name will be established for the duration of the diversion.

Normal R output (to connection stdout) is diverted by the default type = "output". Only prompts and (most) messages continue to appear on the console. Messages sent to stderr() (including those from message, warning and stop) can be diverted by sink(type = "message") (see below).
sink() or sink(file = NULL) ends the last diversion (of the specified type). There is a stack of diversions for normal output, so output reverts to the previous diversion (if there was one). The stack is of up to 21 connections (20 diversions).

If file is a connection it will be opened if necessary (in "wt" mode) and closed once it is removed from the stack of diversions.

split = TRUE only splits R output (via Rvprintf) and the default output from writeLines: it does not split all output that might be sent to stdout().

Sink-ing the messages stream should be done only with great care. For that stream file must be an already open connection, and there is no stack of connections.

If file is a character string, the file will be opened using the current encoding. If you want a different encoding (e.g., to represent strings which have been stored in UTF-8), use a file connection — but some ways to produce R output will already have converted such strings to the current encoding.
Value

sink returns NULL.

For sink.number() the number (0, 1, 2, ...) of diversions of output in place.

For sink.number("message") the connection number used for messages, 2 if no diversion has been used.

Warning

Do not use a connection that is open for sink for any other purpose. The software will stop you closing one such inadvertently.

Do not sink the messages stream unless you understand the source code implementing it and hence the pitfalls.

References


See Also

capture.output

Examples

sink("sink-examp.txt")
i <- 1:10
outer(i, i)
sink()

## capture all the output to a file.
z <- file("all.Rout", open = "wt")
sink(z)
sink(z, type = "message")
try(log("a"))
## revert output back to the console -- only then access the file!
sink(type = "message")
sink()
file.show("all.Rout")

slice.index  Slice Indexes in an Array

Description

Returns a matrix of integers indicating the number of their slice in a given array.

Usage

slice.index(x, MARGIN)
Arguments

\( x \) an array. If \( x \) has no dimension attribute, it is considered a one-dimensional array.

MARGIN an integer vector giving the dimension numbers to slice by.

Details

If MARGIN gives a single dimension, then all elements of slice number \( i \) with respect to this have value \( i \). In general, slice numbers are obtained by numbering all combinations of indices in the dimensions given by MARGIN in column-major order. I.e., with \( m_1, \ldots, m_k \) the dimension numbers (elements of MARGIN) sliced by and \( d_{m_1}, \ldots, d_{m_k} \) the corresponding extents, and \( n_1 = 1, n_2 = d_{m_1}, \ldots, n_k = d_{m_1} \cdots d_{m_k-1} \), the number of the slice where dimension \( m_1 \) has value \( i_1 \), \ldots, dimension \( m_k \) has value \( i_k \) is \( 1 + n_1(i_1 - 1) + \cdots + n_k(i_k - 1) \).

Value

An integer array \( y \) with dimensions corresponding to those of \( x \).

See Also

row and col for determining row and column indexes; in fact, these are special cases of slice.index corresponding to MARGIN equal to 1 and 2, respectively when \( x \) is a matrix.

Examples

\[
\begin{align*}
x & \leftarrow \text{array}(1:24, c(2, 3, 4)) \\
slice.index(x, 2) \\
slice.index(x, c(1, 3)) \\
\#\# \text{When slicing by dimensions 1 and 3, slice index 5 is obtained for} \\
\#\# \text{dimension 1 has value 1 and dimension 3 has value 3 (see above):} \\
\text{which(slice.index(x, c(1, 3)))} & = 5, \text{arr.ind} = \text{TRUE}
\end{align*}
\]

slotOp

Extract or Replace a Slot or Property

Description

Extract or replace the contents of a slot or property of an object.

Usage

object@name

object@name <- value

Arguments

object An object from a formally defined (S4) class, or an object with a class for which ‘@’ or ‘@<-' S3 methods are defined.

name The name of the slot or property, supplied as a character string or unquoted symbol. If object has an S4 class, then name must be the name of a slot in the definition of the class of object.
value  A suitable replacement value for the slot or property. For an S4 object this must be from a class compatible with the class defined for this slot in the definition of the class of object.

Details

If object is not an S4 object, then a suitable S3 method for ‘@’ or ‘@<-' is searched for. If no method is found, then an error is signaled.

If object is an S4 object, then these operators are for slot access, and are enabled only when package methods is loaded (as per default). The slot must be formally defined. (There is an exception for the name .Data, intended for internal use only.) The replacement operator checks that the slot already exists on the object (which it should if the object is really from the class it claims to be). See slot for further details, in particular for the differences between slot() and the @ operator.

These are internal generic operators: see InternalMethods.

Value

The current contents of the slot.

See Also

Extract, slot

socketSelect  Wait on Socket Connections

Description

Waits for the first of several socket connections and server sockets to become available.

Usage

socketSelect(socklist, write = FALSE, timeout = NULL)

Arguments

socklist  list of open socket connections and server sockets.
write  logical. If TRUE wait for corresponding socket to become available for writing; otherwise wait for it to become available for reading or for accepting an incoming connection (server sockets).
timeout  numeric or NULL. Time in seconds to wait for a socket to become available; NULL means wait indefinitely.

Details

The values in write are recycled if necessary to make up a logical vector the same length as socklist. Socket connections can appear more than once in socklist; this can be useful if you want to determine whether a socket is available for reading or writing.
Value

Logical the same length as socklist indicating whether the corresponding socket connection is available for output or input, depending on the corresponding value of write. Server sockets can only become available for input.

Examples

```r
## Not run:
## test whether socket connection s is available for writing or reading
socketSelect(list(s, s), c(TRUE, FALSE), timeout = 0)
## End(Not run)
```

## Not run:
```r
## test whether socket connection s is available for writing or reading
socketSelect(list(s, s), c(TRUE, FALSE), timeout = 0)
## End(Not run)
```

solve

Solve a System of Equations

Description

This generic function solves the equation \( a \odot x = b \) for \( x \), where \( b \) can be either a vector or a matrix.

Usage

```r
solve(a, b, ...)
```

## Default S3 method:
```r
solve(a, b, tol, LINPACK = FALSE, ...)
```

Arguments

- **a**: a square numeric or complex matrix containing the coefficients of the linear system. Logical matrices are coerced to numeric.
- **b**: a numeric or complex vector or matrix giving the right-hand side(s) of the linear system. If missing, \( b \) is taken to be an identity matrix and `solve` will return the inverse of \( a \).
- **tol**: the tolerance for detecting linear dependencies in the columns of \( a \). The default is `.Machine$double.eps`.
- **LINPACK**: logical. Defunct and an error.
- **...**: further arguments passed to or from other methods

Details

- \( a \) or \( b \) can be complex, but this uses double complex arithmetic which might not be available on all platforms.
- The row and column names of the result are taken from the column names of \( a \) and of \( b \) respectively. If \( b \) is missing the column names of the result are the row names of \( a \). No check is made that the column names of \( a \) match the row names of \( b \).
- For back-compatibility \( a \) can be a (real) QR decomposition, although `qr.solve` should be called in that case. `qr.solve` can handle non-square systems.
Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

What happens if `a` and/or `b` contain missing, NaN or infinite values is platform-dependent, including on the version of LAPACK in use.

tol is a tolerance for the (estimated 1-norm) 'reciprocal condition number': the check is skipped if tol <= 0.

For historical reasons, the default method accepts `a` as an object of class "qr" (with a warning) and passes it on to `solve.qr`.

### References


### See Also

`solve.qr` for the `qr` method, `chol2inv` for inverting from the Cholesky factor `backsolve`, `qr.solve`.

### Examples

```r
hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
h8 <- hilbert(8); h8
sh8 <- solve(h8)
round(sh8 %*% h8, 3)

A <- hilbert(4)
A[,] <- as.complex(A)
## might not be supported on all platforms
try(solve(A))
```

---

### sort

**Sorting or Ordering Vectors**

#### Description

Sort (or `order`) a vector or factor (partially) into ascending or descending order. For ordering along more than one variable, e.g., for sorting data frames, see `order`.
sort

Usage

sort(x, decreasing = FALSE, ...)  
## Default S3 method:
sort(x, decreasing = FALSE, na.last = NA, ...)  
sort.int(x, partial = NULL, na.last = NA, decreasing = FALSE,  
method = c("auto", "shell", "quick", "radix"), index.return = FALSE)

Arguments

x for sort an R object with a class or a numeric, complex, character or logical  
vector. For sort.int, a numeric, complex, character or logical vector, or a  
factor.
decreasing logical. Should the sort be increasing or decreasing? Not available for partial  
sorting.
... arguments to be passed to or from methods or (for the default methods and  
objects without a class) to sort.int.
na.last for controlling the treatment of NAs. If TRUE, missing values in the data are put  
last; if FALSE, they are put first; if NA, they are removed.
partial NULL or a vector of indices for partial sorting.
method character string specifying the algorithm used. Not available for partial sorting.  
Can be abbreviated.
index.return logical indicating if the ordering index vector should be returned as well. Supported by method == "radix" for any na.last mode and data type, and the  
other methods when na.last = NA (the default) and fully sorting non-factors.

Details

sort is a generic function for which methods can be written, and sort.int is the internal method  
which is compatible with S if only the first three arguments are used.
The default sort method makes use of order for classed objects, which in turn makes use  
of the generic function xtfrm (and can be slow unless a xtfrm method has been defined or  
is.numeric(x) is true).

Complex values are sorted first by the real part, then the imaginary part.
The "auto" method selects "radix" for short (less than 2^{31} elements) numeric vectors, integer  
_vectors, logical vectors and factors; otherwise, "shell".

Except for method "radix", the sort order for character vectors will depend on the collating se-
quence of the locale in use: see Comparison. The sort order for factors is the order of their levels  
(which is particularly appropriate for ordered factors).

If partial is not NULL, it is taken to contain indices of elements of the result which are to be placed  
in their correct positions in the sorted array by partial sorting. For each of the result values in a  
specified position, any values smaller than that one are guaranteed to have a smaller index in the  
sorted array and any values which are greater are guaranteed to have a bigger index in the sorted  
array. (This is included for efficiency, and many of the options are not available for partial sorting.  
It is only substantially more efficient if partial has a handful of elements, and a full sort is done  
(a Quicksort if possible) if there are more than 10.) Names are discarded for partial sorting.

Method "shell" uses Shellsort (an \(O(n^{4/3})\) variant from Sedgewick (1986)). If x has names a  
stable modification is used, so ties are not reordered. (This only matters if names are present.)
Method "quick" uses Singleton (1969)'s implementation of Hoare's Quicksort method and is only available when x is numeric (double or integer) and partial is NULL. (For other types of x Shellsort is used, silently.) It is normally somewhat faster than Shellsort (perhaps 50% faster on vectors of length a million and twice as fast at a billion) but has poor performance in the rare worst case. (Peto's modification using a pseudo-random midpoint is used to make the worst case rarer.) This is not a stable sort, and ties may be reordered.

Method "radix" relies on simple hashing to scale time linearly with the input size, i.e., its asymptotic time complexity is O(n). The specific variant and its implementation originated from the data.table package and are due to Matt Dowle and Arun Srinivasan. For small inputs (< 200), the implementation uses an insertion sort (O(n^2)) that operates in-place to avoid the allocation overhead of the radix sort. For integer vectors of range less than 100,000, it switches to a simpler and faster linear time counting sort. In all cases, the sort is stable; the order of ties is preserved. It is the default method for integer vectors and factors.

The "radix" method generally outperforms the other methods, especially for small integers. Compared to quick sort, it is slightly faster for vectors with large integer or real values (but unlike quick sort, radix is stable and supports all na.last options). The implementation is orders of magnitude faster than shell sort for character vectors, but collation does not respect the locale and so gives incorrect answers even in English locales.

However, there are some caveats for the radix sort:

- If x is a character vector, all elements must share the same encoding. Only UTF-8 (including ASCII) and Latin-1 encodings are supported. Collation follows that with LC_COLLATE=C, that is lexicographically byte-by-byte using numerical ordering of bytes.
- Long vectors (with $2^{31}$ or more elements) and complex vectors are not supported.

Value

For sort, the result depends on the S3 method which is dispatched. If x does not have a class sort.int is used and it description applies. For classed objects which do not have a specific method the default method will be used and is equivalent to x[order(x, ...)]: this depends on the class having a suitable method for [ and also that order will work, which requires a xtfrm method).

For sort.int the value is the sorted vector unless index.return is true, when the result is a list with components named x and ix containing the sorted numbers and the ordering index vector. In the latter case, if method == "quick" ties may be reversed in the ordering (unlike sort.list) as quicksort is not stable. For method == "radix", index.return is supported for all na.last modes. The other methods only support index.return when na.last is NA. The index vector refers to element numbers after removal of NAs: see order if you want the original element numbers.

All attributes are removed from the return value (see Becker et al, 1988, p.146) except names, which are sorted. (If partial is specified even the names are removed.) Note that this means that the returned value has no class, except for factors and ordered factors (which are treated specially and whose result is transformed back to the original class).

References


**See Also**

‘Comparison’ for how character strings are collated.

`order` for sorting on or reordering multiple variables.

`is.unsorted`, `rank`.

**Examples**

```r
require(stats)

x <- swiss$Education[1:25]
x; sort(x); sort(x, partial = c(10, 15))

## illustrate 'stable' sorting (of ties):
sort(c(10:3, 2:12), method = "shell", index.return = TRUE) # is stable
## $x : 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 11 12
## $ix: 9 8 10 7 11 6 12 5 13 4 14 3 15 2 16 1 17 18 19

sort(c(10:3, 2:12), method = "quick", index.return = TRUE) # is not
## $x : 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 11 12
## $ix: 9 10 8 7 11 6 12 5 13 4 14 3 15 16 2 17 1 18 19

x <- c(1:3, 3:5, 10)
is.unsorted(x)                     # FALSE: is sorted
is.unsorted(x, strictly = TRUE)   # TRUE : is not (and cannot be)
                                  # sorted strictly

## Not run:
## Small speed comparison simulation:
N <- 2000
Sim <- 20
rep <- 1000 # << adjust to your CPU
c1 <- c2 <- numeric(Sim)
for(is in seq_len(Sim)){
  x <- rnorm(N)
c1[is] <- system.time(for(i in 1:rep) sort(x, method = "shell"))[1]
c2[is] <- system.time(for(i in 1:rep) sort(x, method = "quick"))[1]
stopifnot(sort(x, method = "shell") == sort(x, method = "quick"))
}
rbind(ShellSort = c1, QuickSort = c2)
cat("Speedup factor of quick sort():\n")
summary({qq <- c1 / c2; qq[is.finite(qq)]})

## A larger test
x <- rnorm(1e7)

system.time(x1 <- sort(x, method = "shell"))
system.time(x2 <- sort(x, method = "quick"))
system.time(x3 <- sort(x, method = "radix"))
stopifnot(identical(x1, x2))
stopifnot(identical(x1, x3))

## End(Not run)
```
source: Read R Code from a File, a Connection or Expressions

Description

source causes R to accept its input from the named file or URL or connection or expressions directly. Input is read and parsed from that file until the end of the file is reached, then the parsed expressions are evaluated sequentially in the chosen environment.

withAutoprint(exprs) is a wrapper for source(exprs = exprs, ..) with different defaults. Its main purpose is to evaluate and auto-print expressions as if in a toplevel context, e.g., as in the R console.

Usage

source(file, local = FALSE, echo = verbose, print.eval = echo, exprs, spaced = use_file, verbose = getOption("verbose"), prompt.echo = getOption("prompt"), max.deparse.length = 150, width.cutoff = 60L, deparseCtrl = "showAttributes", chdir = FALSE, encoding = getOption("encoding"), continue.echo = getOption("continue"), skip.echo = 0, keep.source = getOption("keep.source"))

withAutoprint(exprs, evaluated = FALSE, local = parent.frame(), print. = TRUE, echo = TRUE, max.deparse.length = Inf, width.cutoff = max(20, getOption("width")), deparseCtrl = c("keepInteger", "showAttributes", "keepNA"), ...

Arguments

file: a connection or a character string giving the pathname of the file or URL to read from. The stdin() connection reads from the console when interactive.
local: TRUE, FALSE or an environment, determining where the parsed expressions are evaluated. FALSE (the default) corresponds to the user’s workspace (the global environment) and TRUE to the environment from which source is called.
echo: logical; if TRUE, each expression is printed after parsing, before evaluation.
print.eval, print.: logical; if TRUE, the result of eval(i) is printed for each expression i; defaults to the value of echo.
exprs: for source() and withAutoprint(*, evaluated=TRUE): instead of specifying file, an expression, call, or list of call's, but not an unevaluated “expression”.
for withAutoprint() (with default evaluated=FALSE): one or more unevaluated “expressions”.
evaluated logical indicating that exprs is passed to source(exprs= *) and hence must be evaluated, i.e., a formal expression, call or list of calls.
source

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source

spaced

logical indicating if newline (hence empty line) should be printed before each
expression (when echo = TRUE).

verbose

if TRUE, more diagnostics (than just echo = TRUE) are printed during parsing and
evaluation of input, including extra info for each expression.

prompt.echo

character; gives the prompt to be used if echo = TRUE.

max.deparse.length

integer; is used only if echo is TRUE and gives the maximal number of characters
output for the deparse of a single expression.

width.cutoff

integer, passed to deparse() which is used (only) when there are no source
references.

deparseCtrl

character vector, passed as control to deparse(), see also .deparseOpts.
In R version <= 3.3.x, this was hardcoded to "showAttributes", which is the
default currently; deparseCtrl = "all" may be preferable, when strict back
compatibility is not of importance.

chdir

logical; if TRUE and file is a pathname, the R working directory is temporarily
changed to the directory containing file for evaluating.

encoding

character vector. The encoding(s) to be assumed when file is a character string:
see file. A possible value is "unknown" when the encoding is guessed: see the
‘Encodings’ section.

continue.echo

character; gives the prompt to use on continuation lines if echo = TRUE.

skip.echo

integer; how many comment lines at the start of the file to skip if echo = TRUE.

keep.source

logical: should the source formatting be retained when echoing expressions, if
possible?

... (for withAutoprint(): further (non-file related) arguments to be passed to
source(.).

Details

Note that running code via source differs in a few respects from entering it at the R command line.
Since expressions are not executed at the top level, auto-printing is not done. So you will need
to include explicit print calls for things you want to be printed (and remember that this includes
plotting by lattice, FAQ Q7.22). Since the complete file is parsed before any of it is run, syntax
errors result in none of the code being run. If an error occurs in running a syntactically correct
script, anything assigned into the workspace by code that has been run will be kept (just as from
the command line), but diagnostic information such as traceback() will contain additional calls
to withVisible.

All versions of R accept input from a connection with end of line marked by LF (as used on Unix),
CRLF (as used on DOS/Windows) or CR (as used on classic Mac OS) and map this to newline. The
final line can be incomplete, that is missing the final end-of-line marker.

If keep.source is true (the default in interactive use), the source of functions is kept so they can be
listed exactly as input.

Unlike input from a console, lines in the file or on a connection can contain an unlimited number of
characters.

When skip.echo > 0, that many comment lines at the start of the file will not be echoed. This does
not affect the execution of the code at all. If there are executable lines within the first skip.echo
lines, echoing will start with the first of them.

If echo is true and a deparsed expression exceeds max.deparse.length, that many characters are
output followed by .... [TRUNCATED].
Encodings

By default the input is read and parsed in the current encoding of the \texttt{R} session. This is usually what is required, but occasionally re-encoding is needed, e.g. if a file from a UTF-8-using system is to be read on Windows (or vice versa).

The rest of this paragraph applies if \texttt{file} is an actual filename or URL (and not a connection). If \texttt{encoding = "unknown"}, an attempt is made to guess the encoding: the result of \texttt{localeToCharset()} is used as a guide. If \texttt{encoding} has two or more elements, they are tried in turn until the file(URL can be read without error in the trial encoding. If an actual encoding is specified (rather than the default or "unknown") in a Latin-1 or UTF-8 locale then character strings in the result will be translated to the current encoding and marked as such (see Encoding).

If \texttt{file} is a connection, it is not possible to re-encode the input inside \texttt{source}, and so the encoding argument is just used to mark character strings in the parsed input in Latin-1 and UTF-8 locales: see \texttt{parse}.

References


See Also

demo which uses source; eval, parse and scan; options("keep.source").
sys.source which is a streamlined version to source a file into an environment.

'The R Language Definition' for a discussion of source directives.

Examples

\begin{verbatim}
someCond <- 7 > 6
## want an if-clause to behave "as top level" wrt auto-printing:
## (all should look "as if on top level", e.g. non-assignments should print:)
if(someCond) withAutoprint({
x <- 1:12
x-1
(y <- (x-5)^2)
z <- y
z - 10
})

## If you want to source() a bunch of files, something like
## the following may be useful:
sourceDir <- function(path, trace = TRUE, ...) {
  op <- options(); on.exit(options(op)) # to reset after each
  for (nm in list.files(path, pattern = "[.]\[RrSsQq\]$")) {
    if(trace) cat(nm,":"
    source(file.path(path, nm), ...)
    if(trace) cat("\n")
    options(op)
  }
}
suppressWarnings( rm(x,y) ) # remove 'x' or 'y' from global env
withAutoprint({ x <- 1:2; cat("x="x,"\n"); y <- x^2 })
## x and y now exist:
stopifnot(identical(x, 1:2), identical(y, x^2))
\end{verbatim}
Special Functions of Mathematics

Description
Special mathematical functions related to the beta and gamma functions.

Usage
beta(a, b)
lbeta(a, b)
gamma(x)
lgamma(x)
psigamma(x, deriv = 0)
digamma(x)
trigamma(x)
choose(n, k)
lchoose(n, k)
factorial(x)
lfactorial(x)

Arguments
a, b non-negative numeric vectors.
x, n numeric vectors.
k, deriv integer vectors.

Details
The functions beta and lbeta return the beta function and the natural logarithm of the beta function,

\[ B(a, b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a + b)}. \]

The formal definition is

\[ B(a, b) = \int_0^1 t^{a-1}(1 - t)^{b-1}dt \]

(Abramowitz and Stegun section 6.2.1, page 258). Note that it is only defined in \( \mathbb{R} \) for non-negative \( a \) and \( b \), and is infinite if either is zero.

The functions gamma and lgamma return the gamma function \( \Gamma(x) \) and the natural logarithm of the absolute value of the gamma function. The gamma function is defined by (Abramowitz and Stegun section 6.1.1, page 255)

\[ \Gamma(x) = \int_0^\infty t^{x-1}e^{-t}dt \]

withAutoprint({ fn(sourceDir); body(sourceDir) },
               max.deparse.length = 20, verbose = TRUE)
for all real \( x \) except zero and negative integers (when NaN is returned). There will be a warning on possible loss of precision for values which are too close (within about \( 10^{-8} \)) to a negative integer less than \( -10 \).

\[ \text{factorial}(x) \text{ ! for non-negative integer } x \text{ is defined to be } \text{gamma}(x+1) \text{ and lfactorial to be lgamma}(x+1). \]

The functions digamma and trigamma return the first and second derivatives of the logarithm of the gamma function. \( \text{psigamma}(x, \text{deriv}) \) (\( \text{deriv} \geq 0 \)) computes the \( \text{deriv} \)-th derivative of \( \psi(x) \).

\[ \text{digamma}(x) = \psi(x) = \frac{d}{dx} \ln \Gamma(x) = \frac{\Gamma'(x)}{\Gamma(x)} \]

\( \psi \) and its derivatives, the psigamma() functions, are often called the ‘polygamma’ functions, e.g. in Abramowitz and Stegun (section 6.4.1, page 260); and higher derivatives (\( \text{deriv} = 2:4 \)) have occasionally been called ‘tetragamma’, ‘pentagamma’, and ‘hexagamma’.

The functions choose and lchoose return binomial coefficients and the logarithms of their absolute values. Note that choose(n, k) is defined for all real numbers \( n \) and integer \( k \). For \( k \geq 1 \) it is defined as \( n(n-1)\cdots(n-k+1)/k! \), as 1 for \( k = 0 \) and as 0 for negative \( k \). Non-integer values of \( k \) are rounded to an integer, with a warning.

choose(\( *, k \)) uses direct arithmetic (instead of lgamma calls) for small \( k \), for speed and accuracy reasons. Note the function combn (package utils) for enumeration of all possible combinations.

The gamma, lgamma, digamma and trigamma functions are internal generic primitive functions: methods can be defined for them individually or via the Math group generic.

\begin{verbatim}
Source

gamma, lgamma, beta and lbeta are based on C translations of Fortran subroutines by W. Fullerton of Los Alamos Scientific Laboratory (now available as part of SLATEC).

digamma, trigamma and psigamma for \( x \geq 0 \) are based on


For, \( x < 0 \) and \( \text{deriv} <= 5 \), the reflection formula (6.4.7) of Abramowitz and Stegun is used.
\end{verbatim}

References


Chapter 6: Gamma and Related Functions.

See Also

Arithmetic for simple, sqrt for miscellaneous mathematical functions and Bessel for the real Bessel functions.

For the incomplete gamma function see pgamma.
Examples

```r
require(graphics)

choose(5, 2)
for (n in 0:10) print(choose(n, k = 0:n))

factorial(100)
lfactorial(10000)

## gamma has 1st order poles at 0, -1, -2, ...
## this will generate loss of precision warnings, so turn off
op <- options("warn")
options(warn = -1)
x <- sort(c(seq(-3, 4, length.out = 201), outer(0:-3, (-1:1)*1e-6, `+`)))
plot(x, gamma(x), ylim = c(-20,20), col = "red", type = "l", lwd = 2,
     main = expression(Gamma(x)))
abline(h = 0, v = -3:0, lty = 3, col = "midnightblue")
options(op)

x <- seq(0.1, 4, length.out = 201); dx <- diff(x)[1]
par(mfrow = c(2, 3))
for (ch in c("", "l","di","tri","tetra","penta")) {
  is.deriv <- nchar(ch) >= 2
  nm <- paste0(ch, "gamma")
  if (is.deriv) {
    dy <- diff(y) / dx # finite difference
    der <- which(ch == c("di","tri","tetra","penta") - 1
    nm2 <- paste0("psigamma(*, deriv = ", der," )")
    nm <- if(der >= 2) nm2 else paste(nm, nm2, sep = " ==

    y <- psigamma(x, deriv = der)
  } else {
    y <- get(nm)(x)
  }
  plot(x, y, type = "l", main = nm, col = "red")
  abline(h = 0, col = "lightgray")
  if (is.deriv) lines(x[-1], dy, col = "blue", lty = 2)
}
par(mfrow = c(1, 1))

## "Extended" Pascal triangle:
F <- function(n) formatC(n, width=2)
for (n in -4:10) {
  cat(F(n),":", F(choose(n, k = -2:max(3, n+2))))
  cat("n")
}

## R code version of choose() [simplistic; warning for k \leq 0]:
mychoose <- function(r, k)
ifelse(k <= 0, (k == 0),
      sapply(k, function(k) prod(r:(r-k+1))) / factorial(k))
k <- -1:6
cbind(k = k, choose(1/2, k), mychoose(1/2, k))

## Binomial theorem for n = 1/2 ;
## sqrt(1+x) = (1+x)^(1/2) = sum_{k=0}^Inf choose(1/2, k) * x^k :
k <- 0:10 # 10 is sufficient for ~ 9 digit precision:
**split**

\[
\sqrt{1.25} \\
\text{sum}(\text{choose}(1/2, k) \times .25^k)
\]

<table>
<thead>
<tr>
<th>split</th>
<th>Divide into Groups and Reassemble</th>
</tr>
</thead>
</table>

**Description**

split divides the data in the vector x into the groups defined by f. The replacement forms replace values corresponding to such a division. unsplit reverses the effect of split.

**Usage**

split(x, f, drop = FALSE, ...)

## Default S3 method:

split(x, f, drop = FALSE, sep = ".", lex.order = FALSE, ...)

split(x, f, drop = FALSE, ...) <- value

unsplit(value, f, drop = FALSE)

**Arguments**

- **x**: vector or data frame containing values to be divided into groups.
- **f**: a `factor` in the sense that `as.factor(f)` defines the grouping, or a list of such factors in which case their interaction is used for the grouping. If x is a data frame, f can also be a formula of the form `~ g` to split by the variable g, or more generally of the form `~ g1 + ... + gk` to split by the interaction of the variables g1,...,gk, where these variables are evaluated in the data frame x using the usual non-standard evaluation rules.
- **drop**: logical indicating if levels that do not occur should be dropped (if f is a `factor` or a list).
- **value**: a list of vectors or data frames compatible with a splitting of x. Recycling applies if the lengths do not match.
- **sep**: character string, passed to `interaction` in the case where f is a `list`.
- **lex.order**: logical, passed to `interaction` when f is a list.
- **...**: further potential arguments passed to methods.

**Details**

split and split<- are generic functions with default and data.frame methods. The data frame method can also be used to split a matrix into a list of matrices, and the replacement form likewise, provided they are invoked explicitly.

unsplit works with lists of vectors or data frames (assumed to have compatible structure, as if created by split). It puts elements or rows back in the positions given by f. In the data frame case, row names are obtained by unsplitting the row name vectors from the elements of value.

f is recycled as necessary and if the length of x is not a multiple of the length of f a warning is printed.
Any missing values in f are dropped together with the corresponding values of x.

The default method calls interaction when f is a list. If the levels of the factors contain '.' the factors may not be split as expected, unless sep is set to string not present in the factor levels.

Value

The value returned from split is a list of vectors containing the values for the groups. The components of the list are named by the levels of f (after converting to a factor, or if already a factor and drop = TRUE, dropping unused levels).

The replacement forms return their right hand side. unsplit returns a vector or data frame for which split(x, f) equals value

References


See Also

cut to categorize numeric values.

strsplit to split strings.

Examples

```r
require(stats); require(graphics)
n <- 10; nn <- 100
g <- factor(round(n * runif(n * nn)))
x <- rnorm(n * nn) + sqrt(as.numeric(g))
xg <- split(x, g)
boxplot(xg, col = "lavender", notch = TRUE, varwidth = TRUE)
sapply(xg, length)
sapply(xg, mean)
### Calculate 'z-scores' by group (standardize to mean zero, variance one)
z <- unsplit(lapply(split(x, g), scale), g)

# or
zz <- x
split(zz, g) <- lapply(split(x, g), scale)

# and check that the within-group std dev is indeed one
tapply(z, g, sd)
tapply(zz, g, sd)

### data frame variation

## Notice that assignment form is not used since a variable is being added

g <- airquality$Month
l <- split(airquality, g)

## Alternative using a formula
identical(l, split(airquality, ~ Month))
```
l <- lapply(l, transform, Oz.Z = scale(Ozone))
aq2 <- unsplit(l, g)
head(aq2)
with(aq2, tapply(Oz.Z, Month, sd, na.rm = TRUE))

### Split a matrix into a list by columns
ma <- cbind(x = 1:10, y = (-4:5)^2)
split(ma, col(ma))

### Split a matrix into a list by columns
ma <- cbind(x = 1:10, y = (-4:5)^2)
split(ma, col(ma))

---

**sprintf**

*Use C-style String Formatting Commands*

**Description**

A wrapper for the C function sprintf, that returns a character vector containing a formatted combination of text and variable values.

**Usage**

```r
sprintf(fmt, ...)
ggettextf(fmt, ..., domain = NULL, trim = TRUE)
```

**Arguments**

- `fmt` a character vector of format strings, each of up to 8192 bytes.
- `...` values to be passed into `fmt`. Only logical, integer, real and character vectors are supported, but some coercion will be done: see the ‘Details’ section. Up to 100.
- `trim, domain` see `gettext`.

**Details**

`sprintf` is a wrapper for the system `sprintf` C-library function. Attempts are made to check that the mode of the values passed match the format supplied, and R’s special values (NA, Inf, -Inf and NaN) are handled correctly.

`gettextf` is a convenience function which provides C-style string formatting with possible translation of the format string.

The arguments (including `fmt`) are recycled if possible a whole number of times to the length of the longest, and then the formatting is done in parallel. Zero-length arguments are allowed and will give a zero-length result. All arguments are evaluated even if unused, and hence some types (e.g., "symbol" or "language", see `typeof`) are not allowed. Arguments unused by `fmt` result in a warning. (The format %.0s can be used to “skip” an argument.)

The following is abstracted from Kernighan and Ritchie (see References): however the actual implementation will follow the C99 standard and fine details (especially the behaviour under user error) may depend on the platform. References to numbered arguments come from POSIX.
The string `fmt` contains normal characters, which are passed through to the output string, and also conversion specifications which operate on the arguments provided through ... The allowed conversion specifications start with a `%` and end with one of the letters in the set `adifeEgGosxX%`. These letters denote the following types:

- `d, i, o, x, X` Integer value, `o` being octal, `x` and `X` being hexadecimal (using the same case for `a`-`f` as the code). Numeric variables with exactly integer values will be coerced to integer. Formats `d` and `i` can also be used for logical variables, which will be converted to `0`, `1` or `NA`.

- `f` Double precision value, in “fixed point” decimal notation of the form `"[-]mmm.ddd"`. The number of decimal places (“d”) is specified by the precision: the default is `6`; a precision of `0` suppresses the decimal point. Non-finite values are converted to `NA`, `NaN` or (perhaps a sign followed by) `Inf`.

- `e, E` Double precision value, in “exponential” decimal notation of the form `"[-]m.ddde[+-]xx` or `"[-]m.dddE[+-]xx`.

- `g, G` Double precision value, in `%e` or `%E` format if the exponent is less than `-4` or greater than or equal to the precision, and `%f` format otherwise. (The precision (default `6`) specifies the number of significant digits here, whereas in `%f`, `%e`, it is the number of digits after the decimal point.)

- `a, A` Double precision value, in binary notation of the form `"[-]0xh.hhhp[+-]d` This is a binary fraction expressed in hex multiplied by a (decimal) power of `2`. The number of hex digits after the decimal point is specified by the precision: the default is enough digits to represent exactly the internal binary representation. Non-finite values are converted to `NA`, `NaN` or (perhaps a sign followed by) `Inf`. Format `%a` uses lower-case for `x`, `p` and the hex values: format `%A` uses upper-case.

This should be supported on all platforms as it is a feature of C99. The format is not uniquely defined: although it would be possible to make the leading `h` always zero or one, this is not always done. Most systems will suppress trailing zeros, but a few do not. On a well-written platform, for normal numbers there will be a leading one before the decimal point plus (by default) `13` hexadecimal digits, hence `53` bits. The treatment of denormalized (aka ‘subnormal’) numbers is very platform-dependent.

- `s` Character string. Character `NA`s are converted to "NA".

- `%` Literal `%` (none of the extra formatting characters given below are permitted in this case).

Conversion by `as.character` is used for non-character arguments with `s` and by `as.double` for non-double arguments with `f`, `e`, `E`, `g`, `G`. NB: the length is determined before conversion, so do not rely on the internal coercion if this would change the length. The coercion is done only once, so if `length(fmt) > 1` then all elements must expect the same types of arguments.

In addition, between the initial `%` and the terminating conversion character there may be, in any order:

- `m, n` Two numbers separated by a period, denoting the field width (`m`) and the precision (`n`).
- `-` Left adjustment of converted argument in its field.
- `+` Always print number with sign: by default only negative numbers are printed with a sign.
- `a space` Prefix a space if the first character is not a sign.
- `0` For numbers, pad to the field width with leading zeros. For characters, this zero-pads on some platforms and is ignored on others.
- `#` specify “alternate output” for numbers, its action depending on the type: For `x` or `X`, `0x` or `0X` will be prefixed to a non-zero result. For `e`, `e`, `f`, `g` and `G`, the output will always have a decimal point; for `g` and `G`, trailing zeros will not be removed.
Further, immediately after \% may come 1$ to 99$ to refer to a numbered argument: this allows arguments to be referenced out of order and is mainly intended for translators of error messages. If this is done it is best if all formats are numbered: if not the unnumbered ones process the arguments in order. See the examples. This notation allows arguments to be used more than once, in which case they must be used as the same type (integer, double or character).

A field width or precision (but not both) may be indicated by an asterisk \*: in this case an argument specifies the desired number. A negative field width is taken as a '-' flag followed by a positive field width. A negative precision is treated as if the precision were omitted. The argument should be integer, but a double argument will be coerced to integer.

There is a limit of 8192 bytes on elements of \texttt{fmt}, and on strings included from a single \%letter conversion specification.

Field widths and precisions of %s conversions are interpreted as bytes, not characters, as described in the C standard.

The C doubles used for R numerical vectors have signed zeros, which \texttt{sprintf} may output as -0, -0.000 ....

\section*{Value}

A character vector of length that of the longest input. If any element of \texttt{fmt} or any character argument is declared as UTF-8, the element of the result will be in UTF-8 and have the encoding declared as UTF-8. Otherwise it will be in the current locale’s encoding.

\section*{Warning}

The format string is passed down the OS’s \texttt{sprintf} function, and incorrect formats can cause the latter to crash the R process. R does perform sanity checks on the format, but not all possible user errors on all platforms have been tested, and some might be terminal.

The behaviour on inputs not documented here is ‘undefined’, which means it is allowed to differ by platform.

\section*{Author(s)}

Original code by Jonathan Rougier.

\section*{References}


The C Standards, especially ISO/IEC 9899:1999 for ‘C99’. Links can be found at \url{https://developer.r-project.org/Portability.html}.

\url{https://pubs.opengroup.org/onlinepubs/9699919799/functions/snprintf.html} for POSIX extensions such as numbered arguments.

\texttt{man sprintf} on a Unix-alike system.

\section*{See Also}

\texttt{formatC} for a way of formatting vectors of numbers in a similar fashion.

\texttt{paste} for another way of creating a vector combining text and values.

\texttt{gettext} for the mechanisms for the automated translation of text.
Examples

## be careful with the format: most things in R are floats
## only integer-valued reals get coerced to integer.

```r
sprintf("%s is %f feet tall\n", "Sven", 7.1)    # OK
try(sprintf("%s is %i feet tall\n", "Sven", 7.1)) # not OK
    sprintf("%s is %i feet tall\n", "Sven", 7 )   # OK
```

## use a literal % :

```r
sprintf("%.0f%% said yes (out of a sample of size %.0f)", 66.666, 3)
```

## various formats of pi :

```r
sprintf("\%f", pi)
sprintf("\%.3f", pi)
sprintf("\%1.0f", pi)
sprintf("\%5.1f", pi)
sprintf("\%05.1f", pi)
sprintf("\%f", pi)
sprintf("\% f", pi)
sprintf("\%-10f", pi) # left justified
sprintf("\%e", pi)
sprintf("\%E", pi)
sprintf("\%g", pi)
sprintf("\%g", 1e6 * pi) # -> exponential
sprintf("\%g", 1e6 * pi) # -> "fixed"
traîn("\%0", 1e-6 * pi)
```

## no truncation:

```r
sprintf("\%1.f", 101)
```

## re-use one argument three times, show difference between %x and %X

```r
xx <- sprintf("%1$d %1$x %1$X", 0:15)
xx <- matrix(xx, dimnames = list(rep("", 16), "%d%x%X"))
noquote(format(xx, justify = "right"))
```

## More sophisticated:

```r
sprintf("min 10-char string '%%%s'\n", c("a", "ABC", "and an even longer one"))
```

## Platform-dependent bad example from qdapTools 1.0.0:
## may pad with spaces or zeroes.

```r
sprintf("\%09s", month.name)
```

```r
n <- 1:18
sprintf(paste0("e with %2d digits = %.", n, "g"), n, exp(1))
```

## Using arguments out of order

```r
sprintf("second %2$1.0f, first %1$5.2f, third %3$1.0f", pi, 2, 3)
```

## Using asterisk for width or precision

```r
sprintf("precision %.f, width '%%%f'\", 3, pi, 8, pi)
```

## Asterisk and argument re-use, 'e' example reiterated:
```r
sprintf("e with %1$d digits = %2.*1g", n, exp(1))

## re-cycle arguments
sprintf("%s %d", "test", 1:3)

## binary output showing rounding/representation errors
x <- seq(0, 1.0, 0.1); y <- c(0,.1,.2,.3,.4,.5,.6,.7,.8,.9,1)
cbind(x, sprintf("%a", x), sprintf("%a", y))
```

---

### Description

Single or double quote text by combining with appropriate single or double left and right quotation marks.

### Usage

```r
sQuote(x, q = getOption("useFancyQuotes"))
dQuote(x, q = getOption("useFancyQuotes"))
```

### Arguments

- **x**: an R object, to be coerced to a character vector.
- **q**: the kind of quotes to be used, see ‘Details’.

### Details

The purpose of the functions is to provide a simple means of markup for quoting text to be used in the R output, e.g., in warnings or error messages.

The choice of the appropriate quotation marks depends on both the locale and the available character sets. Older Unix/X11 fonts displayed the grave accent (ASCII code 0x60) and the apostrophe (0x27) in a way that they could also be used as matching open and close single quotation marks. Using modern fonts, or non-Unix systems, these characters no longer produce matching glyphs. Unicode provides left and right single quotation mark characters (U+2018 and U+2019); if Unicode markup cannot be assumed to be available, it seems good practice to use the apostrophe as a non-directional single quotation mark.

Similarly, Unicode has left and right double quotation mark characters (U+201C and U+201D); if only ASCII’s typewriter characteristics can be employed, than the ASCII quotation mark (0x22) should be used as both the left and right double quotation mark.

Some other locales also have the directional quotation marks, notably on Windows. TeX uses grave and apostrophe for the directional single quotation marks, and doubled grave and doubled apostrophe for the directional double quotation marks.

What rendering is used depends on `q` which by default depends on the options setting for `useFancyQuotes`. If this is FALSE then the undirectional ASCII quotation style is used. If this is TRUE (the default), Unicode directional quotes are used are used where available (currently, UTF-8 locales on Unix-alikes and all Windows locales except C): if set to "UTF-8" UTF-8 markup is used (whatever the current locale). If set to "TeX", TeX-style markup is used. Finally, if this is set to a character vector of length four, the first two entries are used for beginning and ending single
quotes and the second two for beginning and ending double quotes: this can be used to implement non-English quoting conventions such as the use of guillemets.
Where fancy quotes are used, you should be aware that they may not be rendered correctly as not all fonts include the requisite glyphs: for example some have directional single quotes but not directional double quotes.

Value

A character vector of the same length as x (after any coercion) in the current locale’s encoding.

References

Markus Kuhn, “ASCII and Unicode quotation marks”. https://www.cl.cam.ac.uk/~mgk25/ucs/quotes.html

See Also

Quotes for quoting R code.
shQuote for quoting OS commands.

Examples

op <- options("useFancyQuotes")
paste("argument", sQuote("x"), "must be non-zero")
options(useFancyQuotes = FALSE)
cat("\ndistinguish plain", sQuote("single"), "and",
   dQuote("double"), "quotes\n")
options(useFancyQuotes = TRUE)
cat("\ndistinguish fancy", sQuote("single"), "and",
   dQuote("double"), "quotes\n")
options(useFancyQuotes = "TeX")
cat("\ndistinguish TeX", sQuote("single"), "and",
   dQuote("double"), "quotes\n")
if(l10n_info()$`Latin-1`) {
  options(useFancyQuotes = c("\xab", "\xbb", "\xbf", "?"))
cat("\n", sQuote("guillemet"), "and",
   dQuote("Spanish question"), "styles\n")
} else if(l10n_info()$"UTF-8") {
  options(useFancyQuotes = c("\xc2\xab", "\xc2\xbb", "\xc2\xbf", "?"))
cat("\n", sQuote("guillemet"), "and",
   dQuote("Spanish question"), "styles\n")
}
options(op)

srcfile

References to Source Files and Code

Description

These functions are for working with source files and more generally with “source references” ("srcref"), i.e., references to source code. The resulting data is used for printing and source level debugging, and is typically available in interactive R sessions, namely when options(keep.source = TRUE).
Usage

srcfile(filename, encoding = getOption("encoding"), Enc = "unknown")
srcfilecopy(filename, lines, timestamp = Sys.time(), isFile = FALSE)
srcfilealias(filename, srcfile)
getSrcLines(srcfile, first, last)
srcref(srcfile, lloc)

## S3 method for class 'srcfile'
print(x, ...)  
## S3 method for class 'srcfile'
summary(object, ...)  
## S3 method for class 'srcfile'
open(con, line, ...)  
## S3 method for class 'srcfile'
close(con, ...)  
## S3 method for class 'srcref'
print(x, useSource = TRUE, ...)  
## S3 method for class 'srcref'
summary(object, useSource = FALSE, ...)  
## S3 method for class 'srcref'
as.character(x, useSource = TRUE, to = x, ...)
.isOpen(srcfile)

Arguments

filename The name of a file.
encoding The character encoding to assume for the file.
Enc The encoding with which to make strings: see the encoding argument of parse.
lines A character vector of source lines. Other R objects will be coerced to character.
timestamp The timestamp to use on a copy of a file.
isFile Is this srcfilecopy known to come from a file system file?
srcfile A srcfile object.
first, last, line Line numbers.
lloc A vector of four, six or eight values giving a source location; see ‘Details’.
x, object, con An object of the appropriate class.
useSource Whether to read the srcfile to obtain the text of a srcref.
to An optional second srcref object to mark the end of the character range.
... Additional arguments to the methods; these will be ignored.

Details

These functions and classes handle source code references.

The srcfile function produces an object of class srcfile, which contains the name and directory of a source code file, along with its timestamp, for use in source level debugging (not yet implemented) and source echoing. The encoding of the file is saved; see file for a discussion of encodings, and iconvlist for a list of allowable encodings on your platform.

The srcfilecopy function produces an object of the descendant class srcfilecopy, which saves the source lines in a character vector. It copies the value of the isFile argument, to help debuggers identify whether this text comes from a real file in the file system.
The `srcfilealias` function produces an object of the descendant class `srcfilealias`, which gives
an alternate name to another `srcfile`. This is produced by the parser when a `#line` directive is used.
The `getSrcLines` function reads the specified lines from `srcfile`.
The `srcref` function produces an object of class `srcref`, which describes a range of characters in
a `srcfile`. The `lloc` value gives the following values:

```r
c(first_line, first_byte, last_line, last_byte, first_column, 
   last_column, first_parsed, last_parsed)
```

Bytes (elements 2, 4) and columns (elements 5, 6) may be different due to multibyte characters. If
only four values are given, the columns and bytes are assumed to match. Lines (elements 1, 3) and
parsed lines (elements 7, 8) may differ if a `#line` directive is used in code: the former will respect
the directive, the latter will just count lines. If only 4 or 6 elements are given, the parsed lines will
be assumed to match the lines.

Methods are defined for `print`, `summary`, `open`, and `close` for classes `srcfile` and `srcfilecopy`.
The open method opens its internal `file` connection at a particular line; if it was already open, it
will be repositioned to that line.

Methods are defined for `print`, `summary` and `as.character` for class `srcref`. The `as.character`
method will read the associated source file to obtain the text corresponding to the reference. If the
to argument is given, it should be a second `srcref` that follows the first, in the same file; they will
be treated as one reference to the whole range. The exact behaviour depends on the class of the
source file. If the source file inherits from class `srcfilecopy`, the lines are taken from the saved
copy using the "parsed" line counts. If not, an attempt is made to read the file, and the original line
numbers of the `srcref` record (i.e., elements 1 and 3) are used. If an error occurs (e.g., the file no
longer exists), text like `<srcref: "file" chars 1:1 to 2:10>` will be returned instead, indicating
the line:column ranges of the first and last character. The `summary` method defaults to this type of
display.

Lists of `srcref` objects may be attached to expressions as the "srcref" attribute. (The list of
srcref objects should be the same length as the expression.) By default, expressions are printed
by `print.default` using the associated srcref. To see deparsed code instead, call `print` with
argument `useSource = FALSE`. If a `srcref` object is printed with `useSource = FALSE`, the `<srcref:
...>` record will be printed.

`.isOpen` is intended for internal use: it checks whether the connection associated with a `srcfile`
object is open.

**Value**

- `srcfile` returns a `srcfile` object.
- `srcfilecopy` returns a `srcfilecopy` object.
- `getSrcLines` returns a `srcfilecopy` object.
- `srcref` returns a `srcref` object.

**Author(s)**

Duncan Murdoch

**See Also**

`getSrcFilename` for extracting information from a source reference, or `removeSource` to remove
it from a (non-primitive) function (aka 'closure').
Examples

```r
# has timestamp
src <- srcfile(system.file("DESCRIPTION", package = "base"))
summary(src)
getSrcLines(src, 1, 4)
ref <- srcref(src, c(1, 1, 2, 1000))
ref
print(ref, useSource = FALSE)
```

Description

Errors signaled by R when stacks used in evaluation overflow.

Details

R uses several stacks in evaluating expressions: the C stack, the pointer protection stack, and the node stack used by the byte code engine. In addition, the number of nested R expressions currently under evaluation is limited by the value set as `options("expressions")`. Overflowing these stacks or limits signals an error that inherits from classes `stackOverflowError`, `error`, and `condition`.

The specific classes signaled are:

- `CStackOverflowError`: Signaled when the C stack overflows. The usage field of the error object contains the current stack usage.
- `protectStackOverflowError`: Signaled when the pointer protection stack overflows.
- `nodeStackOverflowError`: Signaled when the node stack used by the byte code engine overflows.
- `expressionStackOverflowError`: Signaled when the the evaluation depth, the number of nested R expressions currently under evaluation, exceeds the limit set by `options("expressions")`

Stack overflow errors can be caught and handled by exiting handlers established with `tryCatch()`.

Calling handlers established by `withCallingHandlers()` may fail since there may not be enough stack space to run the handler. In this case the next available exiting handler will be run, or error handling will fall back to the default handler. Default handlers set by `tryCatch("error")` may also fail to run in a stack overflow situation.

See Also

- `Cstack_info` for information on the environment and the evaluation depth limit.
- `Memory` and `options` for information on the protection stack.
standardGeneric

**Description**

The function `standardGeneric` initiates dispatch of S4 methods: see the references and the documentation of the `methods` package. Usually, calls to this function are generated automatically and not explicitly by the programmer.

**Usage**

```
standardGeneric(f, fdef)
```

**Arguments**

- `f`  
The name of the generic.
- `fdef`  
The generic function definition. Never passed when defining a new generic.

**Details**

`standardGeneric` dispatches the method defined for a generic function named `f`, using the actual arguments in the frame from which it is called.

The argument `fdef` is inserted (automatically) when dispatching methods for a primitive function. If present, it must always be the function definition for the corresponding generic. Don’t insert this argument by hand, as there is no validity checking and miss-specifying the function definition will cause certain failure.

For more, use the `methods` package, and see the documentation in `GenericFunctions`.

**Author(s)**

John Chambers

**References**


Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

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startsWith

**Description**

Determines if entries of `x` start or end with string (entries of) `prefix` or `suffix` respectively, where strings are recycled to common lengths.

**Usage**

```
startsWith(x, prefix)
endsWith(x, suffix)
```
Arguments

- **x** (character vector) whose “starts” or “ends” are considered.
- **prefix, suffix** (character vector), typically of length one, i.e., a string.

Details

`startsWith()` is equivalent to but much faster than

```r
substring(x, 1, nchar(prefix)) == prefix
```

or also

```r
grepl("^<prefix>\", x)
```

where `prefix` is not to contain special regular expression characters (and for `grepl`, `x` does not contain missing values, see below).

The code has an optimized branch for the most common usage in which `prefix` or `suffix` is of length one, and is further optimized in a UTF-8 or 8-byte locale if that is an ASCII string.

Value

A **logical** vector, of “common length” of `x` and `prefix` (or `suffix`), i.e., of the longer of the two lengths unless one of them is zero when the result is also of zero length. A shorter input is recycled to the output length.

See Also

`grepl`, `substring`; the partial string matching functions `charmatch` and `pmatch` solve a different task.

Examples

```
startsWith(search(), "package:") # typically at least two FALSE, nowadays often three

x1 <- c("Foobar", "bla bla", "something", "another", "blu", "brown", "blau blüht der Enzian") # non-ASCII
x2 <- cbind(
  startsWith(x1, "b"),
  startsWith(x1, "bl"),
  startsWith(x1, "bla"),
  endsWith(x1, "n"),
  endsWith(x1, "an"))
rownames(x2) <- x1; colnames(x2) <- c("b", "bl", "bla", "n", "an")
x2
```

```
## Non-equivalence in case of missing values in 'x', see Details:
x <- c("all", "but", NA_character_)
cbind(startsWith(x, "a"),
  substring(x, 1L, 1L) == "a",
  grepl("a", x))
```
Description

In R, the startup mechanism is as follows.

Unless ‘--no-environ’ was given on the command line, R searches for site and user files to process for setting environment variables. The name of the site file is the one pointed to by the environment variable R_ENVIRON; if this is unset, ‘R_HOME/etc/Renviron.site’ is used (if it exists, which it does not in a ‘factory-fresh’ installation). The name of the user file can be specified by the R_ENVIRON_USER environment variable; if this is unset, the files searched for are ‘.Renviron’ in the current or in the user’s home directory (in that order). See ‘Details’ for how the files are read.

Then R searches for the site-wide startup profile file of R code unless the command line option ‘--no-site-file’ was given. The path of this file is taken from the value of the R_PROFILE environment variable (after tilde expansion). If this variable is unset, the default is ‘R_HOME/etc/Rprofile.site’, which is used if it exists (which it does not in a ‘factory-fresh’ installation). This code is sourced into the workspace (global environment). Users need to be careful not to unintentionally create objects in the workspace, and it is normally advisable to use local if code needs to be executed: see the examples. .Library.site may be assigned to and the assignment will effectively modify the value of the variable in the base namespace where .libPaths() finds it. One may also assign to .First and .Last, but assigning to other variables in the execution environment is not recommended and does not work in some older versions of R.

Then, unless ‘--no-init-file’ was given, R searches for a user profile, a file of R code. The path of this file can be specified by the R_PROFILE_USER environment variable (and tilde expansion will be performed). If this is unset, a file called ‘.Rprofile’ is searched for in the current directory or in the user’s home directory (in that order). The user profile file is sourced into the workspace. Note that when the site and user profile files are sourced only the base package is loaded, so objects in other packages need to be referred to by e.g. utils::dump.frames or after explicitly loading the package concerned.

R then loads a saved image of the user workspace from ‘.RData’ in the current directory if there is one (unless ‘--no-restore-data’ or ‘--no-restore’ was specified on the command line).

Next, if a function .First is found on the search path, it is executed as .First(). Finally, function .First.sys() in the base package is run. This calls require to attach the default packages specified by options("defaultPackages"). If the methods package is included, this will have been attached earlier (by function .OptRequireMethods()) so that namespace initializations such as those from the user workspace will proceed correctly.

A function .First (and .Last) can be defined in appropriate ‘.profile’ or ‘.profile.site’ files or have been saved in ‘.RData’. If you want a different set of packages than the default ones when you start, insert a call to options in the ‘.profile’ or ‘.profile.site’ file. For example, options(defaultPackages = character()) will attach no extra packages on startup (only the base package) (or set R_DEFAULT_PACKAGES=NULL as an environment variable before running R). Using options(defaultPackages = "") or R_DEFAULT_PACKAGES="" enforces the R system default.

On front-ends which support it, the commands history is read from the file specified by the environment variable R_HISTFILE (default ‘.Rhistory’ in the current directory) unless ‘--no-restore-history’ or ‘--no-restore’ was specified.

The command-line option ‘--vanilla’ implies ‘--no-site-file’, ‘--no-init-file’, ‘--no-environ’ and (except for R CMD) ‘--no-restore’.
Details

Note that there are two sorts of files used in startup: environment files which contain lists of environment variables to be set, and profile files which contain R code.

Lines in a site or user environment file should be either comment lines starting with #, or lines of the form name=value. The latter sets the environmental variable name to value, overriding an existing value. If value contains an expression of the form ${foo-bar}, the value is that of the environmental variable foo if that is set, otherwise bar. For ${foo:-bar}, the value is that of foo if that is set to a non-empty value, otherwise bar. (If it is of the form ${foo}, the default is ".") This construction can be nested, so bar can be of the same form (as in $(foo-$ (bar-blah))). Note that the braces are essential: for example $HOME will not be interpreted.

Leading and trailing white space in value are stripped. value is then processed in a similar way to a Unix shell: in particular (single or double) quotes not preceded by backslash are removed and backslashes are removed except inside such quotes.

For readability and future compatibility it is recommended to only use constructs that have the same behavior as in a Unix shell. Hence, expansions of variables should be in double quotes (e.g. "$HOME", in case they may contain a backslash) and literals including a backslash should be in single quotes. If a variable value may end in a backslash, such as PATH on Windows, it may be necessary to protect the following quote from it, e.g. "$PATH/". It is recommended to use forward slashes instead of backslashes. It is ok to mix text in single and double quotes, see examples below.

On systems with sub-architectures (mainly Windows), the files `Renviron.site` and `Rprofile.site` are looked for first in architecture-specific directories, e.g. `R_HOME/etc/i386/Renviron.site`. And e.g. `~/.Renviron.i386` will be used in preference to `~/.Renviron`.

There is a 100,000 byte limit on the length of a line (after expansions) in environment files.

Note

It is not intended that there be interaction with the user during startup code. Attempting to do so can crash the R process.

On Unix versions of R there is also a file `R_HOME/etc/Renviron` which is read very early in the start-up processing. It contains environment variables set by R in the configure process. Values in that file can be overridden in site or user environment files: do not change `R_HOME/etc/Renviron` itself. Note that this is distinct from `R_HOME/etc/Renviron.site`.

Command-line options may well not apply to alternative front-ends: they do not apply to R.app on macOS.

R CMD check and R CMD build do not always read the standard startup files, but they do always read specific `Renviron` files. The location of these can be controlled by the environment variables R_CHECK_ENVIRON and R_BUILD_ENVIRON. If these are set their value is used as the path for the `Renviron` file; otherwise, files `~/.R/check.Renviron` or `~/.R/build.Renviron` or sub-architecture-specific versions are employed.

If you want `~/.Renviron` or `~/.Rprofile` to be ignored by child R processes (such as those run by R CMD check and R CMD build), set the appropriate environment variable R_ENVIRON_USER or R_PROFILE_USER to (if possible, which it is not on Windows) "" or to the name of a non-existent file.

See Also

For the definition of the ‘home’ directory on Windows see the ‘rw-FAQ’ Q2.14. It can be found from a running R by Sys.getenv("R_USER").
.Last for final actions at the close of an R session. commandArgs for accessing the command line arguments.

There are examples of using startup files to set defaults for graphics devices in the help for X11 and quartz.

An Introduction to R for more command-line options: those affecting memory management are covered in the help file for Memory.

readRenviron to read '.Renviron' files.

For profiling code, see Rprof.

Examples

## Not run:
## Example ~/.Renviron on Unix
R_LIBS=/R/library
PAGER=/usr/local/bin/less

## Example .Renviron on Windows
R_LIBS=C:/R/library
MY_TCLTK="c:/Program Files/Tcl/bin"

# Variable expansion in double quotes, string literals with backslashes in
# single quotes.
R_LIBS_USER="$({APPDATA})"'

## Example of setting R_DEFAULT_PACKAGES (from R CMD check)
R_DEFAULT_PACKAGES='utils,grDevices,graphics,stats'

# this loads the packages in the order given, so they appear on
# the search path in reverse order.

## Example of .Rprofile
options(width=65, digits=5)
options(show.signif.stars=FALSE)
setHook(packageEvent("grDevices", "onLoad"),
    function(...) grDevices::ps.options(horizontal=FALSE))
set.seed(1234)
.First <- function() cat("\n Welcome to R!\n\n")
.Last <- function() cat("\n Goodbye!\n\n")

## Example of Rprofile.site
local({
    # add MASS to the default packages, set a CRAN mirror
    old <- getOption("defaultPackages"); r <- getOption("repos")
    r["CRAN"] <- "http://my.local.cran"
    options(defaultPackages = c(old, "MASS"), repos = r)
    # (for Unix terminal users) set the width from COLUMNS if set
    cols <- Sys.getenv("COLUMNS")
    if(nzchar(cols)) options(width = as.integer(cols))
    # interactive sessions get a fortune cookie (needs fortunes package)
    if (interactive())
        fortunes::fortune()}
}

## if .Renviron contains
FOOBAR="coo\bar"doh\ex"abc"\def"

## then we get
stop

Description

stop stops execution of the current expression and executes an error action.
geterrmessage gives the last error message.

Usage

stop(..., call. = TRUE, domain = NULL)
geterrmessage()

Arguments

... zero or more objects which can be coerced to character (and which are pasted
together with no separator) or a single condition object.
call. logical, indicating if the call should become part of the error message.
domain see gettext. If NA, messages will not be translated.

Details

The error action is controlled by error handlers established within the executing code and by
the current default error handler set by options(error=). The error is first signaled as if using
signalCondition(). If there are no handlers or if all handlers return, then the error mes-
 sage is printed (if options("show.error.messages") is true) and the default error handler is
used. The default behaviour (the NULL error-handler) in interactive use is to return to the top level
prompt or the top level browser, and in non-interactive use to (effectively) call q("no", status =
1, runLast = FALSE). The default handler stores the error message in a buffer; it can be retrieved
by geterrmessage(). It also stores a trace of the call stack that can be retrieved by traceback().
Errors will be truncated to getOption("warning.length") characters, default 1000.
If a condition object is supplied it should be the only argument, and further arguments will be
ignored, with a warning.

Value

geterrmessage gives the last error message, as a character string ending in \"\n\".

Note

Use domain = NA whenever ... contain a result from gettextf() as that is translated already.

References

Brooks/Cole.
See Also

warning, try to catch errors and retry, and options for setting error handlers. stopifnot for validity testing. tryCatch and withCallingHandlers can be used to establish custom handlers while executing an expression.
ggettext for the mechanisms for the automated translation of messages.

Examples

iter <- 12
try(if(iter > 10) stop("too many iterations"))

tst1 <- function(...) stop("dummy error")
try(tst1(1:10, long, calling, expression))

tst2 <- function(...) stop("dummy error", call. = FALSE)
try(tst2(1:10, longcalling, expression, but.not.seen.in.Error))

---

stopifnot

Ensure the Truth of R Expressions

Description

If any of the expressions (in ... or exprs) are not all TRUE, stop is called, producing an error message indicating the first expression which was not (all) true.

Usage

stopifnot(..., exprs, exprObject, local = TRUE)

Arguments

..., exprs any number of \texttt{R} expressions, which should each evaluate to (a logical vector of all) TRUE. Use either ... or exprs, the latter typically an unevaluated expression of the form

\begin{verbatim}
{ 
  expr1 
  expr2
  ...
}
\end{verbatim}

Note that e.g., positive numbers are not TRUE, even when they are coerced to TRUE, e.g., inside if(. ) or in arithmetic computations in \texttt{R}.
If names are provided to ..., they will be used in lieu of the default error message.

exprObject alternative to exprs or ...: an ‘expression-like’ object, typically an expression, but also a call, a name, or atomic constant such as TRUE.

local (only when exprs is used:) indicates the \texttt{environment} in which the expressions should be evaluated; by default the one from where stopifnot() has been called.
Details

This function is intended for use in regression tests or also argument checking of functions, in particular to make them easier to read.

\[
\text{stopifnot}(A, B) \text{ or equivalently stopifnot}(\text{exprs} = \{A ; B\}) \text{ are conceptually equivalent to}
\]

\[
\{ \text{if(any(is.na(A)) || !all(A)) stop(...);}
\text{if(any(is.na(B)) || !all(B)) stop(...)} \}
\]

Since R version 3.6.0, \text{stopifnot()} no longer handles potential errors or warnings (by \text{tryCatch()} etc) for each single expression and may use \text{sys.call(n)} to get a meaningful and short error message in case an expression did not evaluate to all TRUE. This provides considerably less overhead.

Since R version 3.5.0, expressions are evaluated sequentially, and hence evaluation stops as soon as there is a “non-TRUE”, as indicated by the above conceptual equivalence statement.

Also, since R version 3.5.0, \text{stopifnot(exprs = \{ \ldots \})} can be used alternatively and may be preferable in the case of several expressions, as they are more conveniently evaluated interactively (“no extraneous,”).

Since R version 3.4.0, when an expression (from \ldots) is not true and is a call to \text{all.equal}, the error message will report the (first part of the) differences reported by \text{all.equal(*)}; since R 4.3.0, this happens for all calls where “all.equal” \text{pmatch()}es the function called, e.g., when that is called \text{all.equalShow}, see the example in \text{all.equal}.

Value

(\text{NULL} if all statements in \ldots are TRUE.)

Note

Trying to use the \text{stopifnot(exprs = \ldots)} version via a shortcut, say,

\[
\text{assertWRONG <- function(exprs) stopifnot(exprs = exprs)}
\]

is delicate and the above is not a good idea. Contrary to \text{stopifnot()} which takes care to evaluate the parts of \text{exprs} one by one and stop at the first non-TRUE, the above short cut would typically evaluate all parts of \text{exprs} and pass the result, i.e., typically of the last entry of \text{exprs} to \text{stopifnot()}.

However, a more careful version,

\[
\text{assert <- function(exprs) eval.parent(substitute(stopifnot(exprs = exprs)))}
\]

may be a nice short cut for \text{stopifnot(exprs = \*)} calls using the more commonly known verb as function name.

See Also

\text{stop, warning; assertCondition} in package \text{tools} complements \text{stopifnot()} for testing warnings and errors.
Examples

## NB: Some of these examples are expected to produce an error. To
## prevent them from terminating a run with example() they are
## piped into a call to try().

stopifnot(1 == 1, all.equal(pi, 3.14159265), 1 < 2) # all TRUE

m <- matrix(c(1,3,3,1), 2, 2)
stopifnot(m == t(m), diag(m) == rep(1, 2)) # all(.) => TRUE

stopifnot(length(10)) |> try() # gives an error: '1' is *not* TRUE
## even when if(1) "ok" works

stopifnot(all.equal(pi, 3.141593), 2 < 2, (1:10 < 12), "a" < "b") |> try()
## More convenient for interactive "line by line" evaluation:
stopifnot(exprs = {
  all.equal(pi, 3.1415927)
  2 < 2
  1:10 < 12
  "a" < "b"
}) |> try()

eObj <- expression(2 < 3, 3 <= 3:6, 1:10 < 2)
stopifnot(exprObject = eObj) |> try()
stopifnot(exprObject = quote(3 == 3))
stopifnot(exprObject = TRUE)

# long all.equal() error messages are abbreviated:
stopifnot(all.equal(rep(list(pi),4), list(3.1, 3.14, 3.141, 3.1415))) |> try()

# The default error message can be overridden to be more informative:
m[1,2] <- 12
stopifnot("m must be symmetric"= m == t(m)) |> try()
## Error: m must be symmetric

```r
#'' warnifnot(): a "only-warning" version of stopifnot()
#'' (Yes, learn how to use do.call(substitute, ...) in a powerful manner !!)
warnifnot <- stopifnot ; N <- length(bdy <- body(warnifnot))
bdy[1] <- do.call(substitute, list(bdy, list(stopifnot = quote(warnifnot))))
bdy[N] <- do.call(substitute, list(bdy[[N]], list(stop = quote(warning)))))
body(warnifnot) <- bdy
warnifnot(1 == 1, 1 < 2, 2 < 2) # => warns " 2 < 2 is not TRUE ",
warnifnot(exprs = {
  1 == 1
  3 < 3  # => warns "3 < 3 is not TRUE"
})
```

strptime

Date-time Conversion Functions to and from Character

Description

Functions to convert between character representations and objects of classes "POSIXlt" and "POSIXct" representing calendar dates and times.
Usage

```
## S3 method for class 'POSIXct'
format(x, format = "", tz = "", usetz = FALSE, ...)
## S3 method for class 'POSIXlt'
format(x, format = "", usetz = FALSE,
digits = getOption("digits.secs"), ...)
## S3 method for class 'POSIXt'
as.character(x, digits = if(inherits(x, "POSIXlt")) 14L else 6L,
OutDec = ".", ...)
strftime(x, format = "", tz = "", usetz = FALSE, ...)
strptime(x, format, tz = "")
```

Arguments

- **x**: An object to be converted: a character vector for `strptime`, an object which can be converted to "POSIXlt" for `strftime`.
- **tz**: A character string specifying the time zone to be used for the conversion. System-specific (see `as.POSIXlt`), but "" is the current time zone, and "GMT" is UTC. Invalid values are most commonly treated as UTC, on some platforms with a warning.
- **format**: A character string. The default for the format methods is "%Y-%m-%d
%H:%M:%S" if any element has a time component which is not midnight, and "%Y-%m-%d" otherwise. If `options("digits.secs")` is set, up to the specified number of digits will be printed for seconds.
- **...**: Further arguments to be passed from or to other methods.
- **usetz**: logical. Should the time zone abbreviation be appended to the output? This is used in printing times, and more reliable than using "%Z".
- **digits**: integer determining the `format()`ing of seconds when needed. Note that the defaults for `format()` and `as.character()` differ on purpose, `as.character()` giving close to full accuracy as it does for numbers.
- **OutDec**: a 1-character string specifying the decimal point to be used; the default is `notgetOption("OutDec")` on purpose.

Details

The format and as.character methods and strftime convert objects from the classes "POSIXlt" and "POSIXct" to character vectors.

`strptime` converts character vectors to class "POSIXlt": its input x is first converted by as.character. Each input string is processed as far as necessary for the format specified: any trailing characters are ignored.

`strftime` is a wrapper for format.POSIXlt, and it and format.POSIXct first convert to class "POSIXlt" by calling as.POSIXlt (so they also work for class "Date"). Note that only that conversion depends on the time zone. Since R version 4.2.0, as.POSIXlt() conversion now treats the non-finite numeric -Inf, Inf, NA and NaN differently (where previously all were treated as NA). Also the format() method for POSIXlt now treats these different non-finite times and dates analogously to type double.

The usual vector re-cycling rules are applied to x and format so the answer will be of length of the longer of these vectors.
Locale-specific conversions to and from character strings are used where appropriate and available. This affects the names of the days and months, the AM/PM indicator (if used) and the separators in output formats such as %x and %X, via the setting of the LC_TIME locale category. The ‘current locale’ of the descriptions might mean the locale in use at the start of the R session or when these functions are first used. (For input, the locale-specific conversions can be changed by calling Sys.setlocale with category LC_TIME (or LC_ALL). For output, what happens depends on the OS but usually works.)

The details of the formats are platform-specific, but the following are likely to be widely available: most are defined by the POSIX standard. A conversion specification is introduced by %, usually followed by a single letter or O or E and then a single letter. Any character in the format string not part of a conversion specification is interpreted literally (and %%% gives %). Widely implemented conversion specifications include

- `%a` Abbreviated weekday name in the current locale on this platform. (Also matches full name on input: in some locales there are no abbreviations of names.)
- `%A` Full weekday name in the current locale. (Also matches abbreviated name on input.)
- `%b` Abbreviated month name in the current locale on this platform. (Also matches full name on input: in some locales there are no abbreviations of names.)
- `%B` Full month name in the current locale. (Also matches abbreviated name on input.)
- `%c` Date and time. Locale-specific on output, “%a %b %e %H:%M:%S %Y” on input.
- `%C` Century (00–99): the integer part of the year divided by 100.
- `%d` Day of the month as decimal number (01–31).
- `%D` Date format such as %m/%d/%y: the C99 standard says it should be that exact format (but not all OSes comply).
- `%e` Day of the month as decimal number (1–31), with a leading space for a single-digit number.
- `%F` Equivalent to %Y-%m-%d (the ISO 8601 date format).
- `%g` The last two digits of the week-based year (see `%V`). (Accepted but ignored on input.)
- `%G` The week-based year (see `%V`) as a decimal number. (Accepted but ignored on input.)
- `%h` Equivalent to `%b`.
- `%h` Hours as decimal number (00–23). As a special exception strings such as ‘24:00:00’ are accepted for input, since ISO 8601 allows these.
- `%I` Hours as decimal number (01–12).
- `%j` Day of year as decimal number (001–366): For input, 366 is only valid in a leap year.
- `%m` Month as decimal number (01–12).
- `%M` Minute as decimal number (00–59).
- `%n` Newline on output, arbitrary whitespace on input.
- `%p` AM/PM indicator in the locale. Used in conjunction with `%I` and not with `%h`. An empty string in some locales (for example on some OSes, non-English European locales including Russia). The behaviour is undefined if used for input in such a locale.
  - Some platforms accept `%p` for output, which uses a lower-case version (%p may also use lower case): others will output P.
- `%r` For output, the 12-hour clock time (using the locale’s AM or PM): only defined in some locales, and on some OSes misleading in locales which do not define an AM/PM indicator. For input, equivalent to `%I:%M:%S %p`.
- `%R` Equivalent to `%H:%M`. 

...
%S Second as integer (00–61), allowing for up to two leap-seconds (but POSIX-compliant implementations will ignore leap seconds).
%t Tab on output, arbitrary whitespace on input.
%T Equivalent to %H:%M:%S.
%u Weekday as a decimal number (1–7, Monday is 1).
%W Week of the year as decimal number (00–53) using Monday as the first day of the week (and typically with the first Monday of the year as day 1 of week 1). The UK convention.
%V Week of the year as decimal number (01–53) as defined in ISO 8601. If the week (starting on Monday) containing 1 January has four or more days in the new year, then it is considered week 1. Otherwise, it is the last week of the previous year, and the next week is week 1. (Accepted but ignored on input.)
%W Week of the year as decimal number (0–6, Sunday is 0).
%w Weekday as decimal number (0–6, Sunday is 0).
%X Time. Locale-specific on output, "%H:%M:%S" on input.
%Y Year with century. Note that whereas there was no zero in the original Gregorian calendar, ISO 8601:2004 defines it to be valid (interpreted as 1BC): see https://en.wikipedia.org/wiki/0_(year). However, the standards also say that years before 1582 in its calendar should only be used with agreement of the parties involved.
For input, only years 0:9999 are accepted.
%Z (Output only.) Time zone abbreviation as a character string (empty if not available). This may not be reliable when a time zone has changed abbreviations over the years.

Where leading zeros are shown they will be used on output but are optional on input. Names are matched case-insensitively on input: whether they are capitalized on output depends on the platform and the locale. Note that abbreviated names are platform-specific (although the standards specify that in the ‘C’ locale they must be the first three letters of the capitalized English name: this convention is widely used in English-language locales but for example the French month abbreviations are not the same on any two of Linux, macOS, Solaris and Windows). Knowing what the abbreviations are is essential if you wish to use %a, %b or %h as part of an input format: see the examples for how to check.

When %z or %Z is used for output with an object with an assigned time zone an attempt is made to use the values for that time zone — but it is not guaranteed to succeed.

The definition of ‘whitespace’ for %n and %t is platform-dependent: for most it does not include non-breaking spaces.

Not in the standards and less widely implemented are

%k The 24-hour clock time with single digits preceded by a blank.
%l The 12-hour clock time with single digits preceded by a blank.
%s (Output only.) The number of seconds since the epoch.
strptime

%+ (Output only.) Similar to %c, often "%a %b %e %H:%M:%S %Z %Y". May depend on the locale.

For output there are also %O[DHmMVwWY] which may emit numbers in an alternative locale-dependent format (e.g., roman numerals), and %E[cCyYxX] which can use an alternative 'era' (e.g., a different religious calendar). Which of these are supported is OS-dependent. These are accepted for input, but with the standard interpretation.

Specific to R is %OSn, which for output gives the seconds truncated to $0 \leq n \leq 6$ decimal places (and if %OS is not followed by a digit, it uses the setting of getOption("digits.secs"), or if that is unset, $n = 0$). Further, for strptime %S will input seconds including fractional seconds. Note that %S does not read fractional parts on output.

The behaviour of other conversion specifications (and even if other character sequences commencing with % are conversion specifications) is system-specific. Some systems document that the use of multi-byte characters in format is unsupported: UTF-8 locales are unlikely to cause a problem.

Value

The format methods and strftime return character vectors representing the time. NA times are returned as NA_character_.

strftime turns character representations into an object of class "POSIXlt". The time zone is used to set the isdst component and to set the "tzone" attribute if tz != "". If the specified time is invalid (for example "2010-02-30 08:00") all the components of the result are NA. (NB: this does means exactly what it says – if it is an invalid time, not just a time that does not exist in some time zone.)

Printing years

Everyone agrees that years from 1000 to 9999 should be printed with 4 digits, but the standards do not define what is to be done outside that range. For years 0 to 999 most OSes pad with zeros or spaces to 4 characters, but Linux/glibc outputs just the number.

OS facilities will probably not print years before 1 CE (aka 1 AD) 'correctly' (they tend to assume the existence of a year 0: see https://en.wikipedia.org/wiki/0_(year), and some OSes get them completely wrong). Common formats are -45 and -045.

Years after 9999 and before -999 are normally printed with five or more characters.

Some platforms support modifiers from POSIX 2008 (and others). On Linux/glibc the format "%04Y" assures a minimum of four characters and zero-padding (the default is no padding). The internal code (as used on Windows and by default on macOS) uses zero-padding by default (this can be controlled by environment variable R_PAD_YEARS_BY_ZERO). On those platforms, formats %04Y, %_4Y and %_Y can be used for zero, space and no padding respectively. (On macOS, the native code (not the default) supports none of these and uses zero-padding to 4 digits.)

Time zone offsets

Offsets from GMT (also known as UTC) are part of the conversion between timezones and to/from class "POSIXct", but cause difficulties as they are often computed incorrectly.

They conventionally have the opposite sign from time-zone specifications (see Sys.timezone): positive values are East of the meridian. Although there have been time zones with offsets like +00:09:21 (Paris in 1900), and -00:44:30 (Liberia until 1972), offsets are usually treated as whole numbers of minutes, and are most often seen in RFC 5322 email headers in forms like +0800 (e.g., used on the Pacific coast of the USA in winter).

Format %z can be used for input or output: it is a character string, conventionally plus or minus followed by two digits for hours and two for minutes: the standards say that an empty string should
be output if the offset is undetermined, but some systems use +0000 or the offsets for the time zone in use for the current year. (On some platforms this works better after conversion to "POSIXct". Some platforms only recognize hour or half-hour offsets for output.) Using %z for input makes most sense with tz = "UTC".

Sources

Input uses the POSIX function `strptime` and output the C99 function `strftime`.

However, not all OSes (notably Windows) provided `strptime` and many issues were found for those which did, so since 2000 R has used a fork of code from ‘glibc’. The forked code uses the system’s `strftime` to find the locale-specific day and month names and any AM/PM indicator.

On some platforms (including Windows and by default on macOS) the system’s `strftime` is replaced (along with most of the rest of the C-level datetime code) by code modified from IANA’s ‘tzcode’ distribution (https://www.iana.org/time-zones).

Note that as `strftime` is used for output (and not `wcsftime`), argument format is translated if necessary to the session encoding.

Note

The default formats follow the rules of the ISO 8601 international standard which expresses a day as "2001-02-28" and a time as "14:01:02" using leading zeroes as here. (The ISO form uses no space, possibly ‘T’, to separate dates and times: R uses a space by default.)

For `strptime` the input string need not specify the date completely: it is assumed that unspecified seconds, minutes or hours are zero, and an unspecified year, month or day is the current one. (However, if a month is specified, the day of that month has to be specified by %d or %e since the current day of the month need not be valid for the specified month.) Some components may be returned as NA (but an unknown tzone component is represented by an empty string).

If the time zone specified is invalid on your system, what happens is system-specific but it will probably be ignored.

Remember that in most time zones some times do not occur and some occur twice because of transitions to/from ‘daylight saving’ (also known as ‘summer’) time. `strptime` does not validate such times (it does not assume a specific time zone), but conversion by `as.POSIXct` will do so. Conversion by `strftime` and formatting/printing uses OS facilities and may return nonsensical results for non-existent times at DST transitions.

In a C locale `%c` is required to be "%a %b %e %H:%M:%S %Y". As Windows does not comply (and uses a date format not understood outside N. America), that format is used by R on Windows in all locales.

There is a limit of 2048 bytes on each string produced by `strftime` and the `format` methods. As from R 4.3.0 attempting to exceed this is an error (previous versions silently truncated at 255 bytes).

References


The POSIX 1003.1 standard, which is in some respects stricter than ISO 8601.
See Also

DateTimeClasses for details of the date-time classes; locales to query or set a locale.

Your system’s help page on strftime to see how to specify their formats. (On some systems, including Windows, strftime is replaced by more comprehensive internal code.)

Examples

```r
## locale-specific version of date()
format(Sys.time(), "%a %b %d %X %Y %Z")

## time to sub-second accuracy (if supported by the OS)
format(Sys.time(), "%H:%M:%OS3")

## read in date info in format 'ddmmyyyy'
## This will give NA(s) in some non-English locales; setting the C locale as in the commented lines will overcome this on most systems.
## lct <- Sys.getlocale("LC_TIME"); Sys.setlocale("LC_TIME", "C")
x <- c("1jan1960", "2jan1960", "31mar1960", "30jul1960")
z <- strptime(x, "%d%m%Y")
## Sys.setlocale("LC_TIME", lct)

(chz <- as.character(z)) # same w/o TZ
## *here* (but not in general), the same as format():
stopifnot(exprs = {
  identical(chz, format(z))
  grepl("^1960-0[137]-[03][012] $", chz[!is.na(z)])
})

## read in date/time info in format 'm/d/y h:m:s'
dates <- c("02/27/92", "02/27/92", "01/14/92", "02/28/92", "02/01/92")
x <- paste(dates, times)
z2 <- strptime(x, "%m/%d/%y %H:%M:%S")

## *here* (but not in general), the same as format():
stopifnot(identical(format(z2), as.character(z2)))

## time with fractional seconds
z3 <- strptime("20/2/06 11:16:16.683", "%d/%m/%y %H:%M:%OS")
z3 # prints without fractional seconds by default, digits.sec = NULL ("= 0")
op <- options(digits.secs = 3)
z3 # shows the 3 extra digits
as.character(z3) # ditto
options(op)

## time zone names are not portable, but 'EST5EDT' comes pretty close.
z4 <- strptime(c("2006-01-08 10:07:52", "2006-08-07 19:33:02"),
  "%Y-%m-%d %H:%M:%S", tz = "EST5EDT")
attr(z4, "tzone")
as.character(z4)

z4$sec[2] <- pi # "very" fractional seconds
as.character(z4) # shows full precision
format(z4) # no fractional sec
format(z4, digits=8) # shows only 6 (hard-wired maximum)
format(z4, digits=4)
```


strrep

Repeat the Elements of a Character Vector

Description

Repeat the character strings in a character vector a given number of times (i.e., concatenate the respective numbers of copies of the strings).

Usage

strrep(x, times)

Arguments

x a character vector, or an object which can be coerced to a character vector using as.character.
times an integer vector giving the (non-negative) numbers of times to repeat the respective elements of x.

Details

The elements of x and times will be recycled as necessary (if one has no elements, and empty character vector is returned). Missing elements in x or times result in missing elements of the return value.

Value

A character vector with the elements of the given character vector repeated the given numbers of times.

Examples

strrep("ABC", 2)
strrep(c("A", "B", "C"), 1 : 3)
## Create vectors with the given numbers of spaces:
strrep(" ", 1 : 5)
**Description**

Split the elements of a character vector \( x \) into substrings according to the matches to substring \( \text{split} \) within them.

**Usage**

\[
\text{strsplit}(x, \text{split}, \text{fixed} = \text{FALSE}, \text{perl} = \text{FALSE}, \text{useBytes} = \text{FALSE})
\]

**Arguments**

- **x**: character vector, each element of which is to be split. Other inputs, including a factor, will give an error.
- **split**: character vector (or object which can be coerced to such) containing regular expression(s) (unless \text{fixed} = \text{TRUE}) to use for splitting. If empty matches occur, in particular if \text{split} has length 0, \( x \) is split into single characters. If \text{split} has length greater than 1, it is re-cycled along \( x \).
- **fixed**: logical. If \text{TRUE} match \text{split} exactly, otherwise use regular expressions. Has priority over \text{perl}.
- **perl**: logical. Should Perl-compatible regexps be used?
- **useBytes**: logical. If \text{TRUE} the matching is done byte-by-byte rather than character-by-character, and inputs with marked encodings are not converted. This is forced (with a warning) if any input is found which is marked as "bytes" (see \text{Encoding}).

**Details**

Argument \text{split} will be coerced to character, so you will see uses with \text{split} = \text{NULL} to mean \text{split} = \text{character(0)}, including in the examples below.

Note that splitting into single characters can be done via \text{split} = \text{character(0)} or \text{split} = ""; the two are equivalent. The definition of 'character' here depends on the locale: in a single-byte locale it is a byte, and in a multi-byte locale it is the unit represented by a 'wide character' (almost always a Unicode code point).

A missing value of \text{split} does not split the corresponding element(s) of \( x \) at all.

The algorithm applied to each input string is

\[
\text{repeat (}
\begin{align*}
&\text{if the string is empty} \\
&\quad \text{break.} \\
&\text{if there is a match} \\
&\quad \text{add the string to the left of the match to the output.} \\
&\quad \text{remove the match and all to the left of it.} \\
&\text{else} \\
&\quad \text{add the string to the output.} \\
&\quad \text{break.}
\end{align*}
\)
\]
Note that this means that if there is a match at the beginning of a (non-empty) string, the first element of the output is "", but if there is a match at the end of the string, the output is the same as with the match removed.

Invalid inputs in the current locale are warned about up to 5 times.

**Value**

A list of the same length as x, the i-th element of which contains the vector of splits of x[i].

If any element of x or split is declared to be in UTF-8 (see Encoding), all non-ASCII character strings in the result will be in UTF-8 and have their encoding declared as UTF-8. (This also holds if any element is declared to be Latin-1 except in a Latin-1 locale.) For perl = TRUE, useBytes = FALSE all non-ASCII strings in a multibyte locale are translated to UTF-8.

If any element of x or split is marked as "bytes" (see Encoding), all non-ASCII character strings created by the splitting in the result will be marked as "bytes", but encoding of the resulting character strings not split is unspecified (may be "bytes" or the original). If no element of x or split is marked as "bytes", but useBytes = TRUE, even the encoding of the resulting character strings created by splitting is unspecified (may be "bytes" or "unknown", possibly invalid in the current encoding). Mixed use of "bytes" and other marked encodings is discouraged, but if still desired one may use iconv to re-encode the result e.g. to UTF-8 with suitably substituted invalid bytes.

**See Also**

paste for the reverse, grep and sub for string search and manipulation; also nchar, substr. ‘regular expression’ for the details of the pattern specification.

Option PCRE_use_JIT controls the details when perl = TRUE.

**Examples**

noquote(strsplit("A text I want to display with spaces", NULL)[[1]])

x <- c(as = "asfef", qu = "qwerty", "yuiop\[", "b", "stuff.blah.yech")
# split x on the letter e
strsplit(x, "e")

unlist(strsplit("a.b.c", "."))
## [1] "a" "b" "c"
## Note that 'split' is a regexp!
## If you really want to split on ".", use
unlist(strsplit("a.b.c", ".", fixed = TRUE))
## a useful function: rev() for strings
strReverse <- function(x)
sapply(lapply(strsplit(x, NULL), rev), paste, collapse = "")
strReverse(c("abc", "Statistics"))

## get the first names of the members of R-core
a <- readLines(file.path(R.home("doc"),"AUTHORS"))[-(1:8)]
a <- a[0:2]-length(a)
(a <- sub(".*\", "", a))
# and reverse them
strReverse(a)

## Note that final empty strings are not produced:
strsplit(paste(c("", "a", ""), collapse=""), split="")[[1]]
# [1] "" "a"
## and also an empty string is only produced before a definite match:
strsplit("", "")[[1]] # character(0)
strsplit(" ", "")[[1]] # [1] ""

---

**strtoi**

*Convert Strings to Integers*

**Description**

Convert strings to integers according to the given base using the C function `strtol`, or choose a suitable base following the C rules.

**Usage**

```r
strtoi(x, base = 0L)
```

**Arguments**

- `x` a character vector, or something coercible to this by `as.character`.
- `base` an integer which is between 2 and 36 inclusive, or zero (default).

**Details**

Conversion is based on the C library function `strtol`.

For the default `base = 0L`, the base chosen from the string representation of that element of `x`, so different elements can have different bases (see the first example). The standard C rules for choosing the base are that octal constants (prefix `0` not followed by `x` or `X`) and hexadecimal constants (prefix `0x` or `0X`) are interpreted as base 8 and 16; all other strings are interpreted as base 10.

For a base greater than 10, letters `a` to `z` (or `A` to `Z`) are used to represent 10 to 35.

**Value**

An integer vector of the same length as `x`. Values which cannot be interpreted as integers or would overflow are returned as `NA_integer_`.

**See Also**

For decimal strings `as.integer` is equally useful.

**Examples**

```r
strtoi(c("0xff", "077", "123"))
strtoi(c("ffff", "FFFF"), 16L)
strtoi(c("177", "377"), 8L)
```
**strtrim**

**Trim Character Strings to Specified Display Widths**

**Description**
Trim character strings to specified display widths.

**Usage**
```r
strtrim(x, width)
```

**Arguments**
- `x`: a character vector, or an object which can be coerced to a character vector by `as.character`.
- `width`: Positive integer values: recycled to the length of `x`.

**Details**
‘Width’ is interpreted as the display width in a monospaced font. What happens with non-printable characters (such as backspace, tab) is implementation-dependent and may depend on the locale (e.g., they may be included in the count or they may be omitted).

Using this function rather than `substr` is important when there might be double-width (e.g., Chinese/Japanese/Korean) characters in the character vector.

**Value**
A character vector of the same length and with the same attributes as `x` (after possible coercion). Elements of the result will have the encoding declared as that of the current locale (see `Encoding`) if the corresponding input had a declared encoding and the current locale is either Latin-1 or UTF-8.

**Examples**
```r
strtrim(c("abcdef", "abcdef", "abcdef"), c(1,5,10))
```

---

**structure**

**Attribute Specification**

**Description**
`structure` returns the given object with further `attributes` set.

**Usage**
```r
structure(.Data, ...)
```

**Arguments**
- `.Data`: an object which will have various attributes attached to it.
- `...`: attributes, specified in `tag = value` form, which will be attached to data.
Adding a class "factor" will ensure that numeric codes are given integer storage mode.

For historical reasons (these names are used when deparsing), attributes ".Dim", ".Dimnames", ".Names", ".Tsp" and ".Label" are renamed to "dim", "dimnames", "names", "tsp" and "levels".

It is possible to give the same tag more than once, in which case the last value assigned wins. As with other ways of assigning attributes, using tag = NULL removes attribute tag from .Data if it is present.

References

See Also
attributes, attr.

Examples
structure(1:6, dim = 2:3)

Description
Each character string in the input is first split into paragraphs (or lines containing whitespace only). The paragraphs are then formatted by breaking lines at word boundaries. The target columns for wrapping lines and the indentation of the first and all subsequent lines of a paragraph can be controlled independently.

Usage
strwrap(x, width = 0.9 * getOption("width"), indent = 0, exdent = 0, prefix = "", simplify = TRUE, initial = prefix)

Arguments
x a character vector, or an object which can be converted to a character vector by as.character.
width a positive integer giving the target column for wrapping lines in the output.
indent a non-negative integer giving the indentation of the first line in a paragraph.
exdent a non-negative integer specifying the indentation of subsequent lines in paragraphs.
prefix, initial a character string to be used as prefix for each line except the first, for which initial is used.
simplify a logical. If TRUE, the result is a single character vector of line text; otherwise, it is a list of the same length as x the elements of which are character vectors of line text obtained from the corresponding element of x. (Hence, the result in the former case is obtained by unlisting that of the latter.)
subset

Details

Whitespace (space, tab or newline characters) in the input is destroyed. Double spaces after periods, question and explanation marks (thought as representing sentence ends) are preserved. Currently, possible sentence ends at line breaks are not considered specially.

Indentation is relative to the number of characters in the prefix string.

Value

A character vector (if simplify is TRUE), or a list of such character vectors, with declared input encodings preserved.

Examples

```r
## Read in file 'THANKS'.
x <- paste(readLines(file.path(R.home("doc"), "THANKS")), collapse = "\n")
## Split into paragraphs and remove the first three ones
x <- unlist(strsplit(x, "\n\[ \t
\]*\n")[-(1:3)])
## Join the rest
x <- paste(x, collapse = "\n\n")
## Now for some fun:
writeLines(strwrap(x, width = 60))
writeLines(strwrap(x, width = 60, indent = 5))
writeLines(strwrap(x, width = 60, exdent = 5))
writeLines(strwrap(x, prefix = "THANKS> "))

## Note that messages are wrapped AT the target column indicated by 'width' (and not beyond it).
## From an R-devel posting by J. Hosking <jh910@juno.com>.
x <- paste(sapply(sample(10, 100, replace = TRUE),
    function(x) substring("aaaaaaaaaa", 1, x)), collapse = " ")
sapply(10:40,
    function(m)
        c(target = m, actual = max(nchar(strwrap(x, m)))))
```

subset

Subsetting Vectors, Matrices and Data Frames

Description

Return subsets of vectors, matrices or data frames which meet conditions.

Usage

```r
subset(x, ...)
```

## Default S3 method:
```r
subset(x, subset, ...)
```

## S3 method for class 'matrix'
```r
subset(x, subset, select, drop = FALSE, ...)
```

## S3 method for class 'data.frame'
```r
subset(x, subset, select, drop = FALSE, ...)
```
Arguments

- **x**: object to be subsetted.
- **subset**: logical expression indicating elements or rows to keep: missing values are taken as false.
- **select**: expression, indicating columns to select from a data frame.
- **drop**: passed on to \[\] indexing operator.
- **...**: further arguments to be passed to or from other methods.

Details

This is a generic function, with methods supplied for matrices, data frames and vectors (including lists). Packages and users can add further methods.

For ordinary vectors, the result is simply `x[subsets & !is.na(subset)]`.

For data frames, the `subset` argument works on the rows. Note that `subset` will be evaluated in the data frame, so columns can be referred to (by name) as variables in the expression (see the examples).

The `select` argument exists only for the methods for data frames and matrices. It works by first replacing column names in the selection expression with the corresponding column numbers in the data frame and then using the resulting integer vector to index the columns. This allows the use of the standard indexing conventions so that for example ranges of columns can be specified easily, or single columns can be dropped (see the examples).

The `drop` argument is passed on to the indexing method for matrices and data frames: note that the default for matrices is different from that for indexing.

Factors may have empty levels after subsetting; unused levels are not automatically removed. See `droplevels` for a way to drop all unused levels from a data frame.

Value

An object similar to `x` contain just the selected elements (for a vector), rows and columns (for a matrix or data frame), and so on.

Warning

This is a convenience function intended for use interactively. For programming it is better to use the standard subsetting functions like [, and in particular the non-standard evaluation of argument `subset` can have unanticipated consequences.

Author(s)

Peter Dalgaard and Brian Ripley

See Also

-, `transform`, `droplevels`
Examples

```r
subset(airquality, Temp > 80, select = c(Ozone, Temp))
subset(airquality, Day == 1, select = -Temp)
subset(airquality, select = Ozone:Wind)

with(airquality, subset(Ozone, Temp > 80))

## sometimes requiring a logical 'subset' argument is a nuisance
nm <- rownames(state.x77)
start_with_M <- nm %in% grep("^M", nm, value = TRUE)
subset(state.x77, start_with_M, Illiteracy:Murder)
# but in recent versions of R this can simply be
subset(state.x77, grepl("^M", nm), Illiteracy:Murder)
```

---

**substitute**

Substituting and Quoting Expressions

**Description**

substitute returns the parse tree for the (unevaluated) expression expr, substituting any variables bound in env.

quote simply returns its argument. The argument is not evaluated and can be any R expression.

enquote is a simple one-line utility which transforms a call of the form `Foo(...)` into the call `quote(Foo(...))`. This is typically used to protect a call from early evaluation.

**Usage**

```r
substitute(expr, env)
quote(expr)
enquote(cl)
```

**Arguments**

- `expr` any syntactically valid R expression
- `cl` a call, i.e., an R object of class (and mode) "call".
- `env` an environment or a list object. Defaults to the current evaluation environment.

**Details**

The typical use of substitute is to create informative labels for data sets and plots. The myplot example below shows a simple use of this facility. It uses the functions deparse and substitute to create labels for a plot which are character string versions of the actual arguments to the function myplot.

Substitution takes place by examining each component of the parse tree as follows: If it is not a bound symbol in env, it is unchanged. If it is a promise object, i.e., a formal argument to a function or explicitly created using `delayedAssign()`, the expression slot of the promise replaces the symbol. If it is an ordinary variable, its value is substituted, unless env is `.GlobalEnv` in which case the symbol is left unchanged.

Both quote and substitute are 'special' primitive functions which do not evaluate their arguments.
Value

The mode of the result is generally "call" but may in principle be any type. In particular, single-variable expressions have mode "name" and constants have the appropriate base mode.

Note

substitute works on a purely lexical basis. There is no guarantee that the resulting expression makes any sense.

Substituting and quoting often cause confusion when the argument is `expression(...)`. The result is a call to the `expression` constructor function and needs to be evaluated with `eval` to give the actual expression object.

References


See Also

`missing` for argument ‘missingness’, `bquote` for partial substitution, `sQuote` and `dQuote` for adding quotation marks to strings. Quotes about forward, back, and double quotes ‘’, ‘‘’, and "".

`all.names` to retrieve the symbol names from an expression or call.

Examples

```r
require(graphics)
(s.e <- substitute(expression(a + b), list(a = 1))) #> expression(1 + b)
(s.s <- substitute( a + b, list(a = 1))) #> 1 + b
c(mode(s.e), typeof(s.e)) # "call", "language"
c(mode(s.s), typeof(s.s)) # (the same)
# but:
(e.s.e <- eval(s.e)) # expression(1 + b)
c(mode(e.s.e), typeof(e.s.e)) # "expression", "expression"
substitute(x <- x + 1, list(x = 1)) # nonsense

myplot <- function(x, y)
  plot(x, y, xlab = deparse1(substitute(x)),
       ylab = deparse1(substitute(y)))

## Simple examples about lazy evaluation, etc:

f1 <- function(x, y = x) { x <- x + 1; y }
s1 <- function(x, y = substitute(x)) { x <- x + 1; y }
s2 <- function(x, y) { if(missing(y)) y <- substitute(x); x <- x + 1; y }
a <- 10
f1(a) # 11
s1(a) # 11
s2(a) # a
typeof(s2(a)) # "symbol"
```
Description

Extract or replace substrings in a character vector.

Usage

```r
substr(x, start, stop)
substring(text, first, last = 1000000L)
```

```r
substr(x, start, stop) <- value
substring(text, first, last = 1000000L) <- value
```

Arguments

- `x, text`: a character vector.
- `start, first`: integer. The first element to be extracted or replaced.
- `stop, last`: integer. The last element to be extracted or replaced.
- `value`: a character vector, recycled if necessary.

Details

`substring` is compatible with S, with `first` and `last` instead of `start` and `stop`. For vector arguments, it expands the arguments cyclically to the length of the longest `provided` none are of zero length.

When extracting, if `start` is larger than the string length then "" is returned.

For the extraction functions, `x` or `text` will be converted to a character vector by `as.character` if it is not already one.

For the replacement functions, if `start` is larger than the string length then no replacement is done. If the portion to be replaced is longer than the replacement string, then only the portion the length of the string is replaced.

If any argument is an `NA` element, the corresponding element of the answer is `NA`.

Elements of the result will be have the encoding declared as that of the current locale (see `Encoding`) if the corresponding input had a declared Latin-1 or UTF-8 encoding and the current locale is either Latin-1 or UTF-8.

If an input element has declared "bytes" encoding (see `Encoding`), the subsetting is done in units of bytes not characters.

Value

For `substr`, a character vector of the same length and with the same attributes as `x` (after possible coercion).

For `substring`, a character vector of length the longest of the arguments. This will have names taken from `x` (if it has any after coercion, repeated as needed), and other attributes copied from `x` if it is the longest of the arguments).
For the replacement functions, a character vector of the same length as \( x \) or \( \text{text} \), with attributes such as \text{names} preserved. Elements of \( x \) or \( \text{text} \) with a declared encoding (see \text{Encoding}) will be returned with the same encoding.

**Note**

The S version of \text{substring}<- ignores last; this version does not. These functions are often used with \text{nchar} to truncate a display. That does not really work (you want to limit the width, not the number of characters, so it would be better to use \text{strtrim}), but at least make sure you use the default \text{nchar}(\text{type} = \text{"c"}).

**References**


**See Also**

\text{strsplit}, \text{paste}, \text{nchar}.

**Examples**

```r
substr("abcdef", 2, 4)
substring("abcdef", 1:6, 1:6)
## strsplit() is more efficient ...
substr(rep("abcdef", 4), 1:4, 4:5)
x <- c("asfef", "qwerty", "yuiop", "b", "stuff.blah.yech")
substring(x, 2, 5)
substring(x, 2, 4:6)

X <- x
names(X) <- LETTERS[seq_along(x)]
comment(X) <- noquote("is a named vector")
str(aX <- attributes(X))
substring(x, 2) <- c("..", "+++")
substring(X, 2) <- c("..", "+++")
X
stopifnot(x == X, identical(aX, attributes(X)), nzchar(comment(X)))
```

---

### sum

**Sum of Vector Elements**

**Description**

sum returns the sum of all the values present in its arguments.

**Usage**

```r
sum(..., na.rm = FALSE)
```
Arguments

... numeric or complex or logical vectors.
na.rm logical. Should missing values (including NaN) be removed?

Details

This is a generic function: methods can be defined for it directly or via the Summary group generic. For this to work properly, the arguments ... should be unnamed, and dispatch is on the first argument.

If na.rm is FALSE an NA or NaN value in any of the arguments will cause a value of NA or NaN to be returned, otherwise NA and NaN values are ignored.

Logical true values are regarded as one, false values as zero. For historical reasons, NULL is accepted and treated as if it were integer(0).

Loss of accuracy can occur when summing values of different signs: this can even occur for sufficiently long integer inputs if the partial sums would cause integer overflow. Where possible extended-precision accumulators are used, typically well supported with C99 and newer, but possibly platform-dependent.

Value

The sum. If all of the ... arguments are of type integer or logical, then the sum is integer when possible and is double otherwise. Integer overflow should no longer happen since R version 3.5.0. For other argument types it is a length-one numeric (double) or complex vector.

NB: the sum of an empty set is zero, by definition.

S4 methods

This is part of the S4 Summary group generic. Methods for it must use the signature x, ..., na.rm.

'plotmath' for the use of sum in plot annotation.

References


See Also

colSums for row and column sums.

Examples

## Pass a vector to sum, and it will add the elements together.
sum(1:5)

## Pass several numbers to sum, and it also adds the elements.
sum(1, 2, 3, 4, 5)

## In fact, you can pass vectors into several arguments, and everything gets added.
sum(1:2, 3:5)

## If there are missing values, the sum is unknown, i.e., also missing, ....
sum(1:5, NA)
## ... unless we exclude missing values explicitly:
sum(1:5, NA, na.rm = TRUE)

### summary

#### Object Summaries

**Description**

`summary` is a generic function used to produce result summaries of the results of various model fitting functions. The function invokes particular methods which depend on the `class` of the first argument.

**Usage**

```r
summary(object, ...)```

- **Default S3 method:**
  ```r
  summary(object, ..., digits, quantile.type = 7)
  ```

- **S3 method for class 'data.frame':**
  ```r
  summary(object, maxsum = 7, 
          digits = max(3, getOption("digits")-3), ...)
  ```

- **S3 method for class 'factor':**
  ```r
  summary(object, maxsum = 100, ...)
  ```

- **S3 method for class 'matrix':**
  ```r
  summary(object, ...)
  ```

- **S3 method for class 'summaryDefault':**
  ```r
  format(x, digits = max(3L, getOption("digits") - 3L), ...)
  ```

- **S3 method for class 'summaryDefault':**
  ```r
  print(x, digits = max(3L, getOption("digits") - 3L), ...)
  ```

**Arguments**

- `object` an object for which a summary is desired.
- `x` a result of the default method of `summary()`. 
- `maxsum` integer, indicating how many levels should be shown for factors.
- `digits` integer, used for number formatting with `signif()` (for `summary.default`) or `format()` (for `summary.data.frame`). In `summary.default`, if not specified (i.e., `missing()`), `signif()` will not be called anymore (since R >= 3.4.0, where the default has been changed to only round in the print and format methods).
- `quantile.type` integer code used in `quantile(*, type=quantile.type)` for the default method.
- `...` additional arguments affecting the summary produced.
svd

Singular Value Decomposition of a Matrix

Description
Compute the singular-value decomposition of a rectangular matrix.

Usage

svd(x, nu = min(n, p), nv = min(n, p), LINPACK = FALSE)
La.svd(x, nu = min(n, p), nv = min(n, p))
Arguments

- `x` (a numeric or complex matrix) whose SVD decomposition is to be computed. Logical matrices are coerced to numeric.
- `nu` (the number of left singular vectors to be computed. This must be between 0 and \( n = nrow(x) \)).
- `nv` (the number of right singular vectors to be computed. This must be between 0 and \( p = ncol(x) \)).
- `LINPACK` (logical. Defunct and an error).

Details

The singular value decomposition plays an important role in many statistical techniques. `svd` and `La.svd` provide two interfaces which differ in their return values.

Computing the singular vectors is the slow part for large matrices. The computation will be more efficient if both \( nu \leq \min(n, p) \) and \( nv \leq \min(n, p) \), and even more so if both are zero.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code (most often 1): these can only be interpreted by detailed study of the FORTRAN code but mean that the algorithm failed to converge.

Missing, NaN or infinite values in `x` will give an error.

Value

The SVD decomposition of the matrix as computed by LAPACK,

\[ X = UDV', \]

where \( U \) and \( V \) are orthogonal, \( V' \) means \( V \) transposed (and conjugated for complex input), and \( D \) is a diagonal matrix with the (non-negative) singular values \( D_{ii} \) in decreasing order. Equivalently, \( D = U'XV \), which is verified in the examples.

The returned value is a list with components

- `d` (a vector containing the singular values of `x`, of length \( \min(n, p) \), sorted decreasingly).
- `u` (a matrix whose columns contain the left singular vectors of `x`, present if \( nu > 0 \). Dimension \( c(n, nu) \)).
- `v` (a matrix whose columns contain the right singular vectors of `x`, present if \( nv > 0 \). Dimension \( c(p, nv) \)).

Recall that the singular vectors are only defined up to sign (a constant of modulus one in the complex case). If a left singular vector has its sign changed, changing the sign of the corresponding right vector gives an equivalent decomposition.

For `La.svd` the return value replaces `v` by `vt`, the (conjugated if complex) transpose of `v`.

Source

The main functions used are the LAPACK routines `DGESDD` and `ZGESDD`.

LAPACK is from [https://netlib.org/lapack/](https://netlib.org/lapack/) and its guide is listed in the references.
sweep

References


The ‘Singular-value decomposition’ Wikipedia article.

Brooks/Cole.

See Also
eigen, qr.

Examples

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, `+`) }
X <- hilbert(9)[, 1:6]
(s <- svd(X))
D <- diag(s$d)
s$u %*% D %*% t(s$v) # X = U D V'
t(s$u) %*% X %*% s$v # D = U' X V

sweep

Sweep out Array Summaries

Description

Return an array obtained from an input array by sweeping out a summary statistic.

Usage

sweep(x, MARGIN, STATS, FUN = "-", check.margin = TRUE, ...)

Arguments

x an array, including a matrix.
MARGIN a vector of indices giving the extent(s) of x which correspond to STATS. Where
x has named dimnames, it can be a character vector selecting dimension names.
STATS the summary statistic which is to be swept out.
FUN the function to be used to carry out the sweep.
check.margin logical. If TRUE (the default), warn if the length or dimensions of STATS do not
match the specified dimensions of x. Set to FALSE for a small speed gain when
you know that dimensions match.
... optional arguments to FUN.
sweep

Details

FUN is found by a call to \texttt{match.fun}. As in the default, binary operators can be supplied if quoted or back quoted.

FUN should be a function of two arguments: it will be called with arguments \( x \) and an array of the same dimensions generated from \texttt{STATS} by \texttt{aperm}.

The consistency check among \texttt{STATS}, \texttt{MARGIN} and \( x \) is stricter if \texttt{STATS} is an array than if it is a vector. In the vector case, some kinds of recycling are allowed without a warning. Use \texttt{sweep}(\( x \), \texttt{MARGIN}, \texttt{as.array}({\texttt{STATS}})) if \texttt{STATS} is a vector and you want to be warned if any recycling occurs.

Value

An array with the same shape as \( x \), but with the summary statistics swept out.

References


See Also

\texttt{apply} on which \texttt{sweep} used to be based; \texttt{scale} for centering and scaling.

Examples

\begin{verbatim}
require(stats) # for median
med.att <- apply(attitude, 2, median)
sweep(data.matrix(attitude), 2, med.att) # subtract the column medians

## More sweeping:
A <- array(1:24, dim = 4:2)

## no warnings in normal use
sweep(A, 1, 5)
(A.min <- apply(A, 1, min)) # == 1:4
sweep(A, 1, A.min)
sweep(A, 1:2, apply(A, 1:2, median))

## warnings when mismatch
sweep(A, 1, 1:3) # STATS does not recycle
sweep(A, 1, 6:1) # STATS is longer

## exact recycling:
sweep(A, 1, 1:2) # no warning
sweep(A, 1, as.array(1:2)) # warning

## Using named dimnames

dimnames(A) <- list(fee=1:4, fie=1:3, fum=1:2)

mn_fum_fie <- apply(A, c("fum", "fie"), mean)
mn_fum_fie
sweep(A, c("fum", "fie"), mn_fum_fie)
\end{verbatim}
Description

`switch` evaluates `EXPR` and accordingly chooses one of the further arguments (in ...).

Usage

`switch(EXPR, ...)`

Arguments

- `EXPR` an expression evaluating to a number or a character string.
- `...` the list of alternatives. If it is intended that `EXPR` has a character-string value these will be named, perhaps except for one alternative to be used as a ‘default’ value.

Details

`switch` works in two distinct ways depending whether the first argument evaluates to a character string or a number.

If the value of `EXPR` is not a character string it is coerced to integer. Note that this also happens for `factors`, with a warning, as typically the character level is meant. If the integer is between 1 and `nargs()-1` then the corresponding element of `...` is evaluated and the result returned: thus if the first argument is 3 then the fourth argument is evaluated and returned.

If `EXPR` evaluates to a character string then that string is matched (exactly) to the names of the elements in `...`. If there is a match then that element is evaluated unless it is missing, in which case the next non-missing element is evaluated, so for example `switch("cc", a = 1, cc =, cd =, d = 2)` evaluates to 2. If there is more than one match, the first matching element is used. In the case of no match, if there is an unnamed element of `...` its value is returned. (If there is more than one such argument an error is signaled.)

The first argument is always taken to be `EXPR`: if it is named its name must (partially) match.

A warning is signaled if no alternatives are provided, as this is usually a coding error.

This is implemented as a `primitive` function that only evaluates its first argument and one other if one is selected.

Value

The value of one of the elements of `...`, or `NULL`, invisibly (whenever no element is selected).

The result has the visibility (see `invisible`) of the element evaluated.

Warning

It is possible to write calls to `switch` that can be confusing and may not work in the same way in earlier versions of R. For compatibility (and clarity), always have `EXPR` as the first argument, naming it if partial matching is a possibility. For the character-string form, have a single unnamed argument as the default after the named values.
References


Examples

```r
require(stats)
centre <- function(x, type) {
  switch(type,
    mean = mean(x),
    median = median(x),
    trimmed = mean(x, trim = .1))
}
x <- rcauchy(10)
centre(x, "mean")
centre(x, "median")
centre(x, "trimmed")

ccc <- c("b","QQ","a","A","bb")
# note: cat() produces no output for NULL
for(ch in ccc)
  cat(ch,":", switch(EXPR = ch, a = 1, b = 2:3), "\n")
for(ch in ccc)
  cat(ch,":", switch(EXPR = ch, a =, A = 1, b = 2:3, "Otherwise: last"),"\n")

## switch(f, *) with a factor f
ff <- gl(3,1, labels=LETTERS[3:1])
ff[1] # C
## so one might expect " is C" here, but
switch(ff[1], A = "I am A", B="Bb..", C=" is C")# -> "I am A"
## so we give a warning
## Numeric EXPR does not allow a default value to be specified
## -- it is always NULL
for(i in c(-1:3, 9)) print(switch(i, 1, 2 , 3, 4))

## visibility
switch(1, invisible(pi), pi)
switch(2, invisible(pi), pi)
```

Syntax

**Operator Syntax and Precedence**

Description

Outlines R syntax and gives the precedence of operators.

Details

The following unary and binary operators are defined. They are listed in precedence groups, from highest to lowest.

:: access variables in a namespace
Within an expression operators of equal precedence are evaluated from left to right except where indicated. (Note that = is not necessarily an operator.)

The binary operators ::, :::, $ and @ require names or string constants on the right hand side, and the first two also require them on the left.

The links in the See Also section cover most other aspects of the basic syntax.

Note

There are substantial precedence differences between R and S. In particular, in S ? has the same precedence as (binary) + - and && || have equal precedence.

References


See Also

Arithmetic, Comparison, Control, Extract, Logic, NumericConstants, Paren, Quotes, Reserved.

The ‘R Language Definition’ manual.

Examples

## Logical AND ("&&") has higher precedence than OR ("||"): TRUE || TRUE && FALSE # is the same as (TRUE || TRUE) && FALSE

## Special operators have higher precedence than "!" (logical NOT).
## You can use this for %in%:
! 1:10 %in% c(2, 3, 5, 7) # same as !(1:10 %in% c(2, 3, 5, 7))
## but we strongly advise to use the "!( ... )" form in this case!
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Sys.getenv

## '=' has lower precedence than '<-' ... so you should not mix them
##
(and '<-' is considered better style anyway):
## Not run: ## Consequently, this gives a ("non-catchable") error
x <- y = 5 #-> Error in (x <- y) = 5 : ....
## End(Not run)

Sys.getenv

Get Environment Variables

Description
Sys.getenv obtains the values of the environment variables.
Usage
Sys.getenv(x = NULL, unset = "", names = NA)
Arguments
x

a character vector, or NULL.

unset

a character string.

names

logical: should the result be named? If NA (the default) single-element results
are not named whereas multi-element results are.

Details
Both arguments will be coerced to character if necessary.
Setting unset = NA will enable unset variables and those set to the value "" to be distinguished, if
the OS does. POSIX requires the OS to distinguish, and all known current R platforms do.
Value
A vector of the same length as x, with (if names == TRUE) the variable names as its names attribute.
Each element holds the value of the environment variable named by the corresponding component
of x (or the value of unset if no environment variable with that name was found).
On most platforms Sys.getenv() will return a named vector giving the values of all the environment variables, sorted in the current locale. It may be confused by names containing = which some
platforms allow but POSIX does not. (Windows is such a platform: there names including = are
truncated just before the first =.)
When x is missing and names is not false, the result is of class "Dlist" in order to get a nice print
method.
See Also
Sys.setenv, Sys.getlocale for the locale in use, getwd for the working directory.
The help for ‘environment variables’ lists many of the environment variables used by R.


Sys.getpid

Description
Get the process ID of the R Session. It is guaranteed by the operating system that two R sessions running simultaneously will have different IDs, but it is possible that R sessions running at different times will have the same ID.

Usage
Sys.getpid()

Value
An integer, often between 1 and 32767 under Unix-alikes (but for example FreeBSD and macOS use IDs up to 99999) and a positive integer (up to 32767) under Windows.

Examples
Sys.getpid()

## Show files opened from this R process
if(.Platform$OS.type == "unix") ## on Unix-alikes such Linux, macOS, FreeBSD:
  system(paste("lsof -p", Sys.getpid()))

Sys.glob

Wildcard Expansion on File Paths

Description
Function to do wildcard expansion (also known as ‘globbing’) on file paths.

Usage
Sys.glob(paths, dirmark = FALSE)
Arguments

paths character vector of patterns for relative or absolute filepaths. Missing values will be ignored.

dirmark logical: should matches to directories from patterns that do not already end in / have a slash appended? May not be supported on all platforms.

Details

This expands tilde (see tilde expansion) and wildcards in file paths. For precise details of wildcards expansion, see your system’s documentation on the glob system call. There is a POSIX 1003.2 standard (see https://pubs.opengroup.org/onlinepubs/9699917999/functions/glob.html) but some OSes will go beyond this.

All systems should interpret * (match zero or more characters), ? (match a single character) and (probably) [ (begin a character class or range). The handling of paths ending with a separator is system-dependent. On a POSIX-2008 compliant OS they will match directories (only), but as they are not valid filepaths on Windows, they match nothing there. (Earlier POSIX standards allowed them to match files.)

The rest of these details are indicative (and based on the POSIX standard).

If a filename starts with . this may need to be matched explicitly: for example Sys.glob("*.RData") may or may not match `.RData` but will not usually match `.aa.RData`. Note that this is platform-dependent: e.g. on Solaris Sys.glob("*.*") matches `.` and `..`.

[ begins a character class. If the first character in [...] is not !, this is a character class which matches a single character against any of the characters specified. The class cannot be empty, so ] can be included provided it is first. If the first character is !, the character class matches a single character which is none of the specified characters. Whether . in a character class matches a leading . in the filename is OS-dependent.

Character classes can include ranges such as [A-Z]: include ~ as a character by having it first or last in a class. (The interpretation of ranges should be locale-specific, so the example is not a good idea in an Estonian locale.)

One can remove the special meaning of ?, * and [ by preceding them by a backslash (except within a character class).

Value

A character vector of matched file paths. The order is system-specific (but in the order of the elements of paths): it is normally collated in either the current locale or in byte (ASCII) order; however, on Windows collation is in the order of Unicode points.

Directory errors are normally ignored, so the matches are to accessible file paths (but not necessarily accessible files).

See Also

path.expand.

Quotes for handling backslashes in character strings.

Examples

Sys.glob(file.path(R.home(), "library", "*", "R", "*.rdx"))
**Description**

Reports system and user information.

**Usage**

```r
Sys.info()
```

**Details**

This uses POSIX or Windows system calls. Note that OS names (sysname) might not be what you expect: for example macOS identifies itself as `Darwin` and Solaris as `SunOS`.

`Sys.info()` returns details of the platform R is running on, whereas `R.version` gives details of the platform R was built on: the release and version may well be different.

**Value**

A character vector with fields

- `sysname` The operating system name.
- `release` The OS release.
- `version` The OS version.
- `nodename` A name by which the machine is known on the network (if any).
- `machine` A concise description of the hardware, often the CPU type.
- `login` The user's login name, or "unknown" if it cannot be ascertained.
- `user` The name of the real user ID, or "unknown" if it cannot be ascertained.
- `effective_user` The name of the effective user ID, or "unknown" if it cannot be ascertained. This may differ from the real user in 'set-user-ID' processes.

**On Unix-alike platforms:** The first five fields come from the `uname(2)` system call. The login name comes from `getlogin(2)`, and the user names from `getpwuid(getuid())` and `getpwuid(geteuid())`.

**On Windows:** The last three fields give the same value.

**Note**

The meaning of `release` and `version` is system-dependent: on a Unix-alike they normally refer to the kernel. There, usually `release` contains a numeric version and `version` gives additional information. Examples for `release`:

- "4.17.11-200.fc28.x86_64" # Linux (Fedora)
- "3.16.0-5-amd64" # Linux (Debian)
- "17.7.0" # macOS 10.13.6
- "5.11" # Solaris
There is no guarantee that the node or login or user names will be what you might reasonably expect. (In particular on some Linux distributions the login name is unknown from sessions with re-directed inputs.)

The use of alternatives such as `system("whoami")` is not portable: the POSIX command `system("id")` is much more portable on Unix-alikes, provided only the POSIX options `'-[Ggu][nr]'` are used (and not the many BSD and GNU extensions). `whoami` is equivalent to `id -un` (on Solaris, `/usr/xpg4/bin/id -un`).

Windows may report unexpected versions: there, see the help for `whoami`.

See Also

`.Platform` and `R.version`. `sessionInfo()` gives a synopsis of both your system and the `R` session (and gives the OS version in a human-readable form).

Examples

```r
Sys.info()
## An alternative (and probably better) way to get the login name on Unix
Sys.getenv("LOGNAME")
```

### Description

Get details of the numerical and monetary representations in the current locale.

### Usage

```r
Sys.localeconv()
```

### Details

Normally `R` is run without looking at the value of `LC_NUMERIC`, so the decimal point remains `.`. So the first three of these components will only be useful if you have set the locale category `LC_NUMERIC` using `Sys.setlocale` in the current `R` session (when `R` may not work correctly).

The monetary components will only be set to non-default values (see the ‘Examples’ section) if the `LC_MONETARY` category is set. It often is not set: set the examples for how to trigger setting it.

### Value

A character vector with 18 named components. See your ISO C documentation for details of the meaning.

It is possible to compile `R` without support for locales, in which case the value will be `NULL`.

### See Also

`Sys.setlocale` for ways to set locales.
Examples

Sys.localeconv()
## The results in the C locale are
## decimal_point thousands_sep grouping int_curr_symbol
## "." "" "" ""
## currency_symbol mon_decimal_point mon_thousands_sep mon_grouping
## "" "" "" ""
## positive_sign negative_sign int_frac_digits frac_digits
## "" "" "" ""
## p_cs_precedes p_sep_by_space n_cs_precedes n_sep_by_space
## "127" "127" "127" "127"
## p_sign_posn n_sign_posn
## "127" "127"

## Now try your default locale (which might be "C").
old <- Sys.getlocale()
## The category may not be set:
## the following may do so, but it might not be supported.
Sys.setlocale("LC_MONETARY", locale = "")
Sys.localeconv()
## or set an appropriate value yourself, e.g.
Sys.setlocale("LC_MONETARY", "de_AT")
Sys.localeconv()
Sys.setlocale(locale = old)

## Not run: read.table("foo", dec=Sys.localeconv()["decimal_point"])
**Details**

`.GlobalEnv` is given number 0 in the list of frames. Each subsequent function evaluation increases the frame stack by 1. The call, function definition and the environment for evaluation of that function are returned by `sys.call`, `sys.function` and `sys.frame` with the appropriate index.

`sys.call`, `sys.function` and `sys.frame` accept integer values for the argument `which`. Non-negative values of which are frame numbers starting from `.GlobalEnv` whereas negative values are counted back from the frame number of the current evaluation.

The parent frame of a function evaluation is the environment in which the function was called. It is not necessarily numbered one less than the frame number of the current evaluation, nor is it the environment within which the function was defined. `sys.parent` returns the number of the parent frame if `n` is 1 (the default), the grandparent if `n` is 2, and so on. See also the ‘Note’.

`sys.nframe` returns an integer, the number of the current frame as described in the first paragraph.

`sys.calls` and `sys.frames` give a pairlist of all the active calls and frames, respectively, and `sys.parents` returns an integer vector of indices of the parent frames of each of those frames.

Notice that even though the `sys.xxx` functions (except `sys.status`) are interpreted, their contexts are not counted nor are they reported. There is no access to them.

`sys.status()` returns a list with components `sys.calls`, `sys.parents` and `sys.frames`, the results of calls to those three functions (which will include the call to `sys.status`: see the first example).

`sys.on.exit()` returns the expression stored for use by `on.exit` in the function currently being evaluated. (Note that this differs from S, which returns a list of expressions for the current frame and its parents.)

`parent.frame(n)` is a convenient shorthand for `sys.frame(sys.parent(n))` (implemented slightly more efficiently).

**Value**

`sys.call` returns a call, `sys.function` a function definition, and `sys.frame` and `parent.frame` return an environment.

For the other functions, see the ‘Details’ section.

**Note**

Strictly, `sys.parent` and `parent.frame` refer to the context of the parent interpreted function. So internal functions (which may or may not set contexts and so may or may not appear on the call stack) may not be counted, and S3 methods can also do surprising things.

As an effect of lazy evaluation, these functions look at the call stack at the time they are evaluated, not at the time they are called. Passing calls to them as function arguments is unlikely to be a good idea, but these functions still look at the call stack and count frames from the frame of the function evaluation from which they were called.

Hence, when these functions are called to provide default values for function arguments, they are evaluated in the evaluation of the called function and they count frames accordingly (see e.g. the `envir` argument of `eval`).

**References**

See Also

eval for a usage of sys.frame and parent.frame.

Examples

```r
require(utils)

## Note: the first two examples will give different results
## if run by example().
ff <- function(x) gg(x)
gg <- function(y) sys.status()
str(ff(1))

gg <- function(y) {
    ggg <- function() {
        cat("current frame is", sys.nframe(), "\n")
        cat("parents are", sys.parents(), "\n")
        print(sys.function(0)) # ggg
        print(sys.function(2)) # gg
    }
    if(y > 0) gg(y-1) else ggg()
}

gg(3)

## in frame 2 here
## list with two components t1() and t2()
## 0 1

test.sys.on.exit <- function() {
    on.exit(print(1))
ex <- sys.on.exit()
    str(ex)
}
test.sys.on.exit()

as.double.foo <- function(x)
{ str(sys.calls())
    print(sys.frames())
    print(sys.parents())
    print(sys.frame(-1)); print(parent.frame())
    x
}
```

Sys.readlink(t2 <- function(x) as.double(x)
a <- structure(pi, class = "foo")
t2(a)

Sys.readlink

Read File Symbolic Links

Description

Find out if a file path is a symbolic link, and if so what it is linked to, via the system call readlink.
Symbolic links are a POSIX concept, not implemented on Windows but for most filesystems on Unix-alikes.

Usage

Sys.readlink(paths)

Arguments

paths character vector of file paths. Tilde expansion is done: see path.expand.

Value

A character vector of the same length as paths. The entries are the path of the file linked to, "" if
the path is not a symbolic link, and NA if there is an error (e.g., the path does not exist or cannot be
converted to the native encoding).

On platforms without the readlink system call, all elements are "".

See Also

file.symlink for the creation of symbolic links (and their Windows analogues), file.info

Examples

## To check if files (incl. directories) are symbolic links:
is.symlink <- function(paths) isTRUE(nzchar(Sys.readlink(paths), keepNA=TRUE))
## will return all FALSE when the platform has no 'readlink' system call.
is.symlink("/foo/bar")
Sys.setenv

Set or Unset Environment Variables

Description

Sys.setenv sets environment variables (for other processes called from within R or future calls to Sys.getenv from this R process).
Sys.unsetenv removes environment variables.

Usage

Sys.setenv(...)
Sys.unsetenv(x)

Arguments

... named arguments with values coercible to a character string.
x a character vector, or an object coercible to character.

Details

Non-standard R names must be quoted in Sys.setenv: see the examples. Most platforms (and POSIX) do not allow names containing "=". Windows does, but the facilities provided by R may not handle these correctly so they should be avoided. Most platforms allow setting an environment variable to "", but Windows does not and there Sys.setenv(FOO = "") unsets FOO.

There may be system-specific limits on the maximum length of the values of individual environment variables or of names+values of all environment variables.

Recent versions of Windows have a maximum length of 32,767 characters for a environment variable; however cmd.exe has a limit of 8192 characters for a command line, hence set can only set 8188.

Value

A logical vector, with elements being true if (un)setting the corresponding variable succeeded. (For Sys.unsetenv this includes attempting to remove a non-existent variable.)

Note

On Unix-alikes, if Sys.unsetenv is not supported, it will at least try to set the value of the environment variable to "", with a warning.

See Also

Sys.getenv, Startup for ways to set environment variables for the R session.
setwd for the working directory.
Sys.setlocale to set (and get) language locale variables, and notably Sys.setLanguage to set the LANGUAGE environment variable which is used for conditionMessage translations.
The help for ‘environment variables’ lists many of the environment variables used by R.
Examples

print(Sys.setenv(R_TEST = "testit", "A+C" = 123)) # 'A+C' could also be used
Sys.getenv("R_TEST")
Sys.unsetenv("R_TEST") # on Unix-alike may warn and not succeed
Sys.getenv("R_TEST", unset = NA)

Description

Uses system calls to set the times on a file or directory.

Usage

Sys.setFileTime(path, time)

Arguments

path A character vector containing file or directory paths.
time A date-time of class "POSIXct" or an object which can be coerced to one. Fractions of a second may be ignored. Recycled along paths.

Details

This attempts sets the file time to the value specified.

On a Unix-alike it uses the system call utimensat if that is available, otherwise utimes or utime. On a POSIX file system it sets both the last-access and modification times. Fractional seconds will set as from R 3.4.0 on OSes with the requisite system calls and suitable filesystems.

On Windows it uses the system call SetFileTime to set the 'last write time'. Some Windows file systems only record the time at a resolution of two seconds.

Sys.setFileTime has been vectorized in R 3.6.0. Earlier versions of R required path and time to be vectors of length one.

Value

A logical vector indicating if the operation succeeded for each of the files and directories attempted, returned invisibly.
Description

Suspend execution of R expressions for a specified time interval.

Usage

Sys.sleep(time)

Arguments

time The time interval to suspend execution for, in seconds.

Details

Using this function allows R to temporarily be given very low priority and hence not to interfere with more important foreground tasks. A typical use is to allow a process launched from R to set itself up and read its input files before R execution is resumed.

The intention is that this function suspends execution of R expressions but wakes the process up often enough to respond to GUI events, typically every half second. It can be interrupted (e.g. by ‘Ctrl-C’ or ‘Esc’ at the R console).

There is no guarantee that the process will sleep for the whole of the specified interval (sleep might be interrupted), and it may well take slightly longer in real time to resume execution.

time must be non-negative (and not NA nor NaN): Inf is allowed (and might be appropriate if the intention is to wait indefinitely for an interrupt). The resolution of the time interval is system-dependent, but will normally be 20ms or better. (On modern Unix-alikes it will be better than 1ms.)

Value

Invisible NULL.

Note

Despite its name, this is not currently implemented using the sleep system call (although on Windows it does make use of Sleep).

Examples

testit <- function(x)
{
  p1 <- proc.time()
  Sys.sleep(x)
  proc.time() - p1 # The cpu usage should be negligible
}
testit(3.7)
sys.source  Parse and Evaluate Expressions from a File

Description

Parses expressions in the given file, and then successively evaluates them in the specified environment.

Usage

sys.source(file, envir = baseenv(), chdir = FALSE,
keep.source = getOption("keep.source.pkgs"),
keep.parse.data = getOption("keep.parse.data.pkgs"),
toplevel.env = as.environment(envir))

Arguments

file  a character string naming the file to be read from
envir  an R object specifying the environment in which the expressions are to be evaluated. May also be a list or an integer. The default baseenv() corresponds to evaluation in the base environment. This is probably not what you want; you should typically supply an explicit envir argument, see the ‘Note’.
chdir  logical; if TRUE, the R working directory is changed to the directory containing file for evaluating.
keep.source  logical. If TRUE, functions keep their source including comments, see options(keep.source = *) for more details.
keep.parse.data  logical. If TRUE and keep.source is also TRUE, functions keep parse data with their source, see options(keep.parse.data = *) for more details.
toplevel.env  an R environment to be used as top level while evaluating the expressions. This argument is useful for frameworks running package tests; the default should be used in other cases

Details

For large files, keep.source = FALSE may save quite a bit of memory. Disabling only parse data via keep.parse.data = FALSE can already save a lot.

Note on envir

In order for the code being evaluated to use the correct environment (for example, in global assignments), source code in packages should call toopenv(), which will return the namespace, if any, the environment set up by sys.source, or the global environment if a saved image is being used.

See Also

source, and loadNamespace which is called from library(.) and uses sys.source(.).
Examples

```r
## a simple way to put some objects in an environment
## high on the search path
tmp <- tempfile()
writeLines("aaa <- pi", tmp)
env <- attach(NULL, name = "myenv")
sys.source(tmp, env)
unlink(tmp)
search()
aaa
detach("myenv")
```

Sys.time

Get Current Date and Time

Description

Sys.time and Sys.Date returns the system's idea of the current date with and without time.

Usage

Sys.time()
Sys.Date()

Details

Sys.time returns an absolute date-time value which can be converted to various time zones and
may return different days.

Sys.Date returns the current day in the current time zone.

Value

Sys.time returns an object of class "POSIXct" (see DateTimeClasses). On almost all systems it
will have sub-second accuracy, possibly microseconds or better. On Windows it increments in clock
ticks (usually 1/60 of a second) reported to millisecond accuracy.

Sys.Date returns an object of class "Date" (see Date).

Note

Sys.time may return fractional seconds, but they are ignored by the default conversions (e.g.,
printing) for class "POSIXct". See the examples and format.POSIXct for ways to reveal them.

See Also

date for the system time in a fixed-format character string.
Sys.timezone.

system.time for measuring elapsed/CPU time of expressions.
Sys.which

Find Full Paths to Executables

Description

This is an interface to the system command which, or to an emulation on Windows.

Usage

Sys.which(names)

Arguments

names Character vector of names or paths of possible executables.

Details

The system command which reports on the full path names of an executable (including an executable script) as would be executed by a shell, accepting either absolute paths or looking on the path.

On Windows an ‘executable’ is a file with extension ‘.exe’, ‘.com’, ‘.cmd’ or ‘.bat’. Such files need not actually be executable, but they are what system tries.

On a Unix-alike the full path to which (usually ‘/usr/bin/which’) is found when R is installed.

Value

A character vector of the same length as names, named by names. The elements are either the full path to the executable or some indication that no executable of that name was found. Typically the indication is ‘”, but this does depend on the OS (and the known exceptions are changed to ‘”’). Missing values in names have missing return values.

On Windows the paths will be short paths (8+3 components, no spaces) with \ as the path delimiter.

Note

Except on Windows this calls the system command which: since that is not part of e.g. the POSIX standards, exactly what it does is OS-dependent. It will usually do tilde-expansion and it may make use of csh aliases.
system

Examples

```r
## the first two are likely to exist everywhere
## texi2dvi exists on most Unix-alikes and under MiKTeX
Sys.which(c("ftp", "ping", "texi2dvi", "this-does-not-exist"))
```

system

Invoke a System Command

Description

system invokes the OS command specified by command.

Usage

```r
system(command, intern = FALSE,
       ignore.stdout = FALSE, ignore.stderr = FALSE,
       wait = TRUE, input = NULL, show.output.on.console = TRUE,
       minimized = FALSE, invisible = TRUE, timeout = 0)
```

Arguments

- `command`: the system command to be invoked, as a character string.
- `intern`: a logical (not NA) which indicates whether to capture the output of the command as an R character vector.
- `ignore.stdout`, `ignore.stderr`: a logical (not NA) indicating whether messages written to 'stdout' or 'stderr' should be ignored.
- `wait`: a logical (not NA) indicating whether the R interpreter should wait for the command to finish, or run it asynchronously. This will be ignored (and the interpreter will always wait) if `intern = TRUE`. When running the command asynchronously, no output will be displayed on the Rgui console in Windows (it will be dropped, instead).
- `input`: if a character vector is supplied, this is copied one string per line to a temporary file, and the standard input of `command` is redirected to the file.
- `timeout`: timeout in seconds, ignored if 0. This is a limit for the elapsed time running `command` in a separate process. Fractions of seconds are ignored.
- `show.output.on.console`, `minimized`, `invisible`: arguments that are accepted on Windows but ignored on this platform, with a warning.

Details

This interface has become rather complicated over the years: see `system2` for a more portable and flexible interface which is recommended for new code.

command is parsed as a command plus arguments separated by spaces. So if the path to the command (or a single argument such as a file path) contains spaces, it must be quoted e.g. by `shQuote`. Unix-alikes pass the command line to a shell (normally `/bin/sh`, and POSIX requires that shell), so command can be anything the shell regards as executable, including shell scripts, and it can contain multiple commands separated by ;.
On Windows, `system` does not use a shell and there is a separate function `shell` which passes command lines to a shell.

If `intern` is `TRUE` then `popen` is used to invoke the command and the output collected, line by line, into an R `character` vector. If `intern` is `FALSE` then the C function `system` is used to invoke the command.

`wait` is implemented by appending `&` to the command: this is in principle shell-dependent, but required by POSIX and so widely supported.

When `timeout` is non-zero, the command is terminated after the given number of seconds. The termination works for typical commands, but is not guaranteed: it is possible to write a program that would keep running after the time is out. Timeouts can only be set with `wait = TRUE`.

Timeouts cannot be used with interactive commands: the command is run with standard input redirected from `/dev/null` and it must not modify terminal settings. As long as the `tty` `tostop` option is disabled, which it usually is by default, the executed command may write to standard output and standard error. One cannot rely on that the execution time of the child processes will be included into `user.child` and `sys.child` element of `proc_time` returned by `proc.time`. For the time to be included, all child processes have to be waited for by their parents, which has to be implemented in the parent applications.

The ordering of arguments after the first two has changed from time to time: it is recommended to name all arguments after the first.

There are many pitfalls in using `system` to ascertain if a command can be run — `Sys.which` is more suitable.

**Value**

If `intern = TRUE`, a character vector giving the output of the command, one line per character string. (Output lines of more than 8095 bytes will be split on some systems.) If the command could not be run an R error is generated. If command runs but gives a non-zero exit status this will be reported with a warning and in the attribute "status" of the result: an attribute "errmsg" may also be available.

If `intern = FALSE`, the return value is an error code (0 for success), given the invisible attribute (so needs to be printed explicitly). If the command could not be run for any reason, the value is 127 and a warning is issued (as from R 3.5.0). Otherwise if `wait = TRUE` the value is the exit status returned by the command, and if `wait = FALSE` it is 0 (the conventional success value).

If the command times out, a warning is reported and the exit status is 124.

**Stdout and stderr**

For command-line R, error messages written to `stderr` will be sent to the terminal unless `ignore.stderr = TRUE`. They can be captured (in the most likely shells) by

```r
system("some command 2>&1", intern = TRUE)
```

For GUIs, what happens to output sent to `stdout` or `stderr` if `intern = FALSE` is interface-specific, and it is unsafe to assume that such messages will appear on a GUI console (they do on the macOS GUI’s console, but not on some others).

**Differences between Unix and Windows**

How processes are launched differs fundamentally between Windows and Unix-alike operating systems, as do the higher-level OS functions on which this R function is built. So it should not be surprising that there are many differences between OSes in how `system` behaves. For the benefit of programmers, the more important ones are summarized in this section.
The most important difference is that on a Unix-alike system launches a shell which then runs command. On Windows the command is run directly – use shell for an interface which runs command via a shell (by default the Windows shell cmd.exe, which has many differences from a POSIX shell).

This means that it cannot be assumed that redirection or piping will work in system (redirection sometimes does, but we have seen cases where it stopped working after a Windows security patch), and system2 (or shell) must be used on Windows.

What happens to stdout and stderr when not captured depends on how R is running: Windows batch commands behave like a Unix-alike, but from the Windows GUI they are generally lost. system(intern = TRUE) captures 'stderr' when run from the Windows GUI console unless ignore.stderr = TRUE.

The behaviour on error is different in subtle ways (and has differed between R versions).

The quoting conventions for command differ, but shQuote is a portable interface.

Arguments show.output.on.console, minimized, invisible only do something on Windows (and are most relevant to Rgui there).

See Also

man system and man sh for how this is implemented on the OS in use.

.Platform for platform-specific variables.

pipe to set up a pipe connection.

Examples

```r
# list all files in the current directory using the -F flag
## Not run: system("ls -F")

# t1 is a character vector, each element giving a line of output from who
# (if the platform has who)
t1 <- try(system("who", intern = TRUE))

try(system("ls fizzlipuzzli", intern = TRUE, ignore.stderr = TRUE))
# zero-length result since file does not exist, and will give warning.
```

Description

Finds the full file names of files in packages etc.

Usage

```r
system.file(., package = "base", lib.loc = NULL,
            mustWork = FALSE)
```
system.time

Arguments

... character vectors, specifying subdirectory and file(s) within some package. The default, none, returns the root of the package. Wildcards are not supported.

package a character string with the name of a single package. An error occurs if more than one package name is given.

lib.loc a character vector with path names of R libraries. See ‘Details’ for the meaning of the default value of NULL.

mustWork logical. If TRUE, an error is given if there are no matching files.

Details

This checks the existence of the specified files with file.exists. So file paths are only returned if there are sufficient permissions to establish their existence.

The unnamed arguments in ... are usually character strings, but if character vectors they are recycled to the same length.

This uses find.package to find the package, and hence with the default lib.loc = NULL looks first for attached packages then in each library listed in .libPaths(). Note that if a namespace is loaded but the package is not attached, this will look only on .libPaths().

Value

A character vector of positive length, containing the file paths that matched ..., or the empty string, "", if none matched (unless mustWork = TRUE).

If matching the root of a package, there is no trailing separator.

system.file() with no arguments gives the root of the base package.

See Also

R.home for the root directory of the R installation, list.files.

Sys.glob to find paths via wildcards.

Examples

system.file()  # The root of the 'base' package
system.file(package = "stats")  # The root of package 'stats'

system.file("INDEX")

system.file("help", "AnIndex", package = "splines")


system.time  CPU Time Used

Description

Return CPU (and other) times that expr used.

Usage

system.time(expr, gcFirst = TRUE)
Arguments

expr      Valid R expression to be timed.
gcFirst  Logical - should a garbage collection be performed immediately before the timing? Default is TRUE.

Details

system.time calls the function proc.time, evaluates expr, and then calls proc.time once more, returning the difference between the two proc.time calls.

unix.time has been an alias of system.time, for compatibility with S, has been deprecated in 2016 and finally became defunct in 2022.

Timings of evaluations of the same expression can vary considerably depending on whether the evaluation triggers a garbage collection. When gcFirst is TRUE a garbage collection (gc) will be performed immediately before the evaluation of expr. This will usually produce more consistent timings.

Value

A object of class "proc_time": see proc.time for details.

See Also

proc.time, time which is for time series.
setTimeLimit to limit the (CPU/elapsed) time R is allowed to use.
Sys.time to get the current date & time.

Examples

require(stats)
system.time(for(i in 1:100) mad(runif(1000)))
## Not run:
exT <- function(n = 10000) {
  # Purpose: Test if system.time works ok;  n: loop size
  system.time(for(i in 1:n) x <- mean(rt(1000, df = 4)))
}
#-- Try to interrupt one of the following (using Ctrl-C / Escape):
exT()  # about 4 secs on a 2.5GHz Xeon
system.time(exT())  # +/- same
## End(Not run)

system2  

Invoke a System Command

Description

system2 invokes the OS command specified by command.
Usage

system2(command, args = character(),
        stdout = "", stderr = "", stdin = "", input = NULL,
        env = character(), wait = TRUE,
        minimized = FALSE, invisible = TRUE, timeout = 0)

Arguments

command the system command to be invoked, as a character string.
args a character vector of arguments to command.
stdout, stderr where output to `stdout` or `stderr` should be sent. Possible values are "", to the R console (the default), NULL or FALSE (discard output), TRUE (capture the output in a character vector) or a character string naming a file.
stdin should input be diverted? "" means the default, alternatively a character string naming a file. Ignored if input is supplied.
input if a character vector is supplied, this is copied one string per line to a temporary file, and the standard input of command is redirected to the file.
env character vector of name=value strings to set environment variables.
wait a logical (not NA) indicating whether the R interpreter should wait for the command to finish, or run it asynchronously. This will be ignored (and the interpreter will always wait) if stdout = TRUE or stderr = TRUE. When running the command asynchronously, no output will be displayed on the Rgui console in Windows (it will be dropped, instead).
timeout timeout in seconds, ignored if 0. This is a limit for the elapsed time running command in a separate process. Fractions of seconds are ignored.
minimized, invisible arguments that are accepted on Windows but ignored on this platform, with a warning.

Details

Unlike system, command is always quoted by shQuote, so it must be a single command without arguments.

For details of how command is found see system.

On Windows, env is only supported for commands such as R and make which accept environment variables on their command line.

Some Unix commands (such as some implementations of ls) change their output if they consider it to be piped or redirected: stdout = TRUE uses a pipe whereas stdout = "some_file_name" uses redirection.

Because of the way it is implemented, on a Unix-alike stderr = TRUE implies stdout = TRUE: a warning is given if this is not what was specified.

When timeout is non-zero, the command is terminated after the given number of seconds. The termination works for typical commands, but is not guaranteed: it is possible to write a program that would keep running after the time is out. Timeouts can only be set with wait = TRUE.

Timeouts cannot be used with interactive commands: the command is run with standard input redirected from /dev/null and it must not modify terminal settings. As long as tty tostop option is disabled, which it usually is by default, the executed command may write to standard output and standard error.
Value

If stdout = TRUE or stderr = TRUE, a character vector giving the output of the command, one line per character string. (Output lines of more than 8095 bytes will be split.) If the command could not be run an R error is generated. If command runs but gives a non-zero exit status this will be reported with a warning and in the attribute "status" of the result: an attribute "errmsg" may also be available.

In other cases, the return value is an error code (0 for success), given the invisible attribute (so needs to be printed explicitly). If the command could not be run for any reason, the value is 127 and a warning is issued (as from R 3.5.0). Otherwise if wait = TRUE the value is the exit status returned by the command, and if wait = FALSE it is 0 (the conventional success value).

If the command times out, a warning is issued and the exit status is 124.

Note

system2 is a more portable and flexible interface than system. It allows redirection of output without needing to invoke a shell on Windows, a portable way to set environment variables for the execution of command, and finer control over the redirection of stdout and stderr. Conversely, system (and shell on Windows) allows the invocation of arbitrary command lines.

There is no guarantee that if stdout and stderr are both TRUE or the same file that the two streams will be interleaved in order. This depends on both the buffering used by the command and the OS.

See Also

system.

---

\textit{t} \quad \textit{Matrix Transpose} \quad \begin{tabular}{l}

\textbf{Description} \\

Given a matrix or \texttt{data.frame} \texttt{x}, \texttt{t} returns the transpose of \texttt{x}. \\

\textbf{Usage} \\

\texttt{t(x)} \\

\textbf{Arguments} \\

\texttt{x} \quad a matrix or data frame, typically. \\

\textbf{Details} \\

This is a generic function for which methods can be written. The description here applies to the default and "data.frame" methods. \\

A data frame is first coerced to a matrix: see \texttt{as.matrix}. When \texttt{x} is a vector, it is treated as a column, i.e., the result is a 1-row matrix.

\textbf{Value} \\

A matrix, with \texttt{dim} and \texttt{dimnames} constructed appropriately from those of \texttt{x}, and other attributes except names copied across.
Note

The conjugate transpose of a complex matrix $A$, denoted $A^H$ or $A^*$, is computed as $\text{Conj}(t(A))$.

References


See Also

aperm for permuting the dimensions of arrays.

Examples

```r
a <- matrix(1:30, 5, 6)
ta <- t(a) ##-- i.e., a[i, j] == ta[j, i] for all i,j :
for(j in seq(ncol(a)))
  if(! all(a[, j] == ta[j, ])) stop("wrong transpose")
```

---

**table**

Cross Tabulation and Table Creation

Description

`table()` uses cross-classifying factors to build a contingency table of the counts at each combination of factor levels.

Usage

```r
table(...,
  exclude = if (useNA == "no") c(NA, NaN),
  useNA = c("no", "ifany", "always"),
  dnn = list.names(...), deparse.level = 1)
```

as.table(x, ...)

is.table(x)

## S3 method for class 'table'
as.data.frame(x, row.names = NULL, ...
  responseName = "Freq", stringsAsFactors = TRUE,
  sep = "", base = list(LETTERS))

Arguments

... one or more objects which can be interpreted as factors (including numbers or character strings), or a list (such as a data frame) whose components can be so interpreted. (For as.table, arguments passed to specific methods; for as.data.frame, unused.)

exclude levels to remove for all factors in ... . If it does not contain NA and useNA is not specified, it implies useNA = "ifany". See ‘Details’ for its interpretation for non-factor arguments.
useNA: whether to include NA values in the table. See ‘Details’. Can be abbreviated.
dnn: the names to be given to the dimensions in the result (the *dimnames names*).
deparse.level: controls how the default dnn is constructed. See ‘Details’.
x: an arbitrary R object, or an object inheriting from class "table" for the as.data.frame method. Note that as.data.frame.table(x, *) may be called explicitly for non-table x for “reshaping” arrays.
row.names: a character vector giving the row names for the data frame.
responseName: The name to be used for the column of table entries, usually counts.
stringsAsFactors: logical: should the classifying factors be returned as factors (the default) or character vectors?
sep, base: passed to provideDimnames.

Details

If the argument dnn is not supplied, the internal function list.names is called to compute the ‘dimname names’ as follows: If ... is one list with its own names(), these names are used. Otherwise, if the arguments in ... are named, those names are used. For the remaining arguments, deparse.level = 0 gives an empty name, deparse.level = 1 uses the supplied argument if it is a symbol, and deparse.level = 2 will deparse the argument.

Only when exclude is specified (i.e., not by default) and non-empty, will table potentially drop levels of factor arguments.

useNA controls if the table includes counts of NA values: the allowed values correspond to never ("no"), only if the count is positive ("ifany") and even for zero counts ("always"). Note the somewhat “pathological” case of two different kinds of NAs which are treated differently, depending on both useNA and exclude, see d.patho in the ‘Examples:’ below.

Both exclude and useNA operate on an “all or none” basis. If you want to control the dimensions of a multiway table separately, modify each argument using factor or addNA.

Non-factor arguments a are coerced via factor(a, exclude=exclude). Since R 3.4.0, care is taken not to count the excluded values (where they were included in the NA count, previously).

The summary method for class "table" (used for objects created by table or xtabs) which gives basic information and performs a chi-squared test for independence of factors (note that the function chisq.test currently only handles 2-d tables).

Value

`table()` returns a contingency table, an object of class "table", an array of integer values. Note that unlike S the result is always an array, a 1D array if one factor is given.

as.table and is.table coerce to and test for contingency table, respectively.

The as.data.frame method for objects inheriting from class "table" can be used to convert the array-based representation of a contingency table to a data frame containing the classifying factors and the corresponding entries (the latter as component named by responseName). This is the inverse of xtabs.

References

See Also

`tabulate` is the underlying function and allows finer control.

Use `ftable` for printing (and more) of multidimensional tables. `margin.table`, `prop.table`, `addmargins`.

`addNA` for constructing factors with `NA` as a level.

`xtabs` for cross tabulation of data frames with a formula interface.

Examples

```r
require(stats) # for rpois and xtabs
## Simple frequency distribution
table(rpois(100, 5))
## Check the design:
with(warpbreaks, table(wool, tension))
table(state.division, state.region)

# simple two-way contingency table
with(airquality, table(cut(Temp, quantile(Temp)), Month))
a <- letters[1:3]
table(a, sample(a)) # dnn is c("a","")
table(a, sample(a), deparse.level = 0) # dnn is c("","")
table(a, sample(a), deparse.level = 2) # dnn is c("a", "sample(a)"

## xtabs() <-> as.data.frame.table() :
UCBAdmissions ## already a contingency table
DF <- as.data.frame(UCBAdmissions)
class(tab <- xtabs(Freq ~ ., DF)) # xtabs & table
## tab *is* "the same" as the original table:
all(tab == UCBAdmissions)
all.equal(dimnames(tab), dimnames(UCBAdmissions))
a <- rep(c(NA, 1/0:3), 10)
table(a) # does not report NA's
b <- factor(rep(c("A","B","C"), 10))
table(b)
table(b, exclude="B")
d <- factor(rep(c("A","B","C"), 10), levels = c("A","B","C","D","E"))
table(d, exclude = "B")
print(table(b, d), zero.print = ".")

## NA counting:
is.na(d) <- 3:4
d. <- addNA(d)
d.[1:7]
table(d.) # ", exclude = NULL" is not needed
## i.e., if you want to count the NA's of 'd', use
table(d, useNA = "ifany")

## "pathological" case:
d.patho <- addNA(c(1,NA,1:2,1:3)[-7]; is.na(d.patho) <- 3:4
d.patho
## just 3 consecutive NA's ? --- well, have *two* kinds of NAs here :
as.integer(d.patho) # 1 4 NA NA 1 2
```
In R >= 3.4.0, table() allows to differentiate:
\[
\begin{align*}
table(d.patho) & \quad \# \text{ counts the "unusual" NA} \\
table(d.patho, useNA = "ifany") & \quad \# \text{ counts all three} \\
table(d.patho, exclude = NULL) & \quad \# \text{ (ditto)} \\
table(d.patho, exclude = NA) & \quad \# \text{ counts none}
\end{align*}
\]

Two-way tables with NA counts. The 3rd variant is absurd, but shows
something that cannot be done using exclude or useNA.
\[
\begin{align*}
\text{with(airquality,} & \\
\quad \text{table(OzHi = Ozone > 80, Month, useNA = "ifany")} \\
\text{with(airquality,} & \\
\quad \text{table(OzHi = Ozone > 80, Month, useNA = "always")} \\
\text{with(airquality,} & \\
\quad \text{table(OzHi = Ozone > 80, addNA(Month))}
\end{align*}
\]

---

### `tabulate`

**Tabulation for Vectors**

**Description**

`tabulate` takes the integer-valued vector `bin` and counts the number of times each integer occurs in it.

**Usage**

\[
\text{tabulate(bin, nbins = max(1, bin, na.rm = TRUE))}
\]

**Arguments**

- `bin` a numeric vector (of positive integers), or a factor. **Long vectors** are supported.
- `nbins` the number of bins to be used.

**Details**

`tabulate` is the workhorse for the `table` function.

If `bin` is a factor, its internal integer representation is tabulated.

If the elements of `bin` are numeric but not integers, they are truncated by `as.integer`.

**Value**

An integer valued `integer` or `double` vector (without names). There is a bin for each of the values 1, ..., `nbins`; values outside that range and NAs are (silently) ignored.

On 64-bit platforms `bin` can have $2^{31}$ or more elements (i.e., `length(bin) > .Machine$integer.max`), and hence a count could exceed the maximum integer. For this reason, the return value is of type double for such long `bin` vectors.

**See Also**

`table`, `factor`. 
Examples

```r
tabulate(c(2,3,5))
tabulate(c(2,3,3,5), nbins = 10)
tabulate(c(-2,0,2,3,3,5)) # -2 and 0 are ignored
tabulate(c(-2,0,2,3,3,5), nbins = 3)
tabulate(factor(letters[1:10]))
```

Description

Apply a function to each cell of a ragged array, that is to each (non-empty) group of values or data rows given by a unique combination of the levels of certain factors.

Usage

`tapply(X, INDEX, FUN = NULL, ..., default = NA, simplify = TRUE)`

Arguments

- `X`: an R object for which a `split` method exists. Typically vector-like, allowing subsetting with `[`, or a data frame.
- `INDEX`: a list of one or more factors, each of same length as `X`. The elements are coerced to factors by `as.factor`. Can also be a formula, which is useful if `X` is a data frame; see the `f` argument in `split` for interpretation.
- `FUN`: a function (or name of a function) to be applied, or `NULL`. In the case of functions like `+`, `%*%`, etc., the function name must be backquoted or quoted. If `FUN` is `NULL`, `tapply` returns a vector which can be used to subscript the multi-way array `tapply` normally produces.
- `...`: optional arguments to `FUN`: the Note section.
- `default`: (only in the case of simplification to an array) the value with which the array is initialized as `array(default, dim = ..)`. Before R 3.4.0, this was hard coded to `array()`’s default NA. If it is NA (the default), the missing value of the answer type, e.g. `NA_real_`, is chosen (as.raw(0) for "raw"). In a numerical case, it may be set, e.g., to `FUN(integer(0))`, e.g., in the case of `FUN = sum` or `0L`.
- `simplify`: logical; if FALSE, `tapply` always returns an array of mode "list"; in other words, a `list` with a `dim` attribute. If TRUE (the default), then if `FUN` always returns a scalar, `tapply` returns an array with the mode of the scalar.

Details

If `FUN` is not `NULL`, it is passed to `match.fun`, and hence it can be a function or a symbol or character string naming a function.
Value

When FUN is present, tapply calls FUN for each cell that has any data in it. If FUN returns a single atomic value for each such cell (e.g., functions mean or var) and when simplify is TRUE, tapply returns a multi-way array containing the values, and NA for the empty cells. The array has the same number of dimensions as INDEX has components; the number of levels in a dimension is the number of levels (nlevels()) in the corresponding component of INDEX. Note that if the return value has a class (e.g., an object of class "Date") the class is discarded.

simplify = TRUE always returns an array, possibly 1-dimensional.

If FUN does not return a single atomic value, tapply returns an array of mode list whose components are the values of the individual calls to FUN, i.e., the result is a list with a dim attribute.

When there is an array answer, its dimnames are named by the names of INDEX and are based on the levels of the grouping factors (possibly after coercion).

For a list result, the elements corresponding to empty cells are NULL.

The array2DF function can be used to convert the array returned by tapply into a data frame, which may be more convenient for further analysis.

Note

Optional arguments to FUN supplied by the ... argument are not divided into cells. It is therefore inappropriate for FUN to expect additional arguments with the same length as X.

References


See Also

the convenience functions by and aggregate (using tapply); apply, lapply with its versions sapply and mapply.

array2DF to convert the result into a data frame.

Examples

require(stats)
groups <- as.factor(rbinom(32, n = 5, prob = 0.4))
tapply(groups, groups, length) #~ is almost the same as table(groups)

## contingency table from data.frame: array with named dimnames
tapply(warpbreaks$breaks, warpbreaks[, -1], sum)
tapply(warpbreaks$breaks, warpbreaks[, 3, drop = FALSE], sum)

n <- 17; fac <- factor(rep_len(1:3, n), levels = 1:5)
table(fac)
tapply(1:n, fac, sum)
tapply(1:n, fac, sum, default = 0) # maybe more desirable

tapply(1:n, fac, sum, simplify = FALSE)
tapply(1:n, fac, range)
tapply(1:n, fac, quantile)
tapply(1:n, fac, length) # NA's

tapply(1:n, fac, length, default = 0) # == table(fac)
taskCallback

Add or Remove a Top-Level Task Callback

Description

addTaskCallback registers an R function that is to be called each time a top-level task is completed. removeTaskCallback un-registers a function that was registered earlier via addTaskCallback.

These provide low-level access to the internal/native mechanism for managing task-completion actions. One can use taskCallbackManager at the R-language level to manage R functions that are called at the completion of each task. This is easier and more direct.

Usage

addTaskCallback(f, data = NULL, name = character())
removeTaskCallback(id)

Arguments

f       the function that is to be invoked each time a top-level task is successfully completed. This is called with 5 or 4 arguments depending on whether data is specified or not, respectively. The return value should be a logical value indicating whether to keep the callback in the list of active callbacks or discard it.

data    if specified, this is the 5-th argument in the call to the callback function f.

id      a string or an integer identifying the element in the internal callback list to be removed. Integer indices are 1-based, i.e the first element is 1. The names of currently registered handlers is available using getTaskCallbackNames and is also returned in a call to addTaskCallback.

name    character: names to be used.
Details

Top-level tasks are individual expressions rather than entire lines of input. Thus an input line of the form `expression1 ; expression2` will give rise to 2 top-level tasks.

A top-level task callback is called with the expression for the top-level task, the result of the top-level task, a logical value indicating whether it was successfully completed or not (always TRUE at present), and a logical value indicating whether the result was printed or not. If the data argument was specified in the call to `addTaskCallback`, that value is given as the fifth argument.

The callback function should return a logical value. If the value is FALSE, the callback is removed from the task list and will not be called again by this mechanism. If the function returns TRUE, it is kept in the list and will be called on the completion of the next top-level task.

Value

`addTaskCallback` returns an integer value giving the position in the list of task callbacks that this new callback occupies. This is only the current position of the callback. It can be used to remove the entry as long as no other values are removed from earlier positions in the list first.

`removeTaskCallback` returns a logical value indicating whether the specified element was removed. This can fail (i.e., return FALSE) if an incorrect name or index is given that does not correspond to the name or position of an element in the list.

Note

There is also C-level access to top-level task callbacks to allow C routines rather than R functions be used.

See Also

`getTaskCallbackNames`  `taskCallbackManager`  `https://developer.r-project.org/TaskHandlers.pdf`

Examples

times <- function(total = 3, str = "Task a") {
  ctr <- 0
  function(expr, value, ok, visible) {
    ctr <<- ctr + 1
    cat(str, ctr, "\n")
    keep.me <- (ctr < total)
    if (!keep.me)
      cat("handler removing itself\n")
    
    # return
    keep.me
  }
}

# add the callback that will work for
# 4 top-level tasks and then remove itself.
nt <- addTaskCallback(times(4))

# now remove it, assuming it is still first in the list.
removeTaskCallback(nt)

## See how the handler is called every time till "self destruction":

```r
```
taskCallbackManager

Create an R-level Task Callback Manager

Description

This provides an entirely R-language mechanism for managing callbacks or actions that are invoked at the conclusion of each top-level task. Essentially, we register a single R function from this manager with the underlying, native task-callback mechanism and this function handles invoking the other R callbacks under the control of the manager. The manager consists of a collection of functions that access shared variables to manage the list of user-level callbacks.

Usage

taskCallbackManager(handlers = list(), registered = FALSE, verbose = FALSE)

Arguments

handlers this can be a list of callbacks in which each element is a list with an element named "f" which is a callback function, and an optional element named "data" which is the 5-th argument to be supplied to the callback when it is invoked. Typically this argument is not specified, and one uses add to register callbacks after the manager is created.

registered a logical value indicating whether the evaluate function has already been registered with the internal task callback mechanism. This is usually FALSE and the first time a callback is added via the add function, the evaluate function is automatically registered. One can control when the function is registered by specifying TRUE for this argument and calling addTaskCallback manually.

verbose a logical value, which if TRUE, causes information to be printed to the console about certain activities this dispatch manager performs. This is useful for debugging callbacks and the handler itself.

Value

A list containing 6 functions:

add() register a callback with this manager, giving the function, an optional 5-th argument, an optional name by which the callback is stored in the list, and a register argument which controls whether the evaluate function is registered with the internal C-level dispatch mechanism if necessary.

remove() remove an element from the manager’s collection of callbacks, either by name or position/index.
evaluate() the ‘real’ callback function that is registered with the C-level dispatch mechanism and which invokes each of the R-level callbacks within this manager’s control.

suspend() a function to set the suspend state of the manager. If it is suspended, none of the callbacks will be invoked when a task is completed. One sets the state by specifying a logical value for the status argument.

register() a function to register the evaluate function with the internal C-level dispatch mechanism. This is done automatically by the add function, but can be called manually.

callbacks() returns the list of callbacks being maintained by this manager.

References


See Also

`addTaskCallback`, `removeTaskCallback`, `getTaskCallbackNames` and the reference.

Examples

```r
# create the manager
h <- taskCallbackManager()

# add a callback
h$add(function(expr, value, ok, visible) {
  cat("In handler\n")
  return(TRUE)
}, name = "simpleHandler")

# look at the internal callbacks.
getTaskCallbackNames()

# look at the R-level callbacks
names(h$callbacks())

removeTaskCallback("R-taskCallbackManager")
```

---

**taskCallbackNames**  
Query the Names of the Current Internal Top-Level Task Callbacks

**Description**

This provides a way to get the names (or identifiers) for the currently registered task callbacks that are invoked at the conclusion of each top-level task. These identifiers can be used to remove a callback.

**Usage**

`getTaskCallbackNames()`
Value

A character vector giving the name for each of the registered callbacks which are invoked when a top-level task is completed successfully. Each name is the one used when registering the callbacks and returned as the in the call to `addTaskCallback`.

Note

One can use `taskCallbackManager` to manage user-level task callbacks, i.e., S-language functions, entirely within the S language and access the names more directly.

See Also

`addTaskCallback`, `removeTaskCallback`, `taskCallbackManager`  
https://developer.r-project.org/TaskHandlers.pdf

Examples

```r
n <- addTaskCallback(function(expr, value, ok, visible) {
  cat("In handler\n")
  return(TRUE)
}, name = "simpleHandler")

getTaskCallbackNames()

# now remove it by name
removeTaskCallback("simpleHandler")

h <- taskCallbackManager()
h$h$add(function(expr, value, ok, visible) {
  cat("In handler\n")
  return(TRUE)
}, name = "simpleHandler")

getTaskCallbackNames()
removeTaskCallback("R-taskCallbackManager")
```

```

call

Create Names for Temporary Files

tempfile

description

tempfile returns a vector of character strings which can be used as names for temporary files.

Usage

tempfile(pattern = "file", tmpdir = tempdir(), fileext = "")
tempdir(check = FALSE)
```
**tempfile**

**Arguments**

- **pattern**: a non-empty character vector giving the initial part of the name.
- **tmpdir**: a non-empty character vector giving the directory name.
- **fileext**: a non-empty character vector giving the file extension.
- **check**: logical indicating if `tmpdir()` should be checked and recreated if no longer valid.

**Details**

The length of the result is the maximum of the lengths of the three arguments; values of shorter arguments are recycled.

The names are very likely to be unique among calls to `tempfile` in an R session and across simultaneous R sessions (unless `tmpdir` is specified). The filenames are guaranteed not to be currently in use.

The file name is made by concatenating the path given by `tmpdir`, the `pattern` string, a random string in hex and a suffix of `fileext`.

By default, `tmpdir` will be the directory given by `tempdir()`. This will be a subdirectory of the per-session temporary directory found by the following rule when the R session is started. The environment variables `TMPDIR`, `TMP` and `TEMP` are checked in turn and the first found which points to a writable directory is used: if none succeeds ‘/tmp’ is used. The path must not contain spaces.

Note that setting any of these environment variables in the R session has no effect on `tempdir()`: the per-session temporary directory is created before the interpreter is started.

**Value**

For `tempfile` a character vector giving the names of possible (temporary) files. Note that no files are generated by `tempfile`.

For `tmpdir`, the path of the per-session temporary directory.

On Windows, both will use a backslash as the path separator.

On a Unix-alike, the value will be an absolute path (unless `tmpdir` is set to a relative path), but it need not be canonical (see `normalizePath`) and on macOS it often is not.

**Note on parallel use**

R processes forked by functions such as `mclapply` and `makeForkCluster` in package `parallel` share a per-session temporary directory. Further, the ‘guaranteed not to be currently in use’ applies only at the time of asking, and two children could ask simultaneously. This is circumvented by ensuring that `tempfile` calls in different children try different names.

**Source**

The final component of `tmpdir()` is created by the POSIX system call `mkdtemp`, or if this is not available (e.g. on Windows) a version derived from the source code of GNU `glibc`.

It will be of the form ‘RtmpXXXXXX’ where the last 6 characters are replaced in a platform-specific way. POSIX only requires that the replacements be ASCII, which allows . (so the value may appear to have a file extension) and regexp metacharacters such as .+. Most commonly the replacements are from the regexp pattern [A-Za-z0-9], but . has been seen.
References


See Also

`unlink` for deleting files.

Examples

tempfile(c("ab", "a b c"))  # give file name with spaces in!

tempfile("plot", fileext = c(".ps", ".pdf"))

tempdir()  # works on all platforms with a platform-dependent result

## Show how 'check' is working on some platforms:
if(exists("I'm brave") && 'I'm brave' &&
   identical(.Platform$OS.type, "unix") && grepl("^/tmp/", tempdir())) {
  cat("Current tempdir(): ", tempdir(), 
  cat("Removing it :", file.remove(tempdir()),
  "; dir.exists(tempdir()):", dir.exists(tempdir()), 
  cat("and now tempdir(check = TRUE) :", tempdir(check = TRUE),"
}  

Arguments

- **object**: character. A description of the connection. For an input this is an R character vector object, and for an output connection the name for the R character vector to receive the output, or NULL (for none).
- **open**: character string. Either "r" (or equivalently ") for an input connection or "w" or "a" for an output connection.
- **local**: logical. Used only for output connections. If TRUE, output is assigned to a variable in the calling environment. Otherwise the global environment is used.
- **name**: a character string specifying the connection name.
encoding character string, partially matched. Used only for input connections. How marked strings in object should be handled: converted to the current locale, used byte-by-byte or translated to UTF-8.

con An output text connection.

Details

An input text connection is opened and the character vector is copied at time the connection object is created, and close destroys the copy. object should be the name of a character vector: however, short expressions will be accepted provided they deparse to less than 60 bytes.

An output text connection is opened and creates an R character vector of the given name in the user’s workspace or in the calling environment, depending on the value of the local argument. This object will at all times hold the completed lines of output to the connection, and isIncomplete will indicate if there is an incomplete final line. Closing the connection will output the final line, complete or not. (A line is complete once it has been terminated by end-of-line, represented by \n in R.) The output character vector has locked bindings (see lockBinding) until close is called on the connection. The character vector can also be retrieved via textConnectionValue, which is the only way to do so if object = NULL. If the current locale is detected as Latin-1 or UTF-8, non-ASCII elements of the character vector will be marked accordingly (see Encoding).

Opening a text connection with mode = "a" will attempt to append to an existing character vector with the given name in the user’s workspace or the calling environment. If none is found (even if an object exists of the right name but the wrong type) a new character vector will be created, with a warning.

You cannot seek on a text connection, and seek will always return zero as the position.

Text connections have slightly unusual semantics: they are always open, and throwing away an input text connection without closing it (so it get garbage-collected) does not give a warning.

Value

For textConnection, a connection object of class "textConnection" which inherits from class "connection".

For textConnectionValue, a character vector.

Note

As output text connections keep the character vector up to date line-by-line, they are relatively expensive to use, and it is often better to use an anonymous file() connection to collect output.

On (rare) platforms where vsnprintf does not return the needed length of output there is a 100,000 character limit on the length of line for output connections: longer lines will be truncated with a warning.

References


[S has input text connections only.]

See Also

collections, showConnections, pushBack, capture.output.
Examples

```r
zz <- textConnection(LETTERS)
readLines(zz, 2)
scan(zz, "", 4)
pushBack(c("aa", "bb"), zz)
scan(zz, "", 4)
close(zz)

zz <- textConnection("foo", "w")
writeLines(c("testit1", "testit2"), zz)
cat("testit3 ", file = zz)
isIncomplete(zz)
cat("testit4
", file = zz)
isIncomplete(zz)
close(zz)
foo

# capture R output: use part of example from help(lm)
zz <- textConnection("foo", "w")
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.5, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)
sink(zz)
anova(lm.D9 <- lm(weight ~ group))
cat("\nSummary of Residuals:\n\n")
summary(resid(lm.D9))
sink()
close(zz)
cat(foo, sep = "\n")
```

tilde

Tilde Operator

Description

Tilde is used to separate the left- and right-hand sides in a model formula.

Usage

```r
y ~ model
```

Arguments

```r
y, model symbolic expressions.
```

Details

The left-hand side is optional, and one-sided formulae are used in some contexts. A formula has mode `call`. It can be subsetted by `[[`: the components are `~`, the left-hand side (if present) and the right-hand side in that order. (Thus one-sided formulae have two components.)
References

See Also
formula

timezones    Time Zones

Description
Information about time zones in R. Sys.timezone returns the name of the current time zone.

Usage
Sys.timezone(location = TRUE)
OlsonNames(tzdir = NULL)

Arguments
location      logical: defunct: ignored, with a warning for false values.
tzdir         The time-zone database to be used: the default is to try known locations until one is found.

Details
Time zones are a system-specific topic, but these days almost all R platforms use similar underlying code, used by Linux, macOS, Solaris, AIX and FreeBSD, and installed with R on Windows. (Unfortunately there are many system-specific errors in the implementations.) It is possible to use the R sources’ version of the code on Unix-alikes as well as on Windows: this is the default on macOS.

It should be possible to set the current time zone via the environment variable TZ: see the section on ‘Time zone names’ for suitable values. Sys.timezone() will return the value of TZ if set initially (and on some OSes it is always set), otherwise it will try to retrieve from the OS a value which if set for TZ would give the initial time zone. (‘Initially’ means before any time-zone functions are used: if TZ is being set to override the OS setting or if the ‘try’ does not get this right, it should be set before the R process is started or (probably early enough) in file .Rprofile).

If TZ is set but invalid, most platforms default to ‘UTC’, the time zone colloquially known as ‘GMT’ (see https://en.wikipedia.org/wiki/Coordinated_Universal_Time). (Some but not all platforms will give a warning for invalid values.) If it is unset or empty the system time zone is used (the one returned by Sys.timezone).

Time zones did not come into use until the middle of the nineteenth century and were not widely adopted until the twentieth, and daylight saving time (DST, also known as summer time) was first introduced in the early twentieth century, most widely in 1916. Over the last 100 years places have changed their affiliation between major time zones, have opted out of (or in to) DST in various years or adopted DST rule changes late or not at all. (For example, the UK experimented with DST throughout 1971, only.) In a few countries (one is the Irish Republic) it is the summer time which is the
‘standard’ time and a different name is used in winter. And there can be multiple changes during a year, for example for Ramadan.

A quite common system implementation of POSIXct was as signed 32-bit integers and so only went back to the end of 1901: on such systems R assumes that dates prior to that are in the same time zone as they were in 1902. Most of the world had not adopted time zones by 1902 (so used local ‘mean time’ based on longitude) but for a few places there had been time-zone changes before then. 64-bit representations are becoming by far the most common; unfortunately on some 64-bit OSes the database information is 32-bit and so only available for the range 1901–2038, and incompletely for the end years.

When a time zone location is first found in a session its value is cached in object .sys.timezone in the base environment.

**Value**

Sys.timezone returns an OS-specific character string, possibly NA or an empty string (which on some OSes means ‘UTC’). This will be a location such as "Europe/London" if one can be ascertained.

A time zone region may be known by several names: for example "Europe/London" may also be known as ‘GB’, ‘GB-Eire’, ‘Europe/Belfast’, ‘Europe/Guernsey’, ‘Europe/Isle_of_Man’ and ‘Europe/Jersey’. A few regions are also known by a summary of their time zone, e.g. ‘PST8PDT’ is an alias for ‘America/Los_Angeles’.

OlsonNames returns a character vector, see the examples for typical cases. It may have an attribute "Version", something like "2023a". (It does on systems using ‘--with-internal-tzcode’ and those like Fedora distributing file ‘tzdata.zi’.)

**Time zone names**

Names "UTC" and its synonym "GMT" are accepted on all platforms.

Where OSes describe their valid time zones can be obscure. The help for the C function tzset can be helpful, but it can also be inaccurate. There is a cumbersome POSIX specification (listed under environment variable TZ at https://pubs.opengroup.org/onlinepubs/9699919799/basedefs/V1_chap08.html#tag_08), which is often at least partially supported, but there are other more user-friendly ways to specify time zones.

Almost all R platforms make use of a time-zone database originally compiled by Arthur David Olson and now managed by IANA, in which the preferred way to refer to a time zone is by a location (typically of a city), e.g., Europe/London, America/Los_Angeles, Pacific/Easter within a ‘time zone region’. Some traditional designations are also allowed such as EST5EDT or GB. (Beware that some of these designations may not be what you expect: in particular EST is a time zone used in Canada without daylight saving time, and not EST5EDT nor (Australian) Eastern Standard Time.)

The designation can also be an optional colon prepended to the path to a file giving complied zone information (and the examples above are all files in a system-specific location). See https://data.iana.org/time-zones/tz-link.html for more details and references. By convention, regions with a unique time-zone history since 1970 have specific names in the database, but those with different earlier histories may not. Each time zone has one or two (the second for DST) abbreviations used when formatting times.

The abbreviations used have changed over the years: for example France used ‘PMT’ (‘Paris Mean Time’) from 1891 to 1911 then ‘WET/WEST’ up to 1940 and ‘CET/CEST’ from 1946. (In almost all time zones the abbreviations have been stable since 1970.) The POSIX standard allows only one or two abbreviations per time zone, so you may see the current abbreviation(s) used for older times.

For some time zones abbreviations are like ‘-03’ and '+0845': this is done when there is no official abbreviation. (Negative values are behind (West of) UTC, as for the "%z" format for strftime.)
The function OlsonNames returns the time-zone names known to the currently selected Olson/IANA database. The system-specific location in the file system varies, e.g. `/usr/share/zoneinfo` (Linux, macOS, FreeBSD), `/usr/share/lib/zoneinfo` (Solaris, AIX), .... It is likely that there is a file named something like `zone1970.tab` or (older) `zone.tab` under that directory listing the locations known as time-zone names (but not for example EST5EDT). See also https://en.wikipedia.org/wiki/Zone.tab.

Where R was configured with option `--with-internal-tzcode` (the default on Windows), the database at `file.path(R.home("share"), "zoneinfo")` is used by default: file `VERSION` in that directory states the version. That option is also the default on macOS but there whichever is more recent of the system database at `/var/db/timezone/zoneinfo` and that distributed with R is used by default. Environment variable TZDIR can be used to give the full path to a different `zoneinfo` database: value "internal" indicates the database from the R sources and "macOS" indicates the system database. (Setting either of those values would not be recognized by other software using TZDIR.)

Setting TZDIR is also supported by the native services on some OSes, e.g. Linux using glibc except in secure modes.

Time zones given by name (via environment variable TZ, in tz arguments to functions such as as.POSIXlt and perhaps the system time zone) are loaded from the currently selected `zoneinfo` database.

On Windows only: An attempt is made (once only per session) to map Windows’ idea of the current time zone to a location, following a version of http://unicode.org/repos/cldr/trunk/common/supplemental/windowsZones.xml with additional values deduced from the Windows Registry and documentation. It can be overridden by setting the TZ environment variable before any date-times are used in the session.

Most platforms support time zones of the form `Etc/GMT+n` and `Etc/GMT-n` (possibly also without prefix `Etc/`), which assume a fixed offset from UTC (hence no DST). Contrary to some expectations (but consistent with names such as `PST8PDT`), negative offsets are times ahead of (East of) UTC, positive offsets are times behind (West of) UTC.

Immediately prior to the advent of legislated time zones, most people used time based on their longitude (or that of a nearby town), known as ‘Local Mean Time’ and abbreviated as ‘LMT’ in the databases: in many countries that was codified with a specific name before the switch to a standard time. For example, Paris codified its LMT as ‘Paris Mean Time’ in 1891 (to be used throughout mainland France) and switched to ‘GMT+0’ in 1911.

Some systems (notably Linux) have a tzselect command which allows the interactive selection of a supported time zone name. On systems using systemd (notably Linux), the OS command timedatectl list-timezones will list all available time zone names.

Warnings

There is a system-specific upper limit on the number of bytes in (abbreviated) time-zone names which can be as low as 6 (as required by POSIX). Some OSes allow the setting of time zones with names which exceed their limit, and that can crash the R session.

Information about future times is speculative (‘proleptic’): the database provides the best-known information based on current rules set by civil authorities. For the period 1900–1970 those rules (and which of any authority’s rules were enacted) are often obscure, and the databases do get corrected frequently.

OlsonNames tries to find an Olson database in known locations. It might not succeed (when it returns an empty vector with a warning) and even if it does it might not locate the database used by the date-time code linked into R. Fortunately names are added rarely and most databases are pretty complete. On the other hand, many names which duplicate other named timezones have been
moved to the ‘backward’ list – these are regarded as optional and omitted on minimal installations. Similarly, there are timezones named in file ‘backzone’ which differ only from those in the main lists prior to 1970 – these are usually included but may not be in minimalist systems.

**How the system time zone is found – on Unix-alikes**

This section is of background interest for users of a Unix-alike, but may help if an NA value is returned unexpectedly.

Commercial Unixen such as Solaris and AIX set TZ, so the value when R is started is used.

All other common platforms (Linux, macOS, *BSD) use similar schemes, either derived from tzcode (currently distributed from https://www.iana.org/time-zones) or independently coded (glibc, musl-libc). Such systems read the time-zone information from a file ‘localtime’, usually under ‘/etc’ (but possibly under ‘/usr/local/etc’ or ‘/usr/local/etc/zoneinfo’). As the usual Linux manual page for localtime says

> ‘Because the time zone identifier is extracted from the symlink target name of ‘/etc/localtime’, this file may not be a normal file or hardlink.’

Nevertheless, some Linux distributions (including the one from which that quote was taken) or sysadmins have chosen to copy a time-zone file to ‘localtime’. For a non-symlink, the ultimate fallback is to compare that file to all files in the time-zone database.

Some Linux platforms provide two other mechanisms which are tried in turn before looking at ‘/etc/localtime’.

- ‘Modern’ Linux systems use systemd which provides mechanisms to set and retrieve the time zone (amongst other things). There is a command timedatectl to give details. (Unfortunately RHEL/Centos 6.x were not ‘modern’.)
- Debian-derived systems since ca 2007 have supplied a file ‘/etc/timezone’. Its format is undocumented but empirically it contains a single line of text naming the time zone.

In each case a sanity check is performed that the time-zone name is the name of a file in the time-zone database. (The systems probably use the time-zone file (symlinked to) ‘/etc/localtime’, but the Sys.timezone code does not check that is the same as the named file in the database. This is deliberate as they may be from different dates.)

**Note**

Since 2007 there has been considerable disruption over changes to the timings of the DST transitions, originally aimed at energy conservation. These often have short notice and time-zone databases may not be up to date. (Morocco in 2013 announced a change to the end of DST at a days notice, and in 2015 North Korea gave imprecise information about a change a week in advance. In 2023 there was chaos in Lebanon as the authorities changed their minds repeatedly and some changes were not widely implemented.)

On platforms with case-insensitive file systems, time zone names will be case-insensitive. They may or may not be on other platforms and so, for example, "gmt" is valid on some platforms and not on others.

Note that except where replaced, the operation of time zones is an OS service, and even where replaced a third-party database is used and can be updated (see the section on ‘Time zone names’). Incorrect results will never be an R issue, so please ensure that you have the courtesy not to blame R for them.
See Also

Sys.time, as.POSIXlt.


Examples

Sys.timezone()

str(OlsonNames()) ## typically around six hundred names,
## typically some acronyms/aliases such as "UTC", "NZ", "MET", "Eire", ..., but
## mostly pairs (and triplets) such as "Pacific/Auckland"

table(sl <- grepl("/", OlsonNames()))

OlsonNames()[, sl] # the simple ones

head(Osl <- strsplit(OlsonNames()[sl], "/"))

(tosl <- table(vapply(Osl, `[[`, "", 1))) # Continents, countries, ...

table(lengths(Osl)) # most are pairs, some triplets

str(Osl[lengths(Osl) >= 3]) # "America" South and North ...

toString

Convert an R Object to a Character String

Description

This is a helper function for format to produce a single character string describing an R object.

Usage

toString(x, ...)

Arguments

x The object to be converted.

width Suggestion for the maximum field width. Values of NULL or 0 indicate no maximum. The minimum value accepted is 6 and smaller values are taken as 6.

... Optional arguments passed to or from methods.

Details

This is a generic function for which methods can be written: only the default method is described here. Most methods should honor the width argument to specify the maximum display width (as measured by nchar(type = "width")) of the result.

The default method first converts x to character and then concatenates the elements separated by ", . If width is supplied and is not NULL, the default method returns the first width - 4 characters of the result with .... appended, if the full result would use more than width characters.
Value

A character vector of length 1 is returned.

Author(s)

Robert Gentleman

See Also

format

Examples

x <- c("a", "b", "aaaaaaaaaaa")
toString(x)
toString(x, width = 8)

Description

A call to `trace` allows you to insert debugging code (e.g., a call to `browser` or `recover`) at chosen places in any function. A call to `untrace` cancels the tracing. Specified methods can be traced the same way, without tracing all calls to the generic function. Trace code (tracer) can be any R expression. Tracing can be temporarily turned on or off globally by calling `tracingState`.

Usage

```r
trace(what, tracer, exit, at, print, signature,
     where = topenv(parent.frame()), edit = FALSE)
untrace(what, signature = NULL, where = topenv(parent.frame()))

tracingState(on = NULL)
.doTrace(expr, msg)
returnValue(default = NULL)
```

Arguments

- **what**: the name, possibly `quote()`d, of a function to be traced or untraced. For `untrace` or for `trace` with more than one argument, more than one name can be given in the quoted form, and the same action will be applied to each one. For “hidden” functions such as S3 methods in a namespace, `where = *` typically needs to be specified as well.
- **tracer**: either a `function` or an unevaluated expression. The function will be called or the expression will be evaluated either at the beginning of the call, or before those steps in the call specified by the argument at. See the details section.
- **exit**: either a `function` or an unevaluated expression. The function will be called or the expression will be evaluated on exiting the function. See the details section.
- **at**: optional numeric vector or list. If supplied, tracer will be called just before the corresponding step in the body of the function. See the details section.
If TRUE (as per default), a descriptive line is printed before any trace expression is evaluated.

If this argument is supplied, it should be a signature for a method for function what. In this case, the method, and not the function itself, is traced.

For complicated tracing, such as tracing within a loop inside the function, you will need to insert the desired calls by editing the body of the function. If so, supply the edit argument either as TRUE, or as the name of the editor you want to use. Then trace() will call edit and use the version of the function after you edit it. See the details section for additional information.

where to look for the function to be traced; by default, the top-level environment of the call to trace.

An important use of this argument is to trace functions from a package which are "hidden" or called from another package. The namespace mechanism imports the functions to be called (with the exception of functions in the base package). The functions being called are not the same objects seen from the top-level (in general, the imported packages may not even be attached). Therefore, you must ensure that the correct versions are being traced. The way to do this is to set argument where to a function in the namespace (or that namespace). The tracing computations will then start looking in the environment of that function (which will be the namespace of the corresponding package). (Yes, it's subtle, but the semantics here are central to how namespaces work in R.)

logical; a call to the support function tracingState returns TRUE if tracing is globally turned on, FALSE otherwise. An argument of one or the other of those values sets the state. If the tracing state is FALSE, none of the trace actions will actually occur (used, for example, by debugging functions to shut off tracing during debugging).

arguments to the support function .doTrace, calls to which are inserted into the modified function or method: expr is the tracing action (such as a call to browser()), and msg is a string identifying the place where the trace action occurs.

If returnValue finds no return value (e.g. a function exited because of an error, restart or as a result of evaluating a return from a caller function), it will return default instead.

Details

The trace function operates by constructing a revised version of the function (or of the method, if signature is supplied), and assigning the new object back where the original was found. If only the what argument is given, a line of trace printing is produced for each call to the function (back compatible with the earlier version of trace).

The object constructed by trace is from a class that extends "function" and which contains the original, untraced version. A call to untrace re-assigns this version.

If the argument tracer or exit is the name of a function, the tracing expression will be a call to that function, with no arguments. This is the easiest and most common case, with the functions browser and recover the likeliest candidates; the former browses in the frame of the function being traced, and the latter allows browsing in any of the currently active calls. The arguments tracer and exit are evaluated to see whether they are functions, but only their names are used in the tracing expressions. The lookup is done again when the traced function executes, so it may not be tracer or exit that will be called while tracing.
The tracer or exit argument can also be an unevaluated expression (such as returned by a call to `quote` or `substitute`). This expression itself is inserted in the traced function, so it will typically involve arguments or local objects in the traced function. An expression of this form is useful if you only want to interact when certain conditions apply (and in this case you probably want to supply `print = FALSE` in the call to `trace` also).

When the at argument is supplied, it can be a vector of integers referring to the substeps of the body of the function (this only works if the body of the function is enclosed in `{ . . .}`). In this case tracer is not called on entry, but instead just before evaluating each of the steps listed in at. (Hint: you don’t want to try to count the steps in the printed version of a function; instead, look at `as.list(body(f))` to get the numbers associated with the steps in function f.)

The at argument can also be a list of integer vectors. In this case, each vector refers to a step nested within another step of the function. For example, `at = list(c(3,4))` will call the tracer just before the fourth step of the third step of the function. See the example below.

Using `setBreakpoint` (from package `utils`) may be an alternative, calling `trace(...., at, ...).`

The exit argument is called during on.exit processing. In an on.exit expression, the experimental `returnValue()` function may be called to obtain the value about to be returned by the function. Calling this function in other circumstances will give undefined results.

An intrinsic limitation in the exit argument is that it won’t work if the function itself uses on.exit with `add= FALSE` (the default), since the existing calls will override the one supplied by `trace`.

Tracing does not nest. Any call to `trace` replaces previously traced versions of that function or method (except for edited versions as discussed below), and `untrace` always restores an untraced version. (Allowing nested tracing has too many potentials for confusion and for accidentally leaving traced versions behind.)

When the edit argument is used repeatedly with no call to `untrace` on the same function or method in between, the previously edited version is retained. If you want to throw away all the previous tracing and then edit, call `untrace` before the next call to `trace`. Editing may be combined with automatic tracing; just supply the other arguments such as tracer, and the edit argument as well. The `edit = TRUE` argument uses the default editor (see `edit`).

Tracing primitive functions (builtins and specials) from the base package works, but only by a special mechanism and not very informatively. Tracing a primitive causes the primitive to be replaced by a function with argument ... (only). You can get a bit of information out, but not much. A warning message is issued when `trace` is used on a primitive.

The practice of saving the traced version of the function back where the function came from means that tracing carries over from one session to another, if the traced function is saved in the session image. (In the next session, `untrace` will remove the tracing.) On the other hand, functions that were in a package, not in the global environment, are not saved in the image, so tracing expires with the session for such functions.

Tracing an S4 method is basically just like tracing a function, with the exception that the traced version is stored by a call to `setMethod` rather than by direct assignment, and so is the untraced version after a call to `untrace`.

The version of `trace` described here is largely compatible with the version in S-Plus, although the two work by entirely different mechanisms. The S-Plus `trace` uses the session frame, with the result that tracing never carries over from one session to another (R does not have a session frame). Another relevant distinction has nothing directly to do with `trace`: The browser in S-Plus allows changes to be made to the frame being browsed, and the changes will persist after exiting the browser. The R browser allows changes, but they disappear when the browser exits. This may be relevant in that the S-Plus version allows you to experiment with code changes interactively, but the R version does not. (A future revision may include a ‘destructive’ browser for R.)
Value
In the simple version (just the first argument), trace returns an invisible NULL. Otherwise, the traced function(s) name(s). The relevant consequence is the assignment that takes place.
untrace returns the function name invisibly.
tracingState returns the current global tracing state, and possibly changes it.
When called during on.exit processing, return value returns the value about to be returned by the exiting function. Behaviour in other circumstances is undefined.

Note
Using trace() is conceptually a generalization of debug, implemented differently. Namely by calling browser via its tracer or exit argument.
The version of function tracing that includes any of the arguments except for the function name requires the methods package (because it uses special classes of objects to store and restore versions of the traced functions).
If methods dispatch is not currently on, trace will load the methods namespace, but will not put the methods package on the search list.

References

See Also
browser and recover, the likeliest tracing functions; also, quote and substitute for constructing general expressions.

Examples
require(stats)
## Very simple use
trace(sum)
hist(rnorm(100)) # shows about 3-4 calls to sum()
untrace(sum)

## Show how pt() is called from inside power.t.test():
if(FALSE)
  trace(pt) ## would show ~20 calls, but we want to see more:
  trace(pt, tracer = quote(cat(sprintf("tracing pt(*, ncp = %.15g)\n", ncp))),
        print = FALSE) # <- not showing typical extra
  power.t.test(20, 1, power=0.8, sd=NULL) ##--> showing the ncp root finding:
  untrace(pt)

f <- function(x, y) {
  y <- pmax(y, 0.001)
  if (x > 0) x ^ y else stop("x must be positive")
}

## arrange to call the browser on entering and exiting
## function f
trace("f", quote(browser(skipCalls = 4)), 
    exit = quote(browser(skipCalls = 4)))

## instead, conditionally assign some data, and then browse 
## on exit, but only then. Don’t bother me otherwise
trace("f", quote(if(any(y < 0)) yOrig <- y),
    exit = quote(if(exists("yOrig")) browser(skipCalls = 4),
    print = FALSE))

## Enter the browser just before stop() is called. First, find 
## the step numbers
untrace(f) # (as it has changed f’s body !)
as.list(body(f))
as.list(body(f)[[3]]) # -> stop(...) is [[4]]

## Now call the browser there
trace("f", quote(browser(skipCalls = 4)), at = list(c(3,4)))

## Not run:
f(-1,2) # --> enters browser just before stop(..)

## End(Not run)

## trace a utility function, with recover so we 
## can browse in the calling functions as well.
trace("as.matrix", recover)

## turn off the tracing (that happened above)
untrace(c("f", "as.matrix"))

## Not run:
## Useful to find how system2() is called in a higher-up function:
trace(base::system2, quote(print(ls.str())))

## End(Not run)

#-------- Tracing hidden functions : need 'where = *'
##
## 'where' can be a function whose environment is meant:
trace(quote(ar.yw.default), where = ar)
a <- ar(rnorm(100)) # "Tracing .."
untrace(quote(ar.yw.default), where = ar)

## trace() more than one function simultaneously:
## expression(E1, E2, ...) here is equivalent to
## c(quote(E1), quote(E2), quote(.*, ..))
trace(expression(ar.yw, ar.yw.default), where = ar)
a <- ar(rnorm(100)) # --> 2 x "Tracing .."
# and turn it off:
untrace(expression(ar.yw, ar.yw.default), where = ar)
## Not run:
## trace calls to the function lm() that come from
## the nlme package.
trace("lm", where = asNamespace("nlme"))

lm (len ~ log(dose) * supp, ToothGrowth) -> fit1 # NOT traced
nlme::lmList(len ~ log(dose) | supp, ToothGrowth) -> fit2 # traced
untrace("lm", where = asNamespace("nlme"))

## End(Not run)

### traceback

#### Get and Print Call Stacks

**Description**

By default `traceback()` prints the call stack of the last uncaught error, i.e., the sequence of calls that lead to the error. This is useful when an error occurs with an unidentifiable error message. It can also be used to print the current stack or arbitrary lists of calls.

`.traceback()` now returns the above call stack (and `traceback(x, *)` can be regarded as convenience function for printing the result of `.traceback(x)`).

**Usage**

```r
traceback(x = NULL, max.lines = getOption("traceback.max.lines",
    getOption("deparse.max.lines", -1L)))
```

**Arguments**

- `x` NULL (default, meaning `.Traceback`), or an integer count of calls to skip in the current stack, or a list or pairlist of calls. See the details.
- `max.lines` a number, the maximum number of lines to be printed *per call*. The default is unlimited. Applies only when `x` is `NULL`, a `list` or a `pairlist` of calls, see the details.

**Details**

The default display is of the stack of the last uncaught error as stored as a list of calls in `.Traceback`, which traceback prints in a user-friendly format. The stack of calls always contains all function calls and all foreign function calls (such as `.Call`): if profiling is in progress it will include calls to some primitive functions. (Calls to builtins are included, but not to specials.)

Errors which are caught via `try` or `tryCatch` do not generate a traceback, so what is printed is the call sequence for the last uncaught error, and not necessarily for the last error.

If `x` is numeric, then the current stack is printed, skipping `x` entries at the top of the stack. For example, `options(error = function() traceback(3))` will print the stack at the time of the error, skipping the call to `traceback()` and `.traceback()` and the error function that called it.

Otherwise, `x` is assumed to be a list or pairlist of calls or deparsed calls and will be displayed in the same way.
.traceback() and by extension traceback() may trigger deparsing of calls. This is an expensive operation for large calls so it may be advisable to set max.lines to a reasonable value when such calls are on the call stack.

**Value**

.traceback() returns the deparsed call stack deepest call first as a list or pairlist. The number of lines deparsed from the call can be limited via max.lines. Calls for which max.lines results in truncated output will gain a "truncated" attribute.

traceback() formats, prints, and returns the call stack produced by .traceback() invisibly.

**Warning**

It is undocumented where .Traceback is stored nor that it is visible, and this is subject to change. Currently .Traceback contains the calls as language objects.

**References**


**Examples**

foo <- function(x) { print(1); bar(2) }
bar <- function(x) { x + a.variable.which.does.not.exist }

## Not run:
foo(2) # gives a strange error
traceback()
## End(Not run)
## 2: bar(2)
## 1: foo(2)
bar
## Ah, this is the culprit ...

## This will print the stack trace at the time of the error.
options(error = function() traceback(3))

---

**tracemem**

*Trace Copying of Objects*

**Description**

This function marks an object so that a message is printed whenever the internal code copies the object. It is a major cause of hard-to-predict memory use in R.

**Usage**

tracemem(x)
untracemem(x)
retracemem(x, previous = NULL)
Arguments

- **x**: An R object, not a function or environment or NULL.
- **previous**: A value as returned by tracemem or retracemem.

Details

This functionality is optional, determined at compilation, because it makes R run a little more slowly even when no objects are being traced. tracemem and untracemem give errors when R is not compiled with memory profiling: retracemem does not (so it can be left in code during development).

It is enabled in the CRAN macOS and Windows builds of R.

When an object is traced any copying of the object by the C function duplicate produces a message to standard output, as does type coercion and copying when passing arguments to .C or .Fortran.

The message consists of the string tracemem, the identifying strings for the object being copied and the new object being created, and a stack trace showing where the duplication occurred. retracemem() is used to indicate that a variable should be considered a copy of a previous variable (e.g., after subscipting).

The messages can be turned off with tracingState.

It is not possible to trace functions, as this would conflict with trace and it is not useful to trace NULL, environments, promises, weak references, or external pointer objects, as these are not duplicated.

These functions are primitive.

Value

A character string for identifying the object in the trace output (an address in hex enclosed in angle brackets), or NULL (invisibly).

See Also

- capabilities("profmem") to see if this was enabled for this build of R.
- trace, Rprofmem
- https://developer.r-project.org/memory-profiling.html

Examples

```r
## Not run:
a <- 1:10
tracemem(a)
## b and a share memory
b <- a
b[1] <- 1
untracemem(a)

## copying in lm: less than R <= 2.15.0
d <- stats::rnorm(10)
tracemem(d)
lm(d ~ a+log(b))

## f is not a copy and is not traced
f <- d[-1]
```
transform

Transform an Object, for Example a Data Frame

Description

transform is a generic function, which—at least currently—only does anything useful with data frames. transform.default converts its first argument to a data frame if possible and calls transform.data.frame.

Usage

transform(`_data`, ...)

Arguments

_data The object to be transformed
...
Further arguments of the form tag=value

Details

The ... arguments to transform.data.frame are tagged vector expressions, which are evaluated in the data frame _data. The tags are matched against names(_data), and for those that match, the value replace the corresponding variable in _data, and the others are appended to _data.

Value

The modified value of _data.

Warning

This is a convenience function intended for use interactively. For programming it is better to use the standard subsetting arithmetic functions, and in particular the non-standard evaluation of argument transform can have unanticipated consequences.

Note

If some of the values are not vectors of the appropriate length, you deserve whatever you get!

Author(s)

Peter Dalgaard

See Also

within for a more flexible approach, subset.list, data.frame
Examples

```r
transform(airquality, Ozone = -Ozone)
transform(airquality, new = -Ozone, Temp = (Temp-32)/1.8)
attach(airquality)
transform(Ozone, logOzone = log(Ozone)) # marginally interesting ...
detach(airquality)
```

Trig

Trigonometric Functions

Description

These functions give the obvious trigonometric functions. They respectively compute the cosine, sine, tangent, arc-cosine, arc-sine, arc-tangent, and the two-argument arc-tangent.

`cospi(x)`, `sinpi(x)`, and `tanpi(x)`, compute `cos(pi*x)`, `sin(pi*x)`, and `tan(pi*x)`.

Usage

```r
cos(x)
sin(x)
tan(x)
acos(x)
asin(x)
atan(x)
atan2(y, x)
cospi(x)
sinpi(x)
tanpi(x)
```

Arguments

`x, y` numeric or complex vectors.

Details

The arc-tangent of two arguments `atan2(y, x)` returns the angle between the x-axis and the vector from the origin to `(x, y)`, i.e., for positive arguments `atan2(y, x) == atan(y/x)`.

Angles are in radians, not degrees, for the standard versions (i.e., a right angle is \( \pi/2 \)), and in ‘half-rotations’ for `cospi` etc.

`cospi(x)`, `sinpi(x)`, and `tanpi(x)` are accurate for `x` values which are multiples of a half.

All except `atan2` are internal generic primitive functions: methods can be defined for them individually or via the `Math` group generic.

These are all wrappers to system calls of the same name (with prefix `c` for complex arguments) where available. (`cospi`, `sinpi`, and `tanpi` are part of a C11 extension and provided by e.g. macOS and Solaris: where not yet available call to `cos` etc are used, with special cases for multiples of a half.)
Value

tanpi(0.5) is NaN. Similarly for other inputs with fractional part 0.5.

Complex values

For the inverse trigonometric functions, branch cuts are defined as in Abramowitz and Stegun, figure 4.4, page 79. For asin and acos, there are two cuts, both along the real axis: (−∞, −1] and [1, ∞).

For atan there are two cuts, both along the pure imaginary axis: (−∞i, −1i] and [1i, ∞i).

The behaviour actually on the cuts follows the C99 standard which requires continuity coming round the endpoint in a counter-clockwise direction.

Complex arguments for cospi, sinpi, and tanpi are not yet implemented, and they are a ‘future direction’ of ISO/IEC TS 18661-4.

S4 methods

All except atan2 are S4 generic functions: methods can be defined for them individually or via the Math group generic.

References


Chapter 4. Elementary Transcendental Functions: Logarithmic, Exponential, Circular and Hyperbolic Functions


Examples

```r
x <- seq(-3, 7, by = 1/8)
tx <- cbind(x, cos(pi*x), cospi(x), sin(pi*x), sinpi(x),
            tan(pi*x), tanpi(x), deparse.level=2)
op <- options(digits = 4, width = 90) # for nice formatting
head(tx)
tx[(x %% 1) %in% c(0, 0.5),]
options(op)
```

trimws

Remove Leading/Trailing Whitespace

Description

Remove leading and/or trailing whitespace from character strings.

Usage

```r
trimws(x, which = c("both", "left", "right"), whitespace = "[ \t\r\n"]")
```
Arguments

x
which
whitespace

Arguments

x a character vector
which a character string specifying whether to remove both leading and trailing whitespace (default), or only leading ("left") or trailing ("right"). Can be abbreviated.
whitespace a string specifying a regular expression to match (one character of) "white space", see Details for alternatives to the default.

Details

Internally, sub(re, ",", *, perl = TRUE), i.e., PCRE library regular expressions are used. For portability, the default 'whitespace' is the character class \[ \t\r\n\] (space, horizontal tab, carriage return, newline). Alternatively, [\h\v] is a good (PCRE) generalization to match all Unicode horizontal and vertical white space characters, see also https://www.pcre.org.

Examples

x <- " Some text. "
x
trimws(x)
trimws(x, "l")
trimws(x, "r")

## Unicode --> need "stronger" 'whitespace' to match all :
tt <- "text with unicode 'non breakable space'."
xu <- paste(" \t\v", tt, "\u00a0 \n\r")
(tu <- trimws(xu, whitespace = "[\\h\\v]"))
stopifnot(identical(tu, tt))

try

Try an Expression Allowing Error Recovery

Description

try is a wrapper to run an expression that might fail and allow the user’s code to handle error-recovery.

Usage

try(expr, silent = FALSE,
     outFile = getOption("try.outFile", default = stderr()))

Arguments

expr an R expression to try.
silent logical: should the report of error messages be suppressed?
outFile a connection, or a character string naming the file to print to (via cat(*, file = outFile)); used only if silent is false, as by default.
Details

try evaluates an expression and traps any errors that occur during the evaluation. If an error occurs then the error message is printed to the stderr connection unless options("show.error.messages") is false or the call includes silent = TRUE. The error message is also stored in a buffer where it can be retrieved by geterrmessage. (This should not be needed as the value returned in case of an error contains the error message.)

try is implemented using tryCatch; for programming, instead of try(expr, silent = TRUE), something like tryCatch(expr, error = function(e) e) (or other simple error handler functions) may be more efficient and flexible.

It may be useful to set the default for outFile to stdout(), i.e.,

    options(try.outFile = stdout())

instead of the default stderr(), notably when try() is used inside a Sweave code chunk and the error message should appear in the resulting document.

Value

The value of the expression if expr is evaluated without error: otherwise an invisible object inheriting from class "try-error" containing the error message with the error condition as the "condition" attribute.

Warning

Do not test

    if (class(res) == "try-error")

as if there is no error, the result might (now or in future) have a class of length > 1. Use

    if(inherits(res, "try-error"))

instead.

See Also

options for setting error handlers and suppressing the printing of error messages; geterrmessage for retrieving the last error message. The underlying tryCatch provides more flexible means of catching and handling errors.

assertCondition in package tools is related and useful for testing.

Examples

## this example will not work correctly in example(try), but
## it does work correctly if pasted in
options(show.error.messages = FALSE)
try(log("a"))
print(.Last.value)
options(show.error.messages = TRUE)

## alternatively,
print(try(log("a"), TRUE))

## run a simulation, keep only the results that worked.
set.seed(123)
x <- stats::rnorm(50)
doit <- function(x)
{
    x <- sample(x, replace = TRUE)
    if(length(unique(x)) > 30) mean(x)
    else stop("too few unique points")
}
## alternative 1
res <- lapply(1:100, function(i) try(doit(x), TRUE))
## alternative 2
## Not run: res <- vector("list", 100)
for(i in 1:100) res[[i]] <- try(doit(x), TRUE)
## End(Not run)
unlist(res[sapply(res, function(x) !inherits(x, "try-error"))])

typeof

The Type of an Object

Description

typeof determines the (R internal) type or storage mode of any object

Usage

typeof(x)

Arguments

x  any R object.

Value

A character string. The possible values are listed in the structure TypeTable in 'src/main/util.c'. Current values are the vector types "logical", "integer", "double", "complex", "character", "raw" and "list", "NULL", "closure" (function), "special" and "builtin" (basic functions and operators), "environment", "S4" (some S4 objects) and others that are unlikely to be seen at user level ("symbol", "pairlist", "promise", "language", "char", "...", "any", "expression", "externalptr", "bytecode" and "weakref").

See Also

mode, storage.mode.
isS4 to determine if an object has an S4 class.

Examples

typeof(2)
mode(2)
## for a table of examples, see ?mode / examples(mode)
Extract Unique Elements

**Description**
unique returns a vector, data frame or array like x but with duplicate elements/rows removed.

**Usage**
unique(x, incomparables = FALSE, ...)

## Default S3 method:
unique(x, incomparables = FALSE, fromLast = FALSE, nmax = NA, ...)

## S3 method for class 'matrix'
unique(x, incomparables = FALSE, MARGIN = 1, fromLast = FALSE, ...)

## S3 method for class 'array'
unique(x, incomparables = FALSE, MARGIN = 1, fromLast = FALSE, ...)

**Arguments**
x a vector or a data frame or an array or NULL.
incomparables a vector of values that cannot be compared. FALSE is a special value, meaning that all values can be compared, and may be the only value accepted for methods other than the default. It will be coerced internally to the same type as x.
fromLast logical indicating if duplication should be considered from the last, i.e., the last (or rightmost) of identical elements will be kept. This only matters for names or dimnames.
nmax the maximum number of unique items expected (greater than one). See duplicated.
... arguments for particular methods.
MARGIN the array margin to be held fixed: a single integer.

**Details**
This is a generic function with methods for vectors, data frames and arrays (including matrices). The array method calculates for each element of the dimension specified by MARGIN if the remaining dimensions are identical to those for an earlier element (in row-major order). This would most commonly be used for matrices to find unique rows (the default) or columns (with MARGIN = 2).
Note that unlike the Unix command uniq this omits duplicated and not just repeated elements/rows. That is, an element is omitted if it is equal to any previous element and not just if it is equal the immediately previous one. (For the latter, see rle).
Missing values ("NA") are regarded as equal, numeric and complex ones differing from NaN; character strings will be compared in a "common encoding"; for details, see match (and duplicated) which use the same concept.
Values in `incomparables` will never be marked as duplicated. This is intended to be used for a fairly small set of values and will not be efficient for a very large set.

When used on a data frame with more than one column, or an array or matrix when comparing dimensions of length greater than one, this tests for identity of character representations. This will catch people who unwisely rely on exact equality of floating-point numbers!

**Value**

For a vector, an object of the same type of `x`, but with only one copy of each duplicated element. No attributes are copied (so the result has no names).

For a data frame, a data frame is returned with the same columns but possibly fewer rows (and with row names from the first occurrences of the unique rows).

A matrix or array is subsetted by `[ , drop = FALSE]`, so dimensions and dimnames are copied appropriately, and the result always has the same number of dimensions as `x`.

**Warning**

Using this for lists is potentially slow, especially if the elements are not atomic vectors (see `vector`) or differ only in their attributes. In the worst case it is $O(n^2)$.

**References**


**See Also**

`duplicated` which gives the indices of duplicated elements.

`rle` which is the equivalent of the Unix `uniq -c` command.

**Examples**

```r
x <- c(3:5, 11:8, 8 + 0:5)
(ux <- unique(x))
(u2 <- unique(x, fromLast = TRUE))  # different order
stopifnot(identical(sort(ux), sort(u2)))

length(unique(sample(100, 100, replace = TRUE)))
## approximately 100(1 - 1/e) = 63.21

unique(iris)
```

---

**units**

**Units**

**Description**

Get or set units.

**Usage**

```r
units(x)
units(x) <- value
```
Arguments

x  an R object
value  an R object

Details

These are generic functions, with methods for "difftime" objects.

Description

unlink deletes the file(s) or directories specified by x.

Usage

unlink(x, recursive = FALSE, force = FALSE, expand = TRUE)

Arguments

x  a character vector with the names of the file(s) or directories to be deleted.
recursive  logical. Should directories be deleted recursively?
force  logical. Should permissions be changed (if possible) to allow the file or directory to be removed?
expand  logical. Should wildcards (see 'Details' below) and tilde (see path.expand) be expanded?

Details

If recursive = FALSE directories are not deleted, not even empty ones.
On most platforms 'file' includes symbolic links, fifos and sockets. unlink(x, recursive = TRUE) deletes just the symbolic link if the target of such a link is a directory.

Wildcard expansion (normally '*' and '?' are allowed) is done by the internal code of Sys.glob. Wildcards never match a leading '.' in the filename, and files '.', '..', and '~' will never be considered for deletion. Wildcards will only be expanded if the system supports it. Most systems will support not only '* and '?' but also character classes such as '[a-z]' (see the man pages for the system call glob on your OS). The metacharacters * ? [ can occur in Unix filenames, and this makes it difficult to use unlink to delete such files (see file.remove), although escaping the metacharacters by backslashes usually works. If a metacharacter matches nothing it is considered as a literal character.

recursive = TRUE might not be supported on all platforms, when it will be ignored, with a warning: however there are no known current examples.

Value

0 for success, 1 for failure, invisibly. Not deleting a non-existent file is not a failure, nor is being unable to delete a directory if recursive = FALSE. However, missing values in x are regarded as failures.
References


See Also

`file.remove`.

---

**unlist**

**Flatten Lists**

**Description**

Given a list structure `x`, `unlist` simplifies it to produce a vector which contains all the atomic components which occur in `x`.

**Usage**

```r
unlist(x, recursive = TRUE, use.names = TRUE)
```

**Arguments**

- `x` an R object, typically a list or vector.
- `recursive` logical. Should unlisting be applied to list components of `x`?
- `use.names` logical. Should names be preserved?

**Details**

`unlist` is generic: you can write methods to handle specific classes of objects, see `InternalMethods`, and note, e.g., `relist` with the `unlist` method for `relistable` objects.

If `recursive = FALSE`, the function will not recurse beyond the first level items in `x`.

Factors are treated specially. If all non-list elements of `x` are `factor` (or ordered factor) objects then the result will be a factor with levels the union of the level sets of the elements, in the order the levels occur in the level sets of the elements (which means that if all the elements have the same level set, that is the level set of the result).

`x` can be an atomic vector, but then `unlist` does nothing useful, not even drop names.

By default, `unlist` tries to retain the naming information present in `x`. If `use.names = FALSE` all naming information is dropped.

Where possible the list elements are coerced to a common mode during the unlisting, and so the result often ends up as a character vector. Vectors will be coerced to the highest type of the components in the hierarchy `NULL < raw < logical < integer < double < complex < character < list < expression`: pairlists are treated as lists.

A list is a (generic) vector, and the simplified vector might still be a list (and might be unchanged). Non-vector elements of the list (for example language elements such as names, formulas and calls) are not coerced, and so a list containing one or more of these remains a list. (The effect of unlisting an `lm` fit is a list which has individual residuals as components.) Note that `unlist(x)` now returns `x` unchanged also for non-vector `x`, instead of signalling an error in that case.
Value

NULL or an expression or a vector of an appropriate mode to hold the list components.
The output type is determined from the highest type of the components in the hierarchy
NULL < raw < logical < integer < double < complex < character < list < expression, after coercion of pairlists
to lists.

References

Brooks/Cole.

See Also

c, as.list, relist.

Examples

unlist(options())
unlist(options(), use.names = FALSE)

l.ex <- list(a = list(1:5, LETTERS[1:5]), b = "Z", c = NA)
unlist(l.ex, recursive = FALSE)
unlist(l.ex, recursive = TRUE)

l1 <- list(a = "a", b = 2, c = pi+2i)
unlist(l1) # a character vector
l2 <- list(a = "a", b = as.name("b"), c = pi+2i)
unlist(l2) # remains a list

ll <- list(as.name("sinc"), quote( a + b ), 1:10, letters, expression(1+x))
utils::str(ll)
for(x in ll)
  stopifnot(identical(x, unlist(x)))

\begin{tabular}{ll}
\hline
\textbf{uname} & \textbf{Remove names or dimnames} \\
\hline
\end{tabular}

Description

Remove the \texttt{names} or \texttt{dimnames} attribute of an \texttt{R} object.

Usage

\texttt{unname(obj, force = FALSE)}

Arguments

\begin{itemize}
\item \texttt{obj} \hspace{1cm} an \texttt{R} object.
\item \texttt{force} \hspace{1cm} logical; if true, the \texttt{dimnames} (names and row names) are removed even from \texttt{data.frames}.
\end{itemize}
Value
Object as obj but without names or dimnames.

Examples
require(graphics); require(stats)
## Answering a question on R-help (14 Oct 1999):
col3 <- 750+ 100*rt(1500, df = 3)
breaks <- factor(cut(col3, breaks = 360+5*(0:155)))
z <- table(breaks)
z[1:5] # The names are larger than the data ...
barplot(unname(z), axes = FALSE)

Description
R possesses a simple generic function mechanism which can be used for an object-oriented style of programming. Method dispatch takes place based on the class(es) of the first argument to the generic function or of the object supplied as an argument to UseMethod or NextMethod.

Usage
UseMethod(generic, object)
NextMethod(generic = NULL, object = NULL, ...)

Arguments
generic a character string naming a function (and not a built-in operator). Required for UseMethod.
object for UseMethod: an object whose class will determine the method to be dis-patched. Defaults to the first argument of the enclosing function.
... further arguments to be passed to the next method.

Details
An R object is a data object which has a class attribute (and this can be tested by is.object). A class attribute is a character vector giving the names of the classes from which the object inherits.

If the object does not have a class attribute, it has an implicit class. Matrices and arrays have class "matrix" or "array" followed by the class of the underlying vector. Most vectors have class the result of mode(x), except that integer vectors have class c("integer", "numeric") and real vectors have class c("double", "numeric"). Function .class2(x) (since R 4.0.x) returns the full implicit (or explicit) class vector of x.

When a function calling UseMethod("fun") is applied to an object with class vector c("first", "second"), the system searches for a function called fun.first and, if it finds it, applies it to the object. If no such function is found a function called fun.second is tried. If no class name produces a suitable function, the function fun.default is used, if it exists, or an error results.
Function \texttt{methods} can be used to find out about the methods for a particular generic function or class.

\texttt{UseMethod} is a primitive function but uses standard argument matching. It is not the only means of dispatch of methods, for there are \texttt{internal generic} and \texttt{group generic} functions. \texttt{UseMethod} currently dispatches on the implicit class even for arguments that are not objects, but the other means of dispatch do not.

\texttt{NextMethod} invokes the next method (determined by the class vector, either of the object supplied to the generic, or of the first argument to the function containing \texttt{NextMethod} if a method was invoked directly). Normally \texttt{NextMethod} is used with only one argument, \texttt{generic}, but if further arguments are supplied these modify the call to the next method.

\texttt{NextMethod} should not be called except in methods called by \texttt{UseMethod} or from internal generics (see \texttt{InternalGenerics}). In particular it will not work inside anonymous calling functions (e.g., \texttt{get("print.ts")}(AirPassengers)).

Namespaces can register methods for generic functions. To support this, \texttt{UseMethod} and \texttt{NextMethod} search for methods in two places: in the environment in which the generic function is called, and in the registration data base for the environment in which the generic is defined (typically a namespace). So methods for a generic function need to be available in the environment of the call to the generic, or they must be registered. (It does not matter whether they are visible in the environment in which the generic is defined.) As from \texttt{R 3.5.0}, the registration data base is searched after the top level environment (see \texttt{topenv}) of the calling environment (but before the parents of the top level environment).

**Technical Details**

Now for some obscure details that need to appear somewhere. These comments will be slightly different than those in Chambers(1992). (See also the draft ‘R Language Definition’.) \texttt{UseMethod} creates a new function call with arguments matched as they came in to the generic. Any local variables defined before the call to \texttt{UseMethod} are retained (unlike S). Any statements after the call to \texttt{UseMethod} will not be evaluated as \texttt{UseMethod} does not return. \texttt{UseMethod} can be called with more than two arguments: a warning will be given and additional arguments ignored. (They are not completely ignored in S.) If it is called with just one argument, the class of the first argument of the enclosing function is used as \texttt{object}: unlike S this is the first actual argument passed and not the current value of the object of that name.

\texttt{NextMethod} works by creating a special call frame for the next method. If no new arguments are supplied, the arguments will be the same in number, order and name as those to the current method but their values will be promises to evaluate their name in the current method and environment. Any named arguments matched to ... are handled specially: they either replace existing arguments of the same name or are appended to the argument list. They are passed on as the promise that was supplied as an argument to the current environment. (S does this differently!) If they have been evaluated in the current (or a previous environment) they remain evaluated. (This is a complex area, and subject to change: see the draft ‘R Language Definition’.)

The search for methods for \texttt{NextMethod} is slightly different from that for \texttt{UseMethod}. Finding no \texttt{fun.default} is not necessarily an error, as the search continues to the generic itself. This is to pick up an \texttt{internal generic} like [ which has no separate default method, and succeeds only if the generic is a \texttt{primitive} function or a wrapper for a .\texttt{Internal} function of the same name. (When a primitive is called as the default method, argument matching may not work as described above due to the different semantics of primitives.)

You will see objects such as .\texttt{Generic}, .\texttt{Method}, and .\texttt{Class} used in methods. These are set in the environment within which the method is evaluated by the dispatch mechanism, which is as follows:
1. Find the context for the calling function (the generic): this gives us the unevaluated arguments for the original call.

2. Evaluate the object (usually an argument) to be used for dispatch, and find a method (possibly the default method) or throw an error.

3. Create an environment for evaluating the method and insert special variables (see below) into that environment. Also copy any variables in the environment of the generic that are not formal (or actual) arguments.

4. Fix up the argument list to be the arguments of the call matched to the formals of the method.

GenericType is a length-one character vector naming the generic function.

Method is a character vector (normally of length one) naming the method function. (For functions in the group generic Ops it is of length two.)

Class is a character vector of classes used to find the next method. NextMethod adds an attribute "previous" to .Class giving the .Class last used for dispatch, and shifts .Class along to that used for dispatch.

GenericCallEnv and GenericDefEnv are the environments of the call to be generic and defining the generic respectively. (The latter is used to find methods registered for the generic.)

Note that .Class is set when the generic is called, and is unchanged if the class of the dispatching argument is changed in a method. It is possible to change the method that NextMethod would dispatch by manipulating .Class, but 'this is not recommended unless you understand the inheritance mechanism thoroughly' (Chambers & Hastie, 1992, p. 469).

Note

This scheme is called S3 (S version 3). For new projects, it is recommended to use the more flexible and robust S4 scheme provided in the methods package.

References


See Also

The draft ‘R Language Definition’.
methods, class incl .class2(); getS3method, is.object.

userhooks Functions to Get and Set Hooks for Load, Attach, Detach and Unload

Description

These functions allow users to set actions to be taken before packages are attached/detached and namespaces are (un)loaded.
Usage

getHook(hookName)
setHook(hookName, value,
    action = c("append", "prepend", "replace"))
packageEvent(pkgname,
    event = c("onLoad", "attach", "detach", "onUnload"))

Arguments

hookName
    character string: the hook name
pkgname
    character string: the package/namespace name
event
    character string: an event for the package. Can be abbreviated.
value
    A function or a list of functions, or for action = "replace", NULL
action
    The action to be taken. Can be abbreviated.

Details

setHook provides a general mechanism for users to register hooks, a list of functions to be called from system (or user) functions. The initial set of hooks was associated with events on packages/namespaces: these hooks are named via calls to packageEvent.

To remove a hook completely, call setHook(hookName, NULL, "replace").

When an R package is attached by library or loaded by other means, it can call initialization code. See .onLoad for a description of the package hook functions called during initialization. Users can add their own initialization code via the hooks provided by setHook(), functions which will be called as funname(pkgname, pkgpath) inside a try call.

The sequence of events depends on which hooks are defined, and whether a package is attached or just loaded. In the case where all hooks are defined and a package is attached, the order of initialization events is as follows:

1. The package namespace is loaded.
2. The package’s .onLoad function is run.
3. If S4 methods dispatch is on, any actions set by setLoadAction are run.
4. The namespace is sealed.
5. The user’s "onLoad" hook is run.
6. The package is added to the search path.
7. The package’s .onAttach function is run.
8. The package environment is sealed.
9. The user’s "attach" hook is run.

A similar sequence (but in reverse) is run when a package is detached and its namespace unloaded:

1. The user’s "detach" hook is run.
2. The package’s .Last.lib function is run.
3. The package is removed from the search path.
4. The user’s "onUnload" hook is run.
5. The package’s .onUnload function is run.
6. The package namespace is unloaded.

Note that when an R session is finished, packages are not detached and namespaces are not unloaded, so the corresponding hooks will not be run.

Also note that some of the user hooks are run without the package being on the search path, so in those hooks objects in the package need to be referred to using the double (or triple) colon operator, as in the example.

If multiple hooks are added, they are normally run in the order shown by getHook, but the "detach" and "onUnload" hooks are run in reverse order so the default for package events is to add hooks ‘inside’ existing ones.

The hooks are stored in the environment .userHooksEnv in the base package, with ‘mangled’ names.

Value

For getHook function, a list of functions (possibly empty). For setHook function, no return value. For packageEvent, the derived hook name (a character string).

Note

Hooks need to be set before the event they modify: for standard packages this can be problematic as methods is loaded and attached early in the startup sequence. The usual place to set hooks such as the example below is in the ‘.Rprofile’ file, but that will not work for methods.

See Also

library, detach, loadNamespace.

See :: for a discussion of the double and triple colon operators.

Other hooks may be added later: functions plot.new and persp already have them.

Examples

setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::ps.options(horizontal = FALSE))

utf8Conversion Convert Integer Vectors to or from UTF-8-encoded Character Vectors

Description

Conversion of UTF-8 encoded character vectors to and from integer vectors representing a UTF-32 encoding.

Usage

utf8ToInt(x)
intToUtf8(x, multiple = FALSE, allow_surrogate_pairs = FALSE)
Arguments

- **x**: object to be converted.
- **multiple**: logical: should the conversion be to a single character string or multiple individual characters?
- **allow_surrogate_pairs**: logical: should interpretation of surrogate pairs be attempted? (See ‘Details’.)
  Only supported for `multiple = FALSE`.

Details

These will work in any locale, including on platforms that do not otherwise support multi-byte character sets.

Unicode defines a name and a number of all of the glyphs it encompasses: the numbers are called *code points*: since RFC3629 they run from 0 to 0x10FFFF (with about 5% being assigned by version 13.0 of the Unicode standard and 7% reserved for ‘private use’).

`intToUtf8` does not by default handle surrogate pairs: inputs in the surrogate ranges are mapped to `NA`. They might occur if a UTF-16 byte stream has been read as 2-byte integers (in the correct byte order), in which case `allow_surrogate_pairs = TRUE` will try to interpret them (with unmatched surrogate values still treated as `NA`).

Value

`utf8ToInt` converts a length-one character string encoded in UTF-8 to an integer vector of Unicode code points.

`intToUtf8` converts a numeric vector of Unicode code points either (default) to a single character string or a character vector of single characters. Non-integral numeric values are truncated to integers. For output to a single character string 0 is silently omitted: otherwise 0 is mapped to “”. The *Encoding* of a non-NA return value is declared as “UTF-8”.

Invalid and NA inputs are mapped to NA output.

Validity

Which code points are regarded as valid has changed over the lifetime of UTF-8. Originally all 32-bit unsigned integers were potentially valid and could be converted to up to 6 bytes in UTF-8. Since 2003 it has been stated that there will never be valid code points larger than 0x10FFFF, and so valid UTF-8 encodings are never more than 4 bytes.

The code points in the surrogate-pair range 0xD800 to 0xDFFF are prohibited in UTF-8 and so are regarded as invalid by `utf8ToInt` and by default by `intToUtf8`.

The position of ‘noncharacters’ (notably 0xFFFE and 0xFFFF) was clarified by ‘Corrigendum 9’ in 2013. These are valid but will never be given an official interpretation. (In some earlier versions of R `utf8ToInt` treated them as invalid.)

References

Examples

```r
## will only display in some locales and fonts
intToUtf8(0x03B2L) # Greek beta

utf8ToInt("b\u00dfchen")
utf8ToInt("\xa4\xb4\xbfunf")

## A valid UTF-16 surrogate pair (for U+10437)
x <- c(0x0801, 0xDC37)
intToUtf8(x)
intToUtf8(x, TRUE)
(xx <- intToUtf8(x, , TRUE)) # will only display in some locales and fonts
charToRaw(xx)

## An example of how surrogate pairs might occur
x <- "\U10437"
charToRaw(x)
foo <- tempfile()
writeLines(x, file(foo, encoding = "UTF-16LE"))

## next two are OS-specific, but are mandated by POSIX
system(paste("od -x", foo)) # 2-byte units, correct on little-endian platforms
system(paste("od -t x1", foo)) # single bytes as hex
y <- readBin(foo, "integer", 2, 2, FALSE, endian = "little")
sprintf("%X", y)
intToUtf8(y, , TRUE)
```

Description

Most modern file systems store file-path components (names of directories and files) in a character encoding of wide scope: usually UTF-8 on a Unix-alike and UCS-2/UTF-16 on Windows. However, this was not true when R was first developed and there are still exceptions amongst file systems, e.g. FAT32.

This was not something anticipated by the C and POSIX standards which only provide means to access files *via* file paths encoded in the current locale, for example those specified in Latin-1 in a Latin-1 locale.

Everything here apart from the specific section on Windows is about Unix-alikes.

Details

It is possible to mark character strings (elements of character vectors) as being in UTF-8 or Latin-1 (see Encoding). This allows file paths not in the native encoding to be expressed in R character vectors but there is almost no way to use them unless they can be translated to the native encoding. That is of course not a problem if that is UTF-8, so these details are really only relevant to the use of a non-UTF-8 locale (including a C locale) on a Unix-alike.

Functions to open a file such as `file`, `fifo`, `gzfile`, `bzfile`, `xzfile` and `unz` give an error for non-native filepaths. Where functions look at existence such as `file.exists`, `dir.exists`, `unlink`, `file.info` and `list.files`, non-native filepaths are treated as non-existent.
Many other functions use `file` or `gzfile` to open their files.
`file.path` allows non-native file paths to be combined, marking them as UTF-8 if needed.
`path.expand` only handles paths in the native encoding.

### Windows

Windows provides proprietary entry points to access its file systems, and these gained ‘wide’ versions in Windows NT that allowed file paths in UCS-2/UTF-16 to be accessed from any locale.

Some R functions use these entry points when file paths are marked as Latin-1 or UTF-8 to allow access to paths not in the current encoding. These include:


and

- `dir.create`, `dir.exists`, `normalizePath`, `path.expand`, `pipe`, `Sys.glob`, `Sys.junction`, `unlink`

but not `gzfile bzipfile`, `xzfile` nor `unz`.

For functions using `gzfile` (including `load`, `readRDS`, `read.dcf` and `tar`), it is often possible to use a `gzcon` connection wrapping a `file` connection.

Other notable exceptions are `list.files`, `list.dirs`, `system` and file-path inputs for graphics devices.

### Historical comment

Before R 4.0.0, file paths marked as being in Latin-1 or UTF-8 were silently translated to the native encoding using escapes such as ‘<e7>’ or ‘\U+00e7’’. This created valid file names but maybe not those intended.

### Note

This document is still a work-in-progress.
Details

These use similar checks to those used by functions such as `grep`.
`validUTF8` ignores any marked encoding (see `Encoding`) and so looks directly if the bytes in each string are valid UTF-8. (For the validity of ‘noncharacters’ see the help for `intToUtf8`.)
`validEnc` regards character strings as validly encoded unless their encodings are marked as UTF-8 or they are unmarked and the R session is in a UTF-8 or other multi-byte locale. (The checks in other multi-byte locales depend on the OS and as with `iconv` not all invalid inputs may be detected.)

Value

A logical vector of the same length as `x`. NA elements are regarded as validly encoded.

Note

It would be possible to check for the validity of character strings in a Latin-1 encoding, but extensions such as CP1252 are widely accepted as ‘Latin-1’ and 8-bit encodings rarely need to be checked for validity.

Examples

```r
x <-
  ## from example(text)
  c("Jetz", "no", "chi", "z\xc3\xbcrit\xc3\xbcr\xc3\xbctsche:",
    "(noch", "ein", "b\xc3\xbch\xc3\xbchen", "\xc3\xbc\xc3\xbch", "deutsch")

validUTF8(x)
validEnc(x) # depends on the locale
Encoding(x) <-"UTF-8"
validEnc(x) # typically the last, x[10], is invalid

## Maybe advantageous to declare it "unknown":
G <- x ; Encoding(G[!validEnc(G)]) <- "unknown"
try( substr(x, 1,1) ) # gives 'invalid multibyte string' error in a UTF-8 locale
try( substr(G, 1,1) ) # works in a UTF-8 locale
nchar(G) # fine, too

## but it is not "more valid" typically:
all.equal(validEnc(x),
  validEnc(G)) # typically TRUE
```

Description

A vector in R is either an atomic vector i.e., one of the atomic types, see ‘Details’, or of type (typeof) or mode `list` or `expression`.

vector produces a ‘simple’ vector of the given length and mode, where a ‘simple’ vector has no attribute, i.e., fulfills is.null(attributes(.)).

as.vector, a generic, attempts to coerce its argument into a vector of mode node (the default is to coerce to whichever vector mode is most convenient): if the result is atomic (is.atomic), all attributes are removed. For mode="any", see ‘Details’.
is.vector(x) returns TRUE if x is a vector of the specified mode having no attributes other than names. For mode="any", see ‘Details’.

Usage

vector(mode = "logical", length = 0)
as.vector(x, mode = "any")
is.vector(x, mode = "any")

Arguments

mode character string naming an atomic mode or "list" or "expression" or (except for vector) "any". Currently, is.vector() allows any type (see typeof) for mode, and when mode is not "any", is.vector(x, mode) is almost the same as typeof(x) == mode.

length a non-negative integer specifying the desired length. For a long vector, i.e., length > .Machine$integer.max, it has to be of type "double". Supplying an argument of length other than one is an error.

x an R object.

Details

The atomic modes are "logical", "integer", "numeric" (synonym "double"), "complex", "character" and "raw".

If mode = "any", is.vector may return TRUE for the atomic modes, list and expression. For any mode, it will return FALSE if x has any attributes except names. (This is incompatible with S.)

On the other hand, as.vector removes all attributes including names for results of atomic mode.

For mode = "any", and atomic vectors x, as.vector(x) strips all attributes (including names), returning a simple atomic vector.

However, when x is of type "list" or "expression", as.vector(x) currently returns the argument x unchanged, unless there is an as.vector method for class(x).

Note that factors are not vectors; is.vector returns FALSE and as.vector converts a factor to a character vector for mode = "any".

Value

For vector, a vector of the given length and mode. Logical vector elements are initialized to FALSE, numeric vector elements to 0, character vector elements to ””, raw vector elements to nul bytes and list/expression elements to NULL.

For as.vector, a vector (atomic or of type list or expression). All attributes are removed from the result if it is of an atomic mode, but not in general for a list or expression result. The default method handles 24 input types and 12 values of type: the details of most coercions are undocumented and subject to change.

For is.vector, TRUE or FALSE. is.vector(x, mode = "numeric") can be true for vectors of types "integer" or "double" whereas is.vector(x, mode = "double") can only be true for those of type "double".

Methods for as.vector()

 Writers of methods for as.vector need to take care to follow the conventions of the default method. In particular
• Argument mode can be "any", any of the atomic modes, "list", "expression", "symbol", "pairlist" or one of the aliases "double" and "name".

• The return value should be of the appropriate mode. For mode = "any" this means an atomic vector or list or expression.

• Attributes should be treated appropriately: in particular when the result is an atomic vector there should be no attributes, not even names.

• is.vector(as.vector(x, m), m) should be true for any mode m, including the default "any".

Currently this is not fulfilled in R when m == "any" and x is of type list or expression with attributes in addition to names — typically the case for (S3 or S4) objects (see is.object) which are lists internally.

Note

as.vector and is.vector are quite distinct from the meaning of the formal class "vector" in the methods package, and hence as(x, "vector") and is(x, "vector").

Note that as.vector(x) is not necessarily a null operation if is.vector(x) is true: any names will be removed from an atomic vector.

Non-vector modes "symbol" (synonym "name") and "pairlist" are accepted but have long been undocumented: they are used to implement as.name and as.pairlist, and those functions should preferably be used directly. None of the description here applies to those modes: see the help for the preferred forms.

References


See Also

c, is.numeric, is.list, etc.

Examples

df <- data.frame(x = 1:3, y = 5:7)
## Error:
try(as.vector(data.frame(x = 1:3, y = 5:7), mode = "numeric"))

x <- c(a = 1, b = 2)
is.vector(x)
as.vector(x)
all.equal(x, as.vector(x)) ## FALSE

###-- All the following are TRUE:
is.list(df)
! is.vector(df)
! is.vector(df, mode = "list")
is.vector(list(), mode = "list")
Description

Vectorize creates a function wrapper that vectorizes the action of its argument FUN.

Usage

Vectorize(FUN, vectorize.args = arg.names, SIMPLIFY = TRUE,
          USE.NAMES = TRUE)

Arguments

FUN function to apply, found via match.fun.
vectorize.args a character vector of arguments which should be vectorized. Defaults to all
arguments of FUN.
SIMPLIFY logical or character string; attempt to reduce the result to a vector, matrix or
higher dimensional array; see the simplify argument of sapply.
USE.NAMES logical; use names if the first ...argument has names, or if it is a character vector,
use that character vector as the names.

Details

The arguments named in the vectorize.args argument to Vectorize are the arguments passed in
the ... list to mapply. Only those that are actually passed will be vectorized; default values will
not. See the examples.

Vectorize cannot be used with primitive functions as they do not have a value for formals.
It also cannot be used with functions that have arguments named FUN, vectorize.args, SIMPLIFY
or USE.NAMES, as they will interfere with the Vectorize arguments. See the combn example below
for a workaround.

Value

A function with the same arguments as FUN, wrapping a call to mapply.

Examples

# We use rep.int as rep is primitive
vrep <- Vectorize(rep.int)
vrep(1:4, 4:1)
vrep(times = 1:4, x = 4:1)

vrep <- Vectorize(rep.int, "times")
vrep(times = 1:4, x = 42)

f <- function(x = 1:3, y) c(x, y)
vf <- Vectorize(f, SIMPLIFY = FALSE)
f(1:3, 1:3)
vf(1:3, 1:3)
vf(y = 1:3) # Only vectorizes y, not x
# Nonlinear regression contour plot, based on nls() example
require(graphics)

SS <- function(Vm, K, resp, conc) {
  pred <- (Vm * conc)/(K + conc)
  sum((resp - pred)^2 / pred)
}

vSS <- Vectorize(SS, c("Vm", "K"))
Treated <- subset(Puromycin, state == "treated")

Vm <- seq(140, 310, length.out = 50)
K <- seq(0, 0.15, length.out = 40)
SSvals <- outer(Vm, K, vSS, Treated$rate, Treated$conc)
contour(Vm, K, SSvals, levels = (1:10)^2, xlab = "Vm", ylab = "K")

# combn() has an argument named FUN
combnV <- Vectorize(function(x, m, FUNV = NULL) combn(x, m, FUN = FUNV),
                    vectorize.args = c("x", "m"))

combnV(4, 1:4)
combnV(4, 1:4, sum)

---

warning  Warning Messages

**Description**

Generates a warning message that corresponds to its argument(s) and (optionally) the expression or function from which it was called.

**Usage**

```r
warning(..., call. = TRUE, immediate. = FALSE, noBreaks. = FALSE,
         domain = NULL)
```

```r
suppressWarnings(expr, classes = "warning")
```

**Arguments**

- `...` zero or more objects which can be coerced to character (and which are pasted together with no separator) or a single condition object.
- `call.` logical, indicating if the call should become part of the warning message.
- `immediate.` logical, indicating if the call should be output immediately, even if `getOption("warn") <= 0`.
- `noBreaks.` logical, indicating as far as possible the message should be output as a single line when `options(warn = 1)`.
- `expr` expression to evaluate.
- `domain` see `gettext`. If NA, messages will not be translated, see also the note in `stop`.
- `classes` character, indicating which classes of warnings should be suppressed.
Details

The result depends on the value of \texttt{options("warn")} and on handlers established in the executing code.

If a condition object is supplied it should be the only argument, and further arguments will be ignored, with a message.

\texttt{warning} signals a warning condition by (effectively) calling \texttt{signalCondition}. If there are no handlers or if all handlers return, then the value of \texttt{warn = getOption("warn")} is used to determine the appropriate action. If \texttt{warn} is negative warnings are ignored; if it is zero they are stored and printed after the top-level function has completed; if it is one they are printed as they occur and if it is \texttt{2} (or larger) warnings are turned into errors. Calling \texttt{warning(immediate. = TRUE)} turns \texttt{warn <= 0} into \texttt{warn = 1} for this call only.

If \texttt{warn} is zero (the default), a read-only variable \texttt{last.warning} is created. It contains the warnings which can be printed via a call to \texttt{warnings}.

Warnings will be truncated to \texttt{getOption("warning.length")} characters, default \texttt{1000}, indicated by \texttt{[... truncated]}

While the warning is being processed, a \texttt{muffleWarning} restart is available. If this restart is invoked with \texttt{invokeRestart}, then \texttt{warning} returns immediately.

An attempt is made to coerce other types of inputs to \texttt{warning} to character vectors.

\texttt{suppressWarnings} evaluates its expression in a context that ignores all warnings.

Value

The warning message as \texttt{character} string, invisibly.

References


See Also

\texttt{stop} for fatal errors, \texttt{message} for diagnostic messages, \texttt{warnings}, and \texttt{options} with argument \texttt{warn=}.

\texttt{gettext} for the mechanisms for the automated translation of messages.

Examples

\begin{verbatim}
  testit <- function() warning("testit")
  testit() ## shows call
  testit <- function() warning("problem in testit", call. = FALSE)
  testit() ## no call
  suppressWarnings(warning("testit"))
\end{verbatim}
warnings

Print Warning Messages

Description

warnings and its print method print the variable last.warning in a pleasing form.

Usage

warnings(...)

## S3 method for class 'warnings'
summary(object, ...)

## S3 method for class 'warnings'
print(x, tags,
        header = ngettext(n, "Warning message:\n", "Warning messages:\n"),
        ...)  
## S3 method for class 'summary.warnings'
print(x, ...)

Arguments

... arguments to be passed to cat (for warnings()).
object a "warnings" object as returned by warnings().
x a "warnings" or "summary.warnings" object.
tags if not missing, a character vector of the same length as x, to "label" the messages. Defaults to paste0(seq_len(n), ": ") for \( n \geq 2 \) where \( n \leftarrow \text{length}(x) \).
header a character string cat()ed before the messages are printed.

Details

See the description of options("warn") for the circumstances under which there is a last.warning object and warnings() is used. In essence this is if options(warn = 0) and warning has been called at least once.

Note that the length(last.warning) is maximallygetOption("nwarnings") (at the time the warnings are generated) which is 50 by default. To increase, use something like

options(nwarnings = 10000)

It is possible that last.warning refers to the last recorded warning and not to the last warning, for example if options(warn) has been changed or if a catastrophic error occurred.

Value

warnings() returns an object of S3 class "warnings", basically a named list.
summary(<warnings>) returns a "summary.warnings" object which is basically the list of unique warnings (unique(object)) with a "counts" attribute, somewhat experimentally.
weekdays

Warning

It is undocumented where last.warning is stored nor that it is visible, and this is subject to change.

References


See Also

warning.

Examples

## NB this example is intended to be pasted in, ## rather than run by example()
ow <- options("warn")
for(w in -1:1) {
  options(warn = w); cat("\n warn =", w, "\n")
  for(i in 1:3) { cat(i,"\n"); m <- matrix(1:7, 3,4) }
  cat("======
")
}
## at the end prints all three warnings, from the 'option(warn = 0)' above
options(ow) # reset to previous, typically 'warn = 0'
tail(warnings(), 2) # see the last two warnings only (via '[' method)

## Often the most useful way to look at many warnings:
summary(warnings())

op <- options(nwarnings = 10000) ## <- get "full statistics"
x <- 1:36; for(n in 1:13) for(m in 1:12) A <- matrix(x, n,m) # There were 105 warnings ... 
summary(warnings())
options(op) # revert to previous (keeping 50 messages by default)

weekdays

Extract Parts of a POSIXt or Date Object

Description

Extract the weekday, month or quarter, or the Julian time (days since some origin). These are generic functions: the methods for the internal date-time classes are documented here.

Usage

weekdays(x, abbreviate)
## S3 method for class 'POSIXt'
weekdays(x, abbreviate = FALSE)
## S3 method for class 'Date'
weekdays(x, abbreviate = FALSE)

months(x, abbreviate)
## S3 method for class 'POSIXt'
months(x, abbreviate = FALSE)
weekdays

## S3 method for class 'Date'
months(x, abbreviate = FALSE)

quarters(x, abbreviate)
## S3 method for class 'POSIXt'
quarters(x, ...)
## S3 method for class 'Date'
quarters(x, ...)

julian(x, ...)
## S3 method for class 'POSIXt'
julian(x, origin = as.POSIXct("1970-01-01", tz = "GMT"), ...)  
## S3 method for class 'Date'
julian(x, origin = as.Date("1970-01-01"), ...)

Arguments

x       an object inheriting from class "POSIXt" or "Date".
abbreviate logical vector (possibly recycled). Should the names be abbreviated?
origin   an length-one object inheriting from class "POSIXt" or "Date".
...      arguments for other methods.

Value

weekdays and months return a character vector of names in the locale in use, i.e.,
Sys.getlocale("LC_TIME").
quarters returns a character vector of "Q1" to "Q4".
julian returns the number of days (possibly fractional) since the origin, with the origin as a
"origin" attribute. All time calculations in R are done ignoring leap-seconds.

Note

Other components such as the day of the month or the year are very easy to compute: just use
as.POSIXlt and extract the relevant component. Alternatively (especially if the components are
desired as character strings), use strftime.

See Also

DateTimeClasses, Date; Sys.getlocale("LC_TIME") crucially for months() and weekdays().

Examples

## first two are locale dependent:
weekdays(.leap.seconds)
months (.leap.seconds)
quarters(.leap.seconds)

## Show how easily you get month, day, year, day (of month, week, yr), ... :
## (remember to count from 0 (!): mon = 0..11, wday = 0..6, etc !!)

##' Transform (Time-)Date vector to convenient data frame :
dt2df <- function(dt, dName = deparse(substitute(dt))) {
  DF <- as.data.frame(unclass(as.POSIXlt( dt )))
}
## is the number of days since noon UTC on the first day of 4317 BCE.
## in the proleptic Julian calendar. To more recently, in
## 'Terrestrial Time' which differs from UTC by a few seconds
## See https://en.wikipedia.org/wiki/Terrestrial_Time
julian(Sys.Date(), -2440588) # from a day
floor(as.numeric(julian(Sys.time())) + 2440587.5) # from a date-time

## Which indices are TRUE?

### Description

Give the TRUE indices of a logical object, allowing for array indices.

### Usage

```r
give
t(x, arr.ind = FALSE, useNames = TRUE) 
arrayInd(ind, .dim, .dimnames = NULL, useNames = FALSE)
```  

### Arguments

- `x` 
  - a logical vector or array. NAs are allowed and omitted (treated as if FALSE).
- `arr.ind` 
  - logical; should array indices be returned when `x` is an array? Anything other than a single true value is treated as false.
- `ind` 
  - integer-valued index vector, as resulting from `which(x)`.
- `.dim` 
  - `dim(.)` integer vector
- `.dimnames` 
  - optional list of character `dimnames(.)`. If useNames is true, to be used for constructing dimnames for `arrayInd()` (and hence, which(x, arr.ind=TRUE)). If names(.dimnames) is not empty, these are used as column names. .dimnames[[1]] is used as row names.
- `useNames` 
  - logical indicating if the value of arrayInd() should have (non-null) dimnames at all.
Value

If arr.ind == FALSE (the default), an integer vector, or a double vector if x is a long vector, with length equal to sum(x), i.e., to the number of TRUEs in x.

Basically, the result is (1:length(x))[x] in typical cases; more generally, including when x has NA’s, which(x) is seq_along(x)[!is.na(x) & x] plus names when x has.

If arr.ind == TRUE and x is an array (has a dim attribute), the result is arrayInd(which(x), dim(x), dimnames(x)), namely a matrix whose rows each are the indices of one element of x; see Examples below.

Note

Unlike most other base R functions this does not coerce x to logical: only arguments with typeof logical are accepted and others give an error.

Author(s)

Werner Stahel and Peter Holzer (ETH Zurich) proposed the arr.ind option.

See Also

Logic, which.min for the index of the minimum or maximum, and match for the first index of an element in a vector, i.e., for a scalar a, match(a, x) is equivalent to min(which(x == a)) but much more efficient.

Examples

which(LETTERS == "R")
which(ll <- c(TRUE, FALSE, TRUE, NA, FALSE, FALSE, TRUE)) #> 1 3 7
names(ll) <- letters[seq(ll)]
which(ll)
which((1:12)%%2 == 0) # which are even?
which(1:10 > 3, arr.ind = TRUE)

( m <- matrix(1:12, 3, 4) )
div.3 <- m %% 3 == 0
which(div.3)
which(div.3, arr.ind = TRUE)
rownames(m) <- paste("Case", 1:3, sep = ",")
which(m %% 5 == 0, arr.ind = TRUE)

dim(m) <- c(2, 2, 3); m
which(div.3, arr.ind = FALSE)
which(div.3, arr.ind = TRUE)

vm <- c(m)
dim(vm) <- length(vm) #-- funny thing with length(dim(...)) == 1
which(div.3, arr.ind = TRUE)
which.min

Where is the Min() or Max() or first TRUE or FALSE?

Description

Determines the location, i.e., index of the (first) minimum or maximum of a numeric (or logical) vector.

Usage

```
which.min(x)
which.max(x)
```

Arguments

- `x` numeric (logical, integer or double) vector or an \( \mathcal{R} \) object for which the internal coercion to `double` works whose `min` or `max` is searched for.

Value

Missing and NaN values are discarded.

- an `integer` or on 64-bit platforms, if `length(x) =: n \geq 2^{31}` an integer valued `double` of length 1 or 0 (iff \( x \) has no non-NAs), giving the index of the first minimum or maximum respectively of \( x \).

If this extremum is unique (or empty), the results are the same as (but more efficient than) `which(x == min(x, na.rm = TRUE))` or `which(x == max(x, na.rm = TRUE))` respectively.

Logical \( x \) – First TRUE or FALSE

For a logical vector \( x \) with both FALSE and TRUE values, `which.min(x)` and `which.max(x)` return the index of the first FALSE or TRUE, respectively, as FALSE < TRUE. However, `match(FALSE, x)` or `match(TRUE, x)` are typically preferred, as they do indicate mismatches.

Author(s)

Martin Maechler

See Also

- `which`, `max.col`, `max`, etc.
- Use `arrayInd()`, if you need array/matrix indices instead of 1D vector ones.
- `which.is.max` in package `nnet` differs in breaking ties at random (and having a ‘fuzz’ in the definition of ties).

Examples

```
x <- c(1:4, 0:5, 11)
which.min(x)
which.max(x)
```

```
## it *does* work with NA's present, by discarding them:
presidents[1:30]
```
range(presidents, na.rm = TRUE)
which.min(presidents)  # 28
which.max(presidents)  # 2

## Find the first occurrence, i.e. the first TRUE, if there is at least one:
x <- rpois(10000, lambda = 10); x[sample.int(50, 20)] <- NA
## where is the first value >= 20 ?
which.max(x >= 20)

## Also works for lists (which can be coerced to numeric vectors):
which.min(list(A = 7, pi = pi))  # -> c(pi = 3.14L)

---

**with**

Evaluate an Expression in a Data Environment

**Description**

Evaluate an R expression in an environment constructed from data, possibly modifying (a copy of) the original data.

**Usage**

```r
with(data, expr, ...)
within(data, expr, ...)
## S3 method for class 'list'
within(data, expr, keepAttrs = TRUE, ...)
```

**Arguments**

- `data` data to use for constructing an environment. For the default `with` method this may be an environment, a list, a data frame, or an integer as in `sys.call`. For `within`, it can be a list or a data frame.
- `expr` expression to evaluate; particularly for `within()` often a “compound” expression, i.e., of the form
  ```r
  {  
  a <- somefun()
  b <- otherfun()
  .....  
  rm(unused1, temp)
  }
  ```
- `keepAttrs` for the `list` method of `within()`, a logical specifying if the resulting list should keep the attributes from data and have its names in the same order. Often this is unneeded as the result is a named list anyway, and then `keepAttrs = FALSE` is more efficient.
- `...` arguments to be passed to (future) methods.
with is a generic function that evaluates expr in a local environment constructed from data. The environment has the caller’s environment as its parent. This is useful for simplifying calls to modeling functions. (Note: if data is already an environment then this is used with its existing parent.) Note that assignments within expr take place in the constructed environment and not in the user’s workspace.

within is similar, except that it examines the environment after the evaluation of expr and makes the corresponding modifications to a copy of data (this may fail in the data frame case if objects are created which cannot be stored in a data frame), and returns it. within can be used as an alternative to transform.

Value
For with, the value of the evaluated expr. For within, the modified object.

Note
For interactive use this is very effective and nice to read. For programming however, i.e., in one’s functions, more care is needed, and typically one should refrain from using with(), as, e.g., variables in data may accidentally override local variables, see the reference.

Further, when using modeling or graphics functions with an explicit data argument (and typically using formulas), it is typically preferred to use the data argument of that function rather than to use with(data, ...).

References

See Also
evalq, attach, assign, transform.

Examples
with(mtcars, mpg[cyl == 8 & disp > 350])
  # is the same as, but nicer than
mtcars$mpg[mtcars$cyl == 8 & mtcars$disp > 350]

require(stats); require(graphics)
  # examples from glm:
with(data.frame(u = c(5,10,15,20,30,40,60,80,100),
  lot1 = c(118,58,42,35,27,25,21,19,18),
  lot2 = c(69,35,26,21,18,16,13,12,12)),
  list(summary(glm(lot1 ~ log(u), family = Gamma)),
       summary(glm(lot2 ~ log(u), family = Gamma))))

aq <- with(airquality, {
  # Notice that multiple vars can be changed
  Ozone <- log(Ozone)
  Month <- factor(month.abb[Month])
  cTemp <- round((Temp - 32) * 5/9, 1) # From Fahrenheit to Celsius
  S.cT <- Solar.R / cTemp # using the newly created variable
  rm(Day, Temp)
# example from boxplot:
with(ToothGrowth, {
    boxplot(len ~ dose, boxwex = 0.25, at = 1:3 - 0.2,
        subset = (supp == "VC"), col = "yellow",
        main = "Guinea Pigs' Tooth Growth",
        xlab = "Vitamin C dose mg",
        ylab = "tooth length", ylim = c(0, 35))
    boxplot(len ~ dose, add = TRUE, boxwex = 0.25, at = 1:3 + 0.2,
        subset = supp == "OJ", col = "orange")
    legend(2, 9, c("Ascorbic acid", "Orange juice"),
        fill = c("yellow", "orange"))
})

# alternate form that avoids subset argument:
with(subset(ToothGrowth, supp == "VC"),
    boxplot(len ~ dose, boxwex = 0.25, at = 1:3 - 0.2,
        col = "yellow", main = "Guinea Pigs' Tooth Growth",
        xlab = "Vitamin C dose mg",
        ylab = "tooth length", ylim = c(0, 35)))
with(subset(ToothGrowth, supp == "OJ"),
    boxplot(len ~ dose, add = TRUE, boxwex = 0.25, at = 1:3 + 0.2,
        col = "orange"))
legend(2, 9, c("Ascorbic acid", "Orange juice"),
    fill = c("yellow", "orange"))

withVisible

Return both a Value and its Visibility

Description

This function evaluates an expression, returning it in a two element list containing its value and a flag showing whether it would automatically print.

Usage

withVisible(x)

Arguments

x an expression to be evaluated.

Details

The argument, not an expression object, rather an (unevaluated function) call, is evaluated in the caller’s context.

This is a primitive function.
Value

- **value**: The value of \( x \) after evaluation.
- **visible**: logical; whether the value would auto-print.

See Also

- `invisible`, `eval`; `withAutoprint()` calls `source()` which itself uses `withVisible()` in order to correctly “auto print”.

Examples

```r
x <- 1
withVisible(x <- 1) # *$visible is FALSE
x
withVisible(x) # *$visible is TRUE

# Wrap the call in evalq() for special handling
df <- data.frame(a = 1:5, b = 1:5)
evalq(withVisible(a + b), envir = df)
```

**write**

**Write Data to a File**

Description

The data (usually a matrix) \( x \) are written to file \( file \). If \( x \) is a two-dimensional matrix you need to transpose it to get the columns in \( file \) the same as those in the internal representation.

Usage

```r
write(x, file = "data",
      ncolumns = if(is.character(x)) 1 else 5,
      append = FALSE, sep = " ")
```

Arguments

- **x**: the data to be written out, usually an atomic vector.
- **file**: a `connection`, or a character string naming the file to write to. If "", print to the standard output connection. When `.Platform$OS.type != "windows"`, and it is "|cmd", the output is piped to the command given by ‘cmd’.
- **ncolumns**: the number of columns to write the data in.
- **append**: if TRUE the data \( x \) are appended to the connection.
- **sep**: a string used to separate columns. Using `sep = "\t"` gives tab delimited output; default is " ".

References

See Also

write is a wrapper for cat, which gives further details on the format used.

save for writing any R objects, write.table for data frames, and scan for reading data.

Examples

# create a 2 by 5 matrix
x <- matrix(1:10, ncol = 5)

fil <- tempfile("data")
# the file data contains x, two rows, five cols
# 1 3 5 7 9 will form the first row
write(t(x), fil)
if(interactive()) file.show(fil)
unlink(fil) # tidy up

# Writing to the "console" 'tab-delimited'
# two rows, five cols but the first row is 1 2 3 4 5
write(x, "", sep = "\t")
xtfrm

Auxiliary Function for Sorting and Ranking

Description

A generic auxiliary function that produces a numeric vector which will sort in the same order as x.

Usage

xtfrm(x)

Arguments

x

an R object.

Details

This is a special case of ranking, but as a less general function than rank is more suitable to be made generic. The default method is similar to rank(x, ties.method = "min", na.last = "keep"), so NA values are given rank NA and all tied values are given equal integer rank.

The factor method extracts the codes.

The default method will unclass the object if is.numeric(x) is true but otherwise make use of == and > methods for the class of x[1] (for integers i), and the is.na method for the class of x, but might be rather slow when doing so.

This is an internal generic primitive, so S3 or S4 methods can be written for it. Differently to other internal generics, the default method is called explicitly when no other dispatch has happened.

Value

A numeric (usually integer) vector of the same length as x.

See Also

rank, sort, order.
**zapsmall**

**Rounding of Numbers: Zapping Small Ones to Zero**

**Description**

zapsmall determines a digits argument dr for calling round(x, digits = dr) such that values close to zero (compared with the maximal absolute value) are ‘zapped’, i.e., replaced by 0.

**Usage**

zapsmall(x, digits = getOption("digits"))

**Arguments**

- **x**: a numeric or complex vector or any R number-like object which has a `round` method and basic arithmetic methods including `log10()`.
- **digits**: integer indicating the precision to be used.

**References**


**Examples**

```r
x2 <- pi * 100^(-1:3)
print(x2 / 1000, digits = 4)
zapsmall(x2 / 1000, digits = 4)
zapsmall(exp(1i*0:4*pi/2))
```

---

**zpackages**

**Listing of Packages**

**Description**

.packages returns information about package availability.

**Usage**

.packages(all.available = FALSE, lib.loc = NULL)

**Arguments**

- **all.available**: logical; if TRUE return a character vector of all available packages in lib.loc.
- **lib.loc**: a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to .libPaths().
Details

.packages() returns the names of the currently attached packages invisibly whereas.packages(all.available = TRUE) gives (visibly) all packages available in the library location path lib.loc.

For a package to be regarded as being ‘available’ it must have valid metadata (and hence be an installed package). However, this will report a package as available if the metadata does not match the directory name: use find.package to confirm that the metadata match or installed.packages for a much slower but more comprehensive check of ‘available’ packages.

Value

A character vector of package base names, invisible unless all.available = TRUE.

Note

.packages(all.available = TRUE) is not a way to find out if a small number of packages are available for use: not only is it expensive when thousands of packages are installed, it is an incomplete test. See the help for find.package for why require should be used.

Author(s)

R core; Guido Masarotto for the all.available = TRUE part of .packages.

See Also

library, .libPaths, installed.packages.

Examples

.packages()            # maybe just "base"
.packages(all.available = TRUE)  # return all available as character vector
require(splines)
.packages()            # "splines", too
detach("package:splines")

zutils

Miscellaneous Internal/Programming Utilities

Description

Miscellaneous internal/programming utilities.

Usage

.standard_regexps()

Details

.standard_regexps returns a list of ‘standard’ regexps, including elements named valid_package_name and valid_package_version with the obvious meanings. The regexps are not anchored.
Chapter 2

The compiler package

---

**compile**  
**Byte Code Compiler**

---

**Description**

These functions provide an interface to a byte code compiler for R.

**Usage**

```r
cmpfun(f, options = NULL)
compile(e, env = .GlobalEnv, options = NULL, srcref = NULL)
cmpfile(infile, outfile, ascii = FALSE, env = .GlobalEnv,
         verbose = FALSE, options = NULL, version = NULL)
loadcmp(file, envir = .GlobalEnv, chdir = FALSE)
disassemble(code)
enableJIT(level)
compilePKGS(enable)
getCompilerOption(name, options)
setCompilerOptions(...)
```

**Arguments**

- **f**  
a closure.
- **options**  
list of named compiler options: see ‘Details’.
- **env**  
the top level environment for the compiling.
- **srcref**  
initial source reference for the expression.
- **file, infile, outfile**  
pathnames; outfile defaults to infile with a ‘.Rc’ extension in place of any existing extension.
- **ascii**  
logical; should the compiled file be saved in ascii format?
- **verbose**  
logical; should the compiler show what is being compiled?
- **version**  
the workspace format version to use. NULL specifies the current default format (3). Version 1 was the default from R 0.99.0 to R 1.3.1 and version 2 from R 1.4.0 to 3.5.0. Version 3 is supported from R 3.5.0.
Details

The function `cmpfun` compiles the body of a closure and returns a new closure with the same formals and the body replaced by the compiled body expression.

`compile` compiles an expression into a byte code object; the object can then be evaluated with `eval`.

`cmpfile` parses the expressions in `infile`, compiles them, and writes the compiled expressions to `outfile`. If `outfile` is not provided, it is formed from `infile` by replacing or appending a `.Rc` suffix.

`loadcmp` is used to load compiled files. It is similar to `sys.source`, except that its default loading environment is the global environment rather than the base environment.

`disassemble` produces a printed representation of the code that may be useful to give a hint of what is going on.

`enableJIT` enables or disables just-in-time (JIT) compilation. JIT is disabled if the argument is 0. If `level` is 1 then larger closures are compiled before their first use. If `level` is 2, then some small closures are also compiled before their second use. If `level` is 3 then in addition all top level loops are compiled before they are executed. JIT level 3 requires the compiler option `optimize` to be 2 or 3. The JIT level can also be selected by starting `R` with the environment variable `R_ENABLE_JIT` set to one of these values. Calling `enableJIT` with a negative argument returns the current JIT level. The default JIT level is 3.

`compilePKGS` enables or disables compiling packages when they are installed. This requires that the package uses lazy loading as compilation occurs as functions are written to the lazy loading data base. This can also be enabled by starting `R` with the environment variable `_R_COMPILE_PKGS_` set to a positive integer value. This should not be enabled outside package installation, because it causes any serialized function to be compiled, which comes with time and space overhead. `R_COMPILE_PKGS` can be used, instead, to instruct `INSTALL` to enable/disable compilation of packages during installation.

Currently the compiler warns about a variety of things. It does this by using `cat` to print messages. Eventually this should use the condition handling mechanism.

The `options` argument can be used to control compiler operation. There are currently four options: `optimize`, `suppressAll`, `suppressUndefined`, and `suppressNoSuperAssignVar`. `optimize` specifies the optimization level, an integer from 0 to 3 (the current out-of-the-box default is 2). `suppressAll` should be a scalar logical; if `TRUE` no messages will be shown (this is the default). `suppressUndefined` can be `TRUE` to suppress all messages about undefined variables, or it can be a character vector of the names of variables for which messages should not be shown. `suppressNoSuperAssignVar` can be `TRUE` to suppress messages about super assignments to a variable for which no binding is visible at compile time. During compilation of packages, `suppressAll` is currently `FALSE`, `suppressUndefined` is `TRUE` and `suppressNoSuperAssignVar` is `TRUE`.

`getCompilerOption` returns the value of the specified option. The default value is returned unless a value is supplied in the `options` argument; the `options` argument is primarily for internal use.
setCompilerOption sets the default option values. Options to set are identified by argument names, e.g. `setCompilerOptions(suppressAll = TRUE, optimize = 3)`. It returns a named list of the previous values.

Calling the compiler a byte code compiler is actually a bit of a misnomer: the external representation of code objects currently uses int operands, and when compiled with gcc the internal representation is actually threaded code rather than byte code.

**Author(s)**

Luke Tierney

**Examples**

```r
oldJIT <- enableJIT(0)  # a simple example
f <- function(x) x+1
fc <- cmpfun(f)
f(2)
disassemble(fc)

# old R version of lapply
la1 <- function(X, FUN, ...) {
  FUN <- match.fun(FUN)
  if (!is.list(X))
    X <- as.list(X)
  rval <- vector("list", length(X))
  for(i in seq_along(X))
    rval[i] <- list(FUN(X[[i]], ...))
  names(rval) <- names(X)  # keep 'names'
  return(rval)
}

# a small variation
la2 <- function(X, FUN, ...) {
  FUN <- match.fun(FUN)
  if (!is.list(X))
    X <- as.list(X)
  rval <- vector("list", length(X))
  for(i in seq_along(X)) {
    v <- FUN(X[[i]], ...)
    if (is.null(v)) rval[i] <- list(v)
    else rval[[i]] <- v
  }
  names(rval) <- names(X)  # keep 'names'
  return(rval)
}

# Compiled versions
la1c <- cmpfun(la1)
la2c <- cmpfun(la2)
# some timings
x <- 1:10
y <- 1:100

system.time(for (i in 1:10000) lapply(x, is.null))
system.time(for (i in 1:10000) la1(x, is.null))
system.time(for (i in 1:10000) la1c(x, is.null))
system.time(for (i in 1:10000) la2(x, is.null))
```
system.time(for (i in 1:10000) la2c(x, is.null))
system.time(for (i in 1:1000) lapply(y, is.null))
system.time(for (i in 1:1000) la1(y, is.null))
system.time(for (i in 1:1000) la1c(y, is.null))
system.time(for (i in 1:1000) la2(y, is.null))
system.time(for (i in 1:1000) la2c(y, is.null))

enableJIT(oldJIT)
Chapter 3

The datasets package

---

datasets-package  The R Datasets Package

Description

Base R datasets

Details

This package contains a variety of datasets. For a complete list, use library(help = "datasets").

Author(s)

R Core Team and contributors worldwide
Maintainer: R Core Team <R-core@r-project.org>

---

ability.cov  Ability and Intelligence Tests

Description

Six tests were given to 112 individuals. The covariance matrix is given in this object.

Usage

ability.cov
Details

The tests are described as

- **general**: a non-verbal measure of general intelligence using Cattell’s culture-fair test.
- **picture**: a picture-completion test
- **blocks**: block design
- **maze**: mazes
- **reading**: reading comprehension
- **vocab**: vocabulary

Bartholomew gives both covariance and correlation matrices, but these are inconsistent. Neither are in the original paper.

Source


References


Examples

```r
require(stats)
(ability.FA <- factanal(factors = 1, covmat = ability.cov))
update(ability.FA, factors = 2)
## The signs of factors and hence the signs of correlations are
## arbitrary with promax rotation.
update(ability.FA, factors = 2, rotation = "promax")
```

|----------|------------------------------------------------------|

Description

The revenue passenger miles flown by commercial airlines in the United States for each year from 1937 to 1960.

Usage

- `airmiles`

Format

AirPassengers

Source

F.A.A. Statistical Handbook of Aviation.

References


Examples

```r
require(graphics)
plot(airmiles, main = "airmiles data",
xlab = "Passenger-miles flown by U.S. commercial airlines", col = 4)
```

AirPassengers

*Monthly Airline Passenger Numbers 1949-1960*

Description

The classic Box & Jenkins airline data. Monthly totals of international airline passengers, 1949 to 1960.

Usage

AirPassengers

Format

A monthly time series, in thousands.

Source


Examples

```r
## Not run:
## These are quite slow and so not run by example(AirPassengers)
## The classic 'airline model', by full ML
(fit <- arima(log10(AirPassengers), c(0, 1, 1),
seasonal = list(order = c(0, 1, 1), period = 12)))
update(fit, method = "CSS")
update(fit, x = window(log10(AirPassengers), start = 1954))
pred <- predict(fit, n.ahead = 24)
tl <- pred$pred - 1.96 * pred$se
tu <- pred$pred + 1.96 * pred$se
ts.plot(AirPassengers, 10^tl, 10^tu, log = "y", lty = c(1, 2, 2))
## full ML fit is the same if the series is reversed, CSS fit is not
ap0 <- rev(log10(AirPassengers))
attributes(ap0) <- attributes(AirPassengers)
arima(ap0, c(0, 1, 1), seasonal = list(order = c(0, 1, 1), period = 12))
```
```r
arima(ap0, c(0, 1, 1), seasonal = list(order = c(0, 1, 1), period = 12),
       method = "CSS")

## Structural Time Series
ap <- log10(AirPassengers) - 2
(fit <- StructTS(ap, type = "BSM"))
par(mfrow = c(1, 2))
plot(cbind(ap, fitted(fit)), plot.type = "single")
plot(cbind(ap, tsSmooth(fit)), plot.type = "single")

## End(Not run)
```

---

### airquality

**New York Air Quality Measurements**

**Description**


**Usage**

`airquality`

**Format**

A data frame with 153 observations on 6 variables.

```r
[,1] Ozone  numeric  Ozone (ppb)
[,3] Wind   numeric  Wind (mph)
[,4] Temp   numeric  Temperature (degrees F)
[,5] Month  numeric  Month (1–12)
```

**Details**

Daily readings of the following air quality values for May 1, 1973 (a Tuesday) to September 30, 1973.

- **Ozone**: Mean ozone in parts per billion from 1300 to 1500 hours at Roosevelt Island
- **Solar.R**: Solar radiation in Langley in the frequency band 4000–7700 Angstroms from 0800 to 1200 hours at Central Park
- **Wind**: Average wind speed in miles per hour at 0700 and 1000 hours at LaGuardia Airport
- **Temp**: Maximum daily temperature in degrees Fahrenheit at LaGuardia Airport.

**Source**

The data were obtained from the New York State Department of Conservation (ozone data) and the National Weather Service (meteorological data).
References

Examples
```r
require(graphics)
pairs(airquality, panel = panel.smooth, main = "airquality data")
```

**anscombe**

*Anscombe’s Quartet of ‘Identical’ Simple Linear Regressions*

Description
Four $x$-$y$ datasets which have the same traditional statistical properties (mean, variance, correlation, regression line, etc.), yet are quite different.

Usage
```r
anscombe
```

Format
A data frame with 11 observations on 8 variables.
- `x1 == x2 == x3` the integers 4:14, specially arranged
- `x4` values 8 and 19
- `y1, y2, y3, y4` numbers in (3, 12.5) with mean 7.5 and sdev 2.03

Source

References

Examples
```r
require(stats); require(graphics)
summary(anscombe)

##-- now some "magic" to do the 4 regressions in a loop:
ff <- y ~ x
mods <- setNames(as.list(1:4), paste0("lm", 1:4))
for(i in 1:4) {
  ff[[2:3]] <- lapply(paste0("y","x"), i, as.name)
  ## or  ff[[2]] <- as.name(paste0("y", i))
  ## ff[[3]] <- as.name(paste0("x", i))
  mods[[i]] <- lmi <- lm(ff, data = anscombe)
  print(anova(lmi))
}
```
## See how close they are (numerically!)
sapply(mods, coef)
lapply(mods, function(fm) coef(summary(fm)))

## Now, do what you should have done in the first place: PLOTS
op <- par(mfrow = c(2, 2), mar = 0.1+c(4,4,1,1), oma = c(0, 0, 2, 0))
for(i in 1:4) {
  ff[2:3] <- lapply(paste0(c("y","x"), i), as.name)
  plot(ff, data = anscombe, col = "red", pch = 21, bg = "orange", cex = 1.2,
       xlim = c(3, 19), ylim = c(3, 13))
  abline(mods[[i]], col = "blue")
}
mtext("Anscombe's 4 Regression data sets", outer = TRUE, cex = 1.5)
par(op)

---

### attenu

The Joyner–Boore Attenuation Data

**Description**

This data gives peak accelerations measured at various observation stations for 23 earthquakes in California. The data have been used by various workers to estimate the attenuating affect of distance on ground acceleration.

**Usage**

attenu

**Format**

A data frame with 182 observations on 5 variables.

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>[.1]</td>
<td>event</td>
<td>numeric Event Number</td>
</tr>
<tr>
<td>[.2]</td>
<td>mag</td>
<td>numeric Moment Magnitude</td>
</tr>
<tr>
<td>[.3]</td>
<td>station</td>
<td>factor Station Number</td>
</tr>
<tr>
<td>[.4]</td>
<td>dist</td>
<td>numeric Station-hypocenter distance (km)</td>
</tr>
<tr>
<td>[.5]</td>
<td>accel</td>
<td>numeric Peak acceleration (g)</td>
</tr>
</tbody>
</table>

**Source**


**References**


**Examples**

```r
require(graphics)
## check the data class of the variables
sapply(attenu, data.class)
summary(attenu)
pairs(attenu, main = "attenu data")
coplot(accel ~ dist | as.factor(event), data = attenu, show.given = FALSE)
coplot(log(accel) ~ log(dist) | as.factor(event),
       data = attenu, panel = panel.smooth, show.given = FALSE)
```

**attitude**  
*The Chatterjee–Price Attitude Data*

**Description**

From a survey of the clerical employees of a large financial organization, the data are aggregated from the questionnaires of the approximately 35 employees for each of 30 (randomly selected) departments. The numbers give the percent proportion of favourable responses to seven questions in each department.

**Usage**

```r
attitude
```

**Format**

A data frame with 30 observations on 7 variables. The first column are the short names from the reference, the second one the variable names in the data frame:

<table>
<thead>
<tr>
<th></th>
<th>rating</th>
<th>numeric</th>
<th>Overall rating</th>
</tr>
</thead>
<tbody>
<tr>
<td>X[1]</td>
<td>complaints</td>
<td>numeric</td>
<td>Handling of employee complaints</td>
</tr>
<tr>
<td>X[2]</td>
<td>privileges</td>
<td>numeric</td>
<td>Does not allow special privileges</td>
</tr>
<tr>
<td>X[3]</td>
<td>learning</td>
<td>numeric</td>
<td>Opportunity to learn</td>
</tr>
<tr>
<td>X[4]</td>
<td>raises</td>
<td>numeric</td>
<td>Raises based on performance</td>
</tr>
<tr>
<td>X[5]</td>
<td>critical</td>
<td>numeric</td>
<td>Too critical</td>
</tr>
<tr>
<td>X[6]</td>
<td>advance</td>
<td>numeric</td>
<td>Advancement</td>
</tr>
</tbody>
</table>

**Source**

beavers

Examples

```
require(stats); require(graphics)
pairs(attitude, main = "attitude data")
summary(attitude)
summary(fm1 <- lm(rating ~ ., data = attitude))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
          mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
summary(fm2 <- lm(rating ~ complaints, data = attitude))
plot(fm2)
par(opar)
```

austres

Quarterly Time Series of the Number of Australian Residents

Description

Numbers (in thousands) of Australian residents measured quarterly from March 1971 to March 1994. The object is of class "ts".

Usage

austres

Source


beavers

Body Temperature Series of Two Beavers

Description

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

Usage

beaver1
beaver2
Format

The beaver1 data frame has 114 rows and 4 columns on body temperature measurements at 10 minute intervals.

The beaver2 data frame has 100 rows and 4 columns on body temperature measurements at 10 minute intervals.

The variables are as follows:

day  Day of observation (in days since the beginning of 1990), December 12–13 (beaver1) and November 3–4 (beaver2).

time  Time of observation, in the form 0330 for 3:30am

temp  Measured body temperature in degrees Celsius.

activ  Indicator of activity outside the retreat.

Note

The observation at 22:20 is missing in beaver1.

Source


Examples

```r
beaver.plot <- function(bdat, ...) {
  nam <- deparse(substitute(bdat))
  with(bdat, {
    # Hours since start of day:
    hours <- time %/% 100 + 24*(day - day[1]) + (time %% 100)/60
    plot (hours, temp, type = "l", ...,
         main = paste(nam, "body temperature"))
    abline(h = 37.5, col = "gray", lty = 2)
    is.act <- activ == 1
    points(hours[is.act], temp[is.act], col = 2, cex = .8)
  })
}

op <- par(mfrow = c(2, 1), mar = c(3, 3, 4, 2), mgp = 0.9 * 2:0)
beaver.plot(beaver1, ylim = yl)
beaver.plot(beaver2, ylim = yl)
par(op)
```
BJsales

Sales Data with Leading Indicator

Description
The sales time series BJsales and leading indicator BJsales.lead each contain 150 observations. The objects are of class "ts".

Usage

BJsales
BJsales.lead

Source
The data are given in Box & Jenkins (1976). Obtained from the Time Series Data Library at https://robjhyndman.com/TSDL/

References

BOD

Biochemical Oxygen Demand

Description
The BOD data frame has 6 rows and 2 columns giving the biochemical oxygen demand versus time in an evaluation of water quality.

Usage

BOD

Format
This data frame contains the following columns:

Time A numeric vector giving the time of the measurement (days).
Demand A numeric vector giving the biochemical oxygen demand (mg/l).

Source
Examples

```r
require(stats)
# simplest form of fitting a first-order model to these data
fm1 <- nls(demand ~ A*(1-exp(-exp(lrc)*Time)), data = BOD,
    start = c(A = 20, lrc = log(.35)))
coef(fm1)
fm1

# using the plinear algorithm (trace o/p differs by platform)
## IGNORE_RDIFF_BEGIN
fm2 <- nls(demand ~ (1-exp(-exp(lrc)*Time)), data = BOD,
    start = c(lrc = log(.35)), algorithm = "plinear", trace = TRUE)
## IGNORE_RDIFF_END

# using a self-starting model
fm3 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
summary(fm3)
```

---

cars

### Description

The data give the speed of cars and the distances taken to stop. Note that the data were recorded in the 1920s.

### Usage

```r
cars
```

### Format

A data frame with 50 observations on 2 variables.

```
[,1] speed  numeric  Speed (mph)
[,2] dist  numeric  Stopping distance (ft)
```

### Source


### References


### Examples

```r
require(stats); require(graphics)
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
    las = 1)
lines(lowess(cars$speed, cars$dist, f = 2/3, iter = 3), col = "red")
title(main = "cars data")
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
    las = 1, log = "xy")
```
ChickWeight

Weight versus age of chicks on different diets

Description

The ChickWeight data frame has 578 rows and 4 columns from an experiment on the effect of diet on early growth of chicks.

Usage

ChickWeight

Format

An object of class c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame") containing the following columns:

weight a numeric vector giving the body weight of the chick (gm).

Time a numeric vector giving the number of days since birth when the measurement was made.

Chick an ordered factor with levels 18 < ... < 48 giving a unique identifier for the chick. The ordering of the levels groups chicks on the same diet together and orders them according to their final weight (lightest to heaviest) within diet.

Diet a factor with levels 1, ..., 4 indicating which experimental diet the chick received.

Details

The body weights of the chicks were measured at birth and every second day thereafter until day 20. They were also measured on day 21. There were four groups on chicks on different protein diets.

This dataset was originally part of package nlme, and that has methods (including for [, as.data.frame, plot and print) for its grouped-data classes.
chickwts

Source

See Also
*SSlogis* for models fitted to this dataset.

Examples
```r
require(graphics)
coplot(weight ~ Time | Chick, data = ChickWeight,
     type = "b", show.given = FALSE)
```

---

### chickwts

*Chicken Weights by Feed Type*

#### Description
An experiment was conducted to measure and compare the effectiveness of various feed supplements on the growth rate of chickens.

#### Usage
`chickwts`

#### Format
A data frame with 71 observations on the following 2 variables.

- `weight` a numeric variable giving the chick weight.
- `feed` a factor giving the feed type.

#### Details
Newly hatched chicks were randomly allocated into six groups, and each group was given a different feed supplement. Their weights in grams after six weeks are given along with feed types.

#### Source

#### References
Examples

```r
require(stats); require(graphics)
boxplot(weight ~ feed, data = chickwts, col = "lightgray",
        varwidth = TRUE, notch = TRUE, main = "chickwt data",
        ylab = "Weight at six weeks (gm)"
anova(fm1 <- lm(weight ~ feed, data = chickwts))
par(opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
     mar = c(4.1, 4.1, 2.1, 1.1)))
plot(fm1)
par(opar)
```

---

**CO2**

*Carbon Dioxide Uptake in Grass Plants*

**Description**

The CO2 data frame has 84 rows and 5 columns of data from an experiment on the cold tolerance of the grass species *Echinochloa crus-galli*.

**Usage**

CO2

**Format**

An object of class c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame") containing the following columns:

- **Plant**: an ordered factor with levels Qn1 < Qn2 < Qn3 < ... < Mc1 giving a unique identifier for each plant.
- **Type**: a factor with levels Quebec Mississippi giving the origin of the plant
- **Treatment**: a factor with levels nonchilled chilled
- **conc**: a numeric vector of ambient carbon dioxide concentrations (mL/L).
- **uptake**: a numeric vector of carbon dioxide uptake rates (µmol/m² sec).

**Details**

The CO2 uptake of six plants from Quebec and six plants from Mississippi was measured at several levels of ambient CO2 concentration. Half the plants of each type were chilled overnight before the experiment was conducted.

This dataset was originally part of package nlme, and that has methods (including for [, as.data.frame, plot and print) for its grouped-data classes.

**Source**


Examples

```r
require(stats); require(graphics)

coplot(uptake ~ conc | Plant, data = CO2, show.given = FALSE, type = "b")
## fit the data for the first plant
fm1 <- nls(uptake ~ SSasymp(conc, Asym, lrc, c0),
  data = CO2, subset = Plant == "Qn1")
summary(fm1)
## fit each plant separately
fmlist <- list()
for (pp in levels(CO2$Plant)) {
  fmlist[[pp]] <- nls(uptake ~ SSasymp(conc, Asym, lrc, c0),
    data = CO2, subset = Plant == pp)
}
## check the coefficients by plant
print(sapply(fmlist, coef), digits = 3)
```

---

co2  

Mauna Loa Atmospheric CO2 Concentration

Description

Atmospheric concentrations of CO2 are expressed in parts per million (ppm) and reported in the preliminary 1997 SIO manometric mole fraction scale.

Usage

co2

Format

A time series of 468 observations; monthly from 1959 to 1997.

Details

The values for February, March and April of 1964 were missing and have been obtained by interpolating linearly between the values for January and May of 1964.

Source

Keeling, C. D. and Whorf, T. P., Scripps Institution of Oceanography (SIO), University of California, La Jolla, California USA 92093-0220.

https://scrippsc02.ucsd.edu/data/atmospheric_co2/.

Note that the data are subject to revision (based on recalibration of standard gases) by the Scripps institute, and hence may not agree exactly with the data provided by R.

References

**Examples**

```r
require(graphics)
plot(co2, ylab = expression("Atmospheric concentration of CO"[2]),
     las = 1)
title(main = "co2 data set")
```

---

**crimtab**

**Student’s 3000 Criminals Data**

**Description**

Data of 3000 male criminals over 20 years old undergoing their sentences in the chief prisons of England and Wales.

**Usage**

```r
crimtab
```

**Format**

A table object of integer counts, of dimension 42 x 22 with a total count, `sum(crimtab)` of 3000. The 42 rownames ("9.4", "9.5", ...) correspond to midpoints of intervals of finger lengths whereas the 22 column names (colnames) ("142.24", "144.78", ...) correspond to (body) heights of 3000 criminals, see also below.

**Details**

Student is the pseudonym of William Sealy Gosset. In his 1908 paper he wrote (on page 13) at the beginning of section VI entitled Practical Test of the foregoing Equations:

“Before I had succeeded in solving my problem analytically, I had endeavoured to do so empirically. The material used was a correlation table containing the height and left middle finger measurements of 3000 criminals, from a paper by W. R. MacDonell (Biometrika, Vol. I., p. 219). The measurements were written out on 3000 pieces of cardboard, which were then very thoroughly shuffled and drawn at random. As each card was drawn its numbers were written down in a book, which thus contains the measurements of 3000 criminals in a random order. Finally, each consecutive set of 4 was taken as a sample—750 in all—and the mean, standard deviation, and correlation of each sample determined. The difference between the mean of each sample and the mean of the population was then divided by the standard deviation of the sample, giving us the z of Section III.”

The table is in fact page 216 and not page 219 in MacDonell(1902). In the MacDonell table, the middle finger lengths were given in mm and the heights in feet/inches intervals, they are both converted into cm here. The midpoints of intervals were used, e.g., where MacDonell has 4\(\frac{7}{8}\)′9/16 − 8\(\frac{9}{16}\)′, we have 142.24 which is 2.54*56 = 2.54*(4\(\frac{7}{8}\)).

MacDonell credited the source of data (page 178) as follows: The data on which the memoir is based were obtained, through the kindness of Dr Garson, from the Central Metric Office, New Scotland Yard... He pointed out on page 179 that: The forms were drawn at random from the mass on the office shelves; we are therefore dealing with a random sampling.

**Source**

References


Examples

```r
require(stats)
dim(crimtab)
utils::str(crimtab)
## for nicer printing:
local({cT <- crimtab
  colnames(cT) <- substring(colnames(cT), 2, 3)
  print(cT, zero.print = " ")})

## Repeat Student's experiment:
# 1) Reconstitute 3000 raw data for heights in inches and rounded to
#    nearest integer as in Student's paper:
(heIn <- round(as.numeric(colnames(crimtab)) / 2.54))
d.hei <- data.frame(height = rep(heIn, colSums(crimtab)))

# 2) shuffle the data:
set.seed(1)
d.hei <- d.hei[sample(1:3000), , drop = FALSE]

# 3) Make 750 samples each of size 4:
d.hei$sample <- as.factor(rep(1:750, each = 4))

# 4) Compute the means and standard deviations (n) for the 750 samples:
  h.mean <- with(d.hei, tapply(height, sample, FUN = mean))
  h.sd <- with(d.hei, tapply(height, sample, FUN = sd)) * sqrt(3/4)

# 5) Compute the difference between the mean of each sample and
#    the mean of the population and then divide by the
#    standard deviation of the sample:
  zobs <- (h.mean - mean(d.hei[, "height"]))/h.sd

# 6) Replace infinite values by +/- 6 as in Student's paper:
  zobs[is.infinite(zobs)] <- 6 * sign(zobs[is.infinite(zobs)])

# 7) Plot the distribution:
require(grDevices); require(graphics)
```
```
hist(x = zobs, probability = TRUE, xlab = "Student's z",
     col = grey(0.8), border = grey(0.5),
     main = "Distribution of Student's z score for 'crimtab' data")
```

---

### discoveries

**Yearly Numbers of Important Discoveries**

**Description**

The numbers of "great" inventions and scientific discoveries in each year from 1860 to 1959.

**Usage**

```r
discoveries
```

**Format**

A time series of 100 values.

**Source**


**References**


**Examples**

```r
require(graphics)
plot(discoveries, ylab = "Number of important discoveries",
     las = 1)
title(main = "discoveries data set")
```

---

### DNase

**Elisa assay of DNase**

**Description**

The DNase data frame has 176 rows and 3 columns of data obtained during development of an ELISA assay for the recombinant protein DNase in rat serum.

**Usage**

```r
DNase
```
esoph

**Format**

An object of class c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame") containing the following columns:

- **Run** an ordered factor with levels 10 < ... < 3 indicating the assay run.
- **conc** a numeric vector giving the known concentration of the protein.
- **density** a numeric vector giving the measured optical density (dimensionless) in the assay. Duplicate optical density measurements were obtained.

**Details**

This dataset was originally part of package nlme, and that has methods (including for [, as.data.frame, plot and print) for its grouped-data classes.

**Source**


**Examples**

```r
require(stats); require(graphics)

coplot(density ~ conc | Run, data = DNase,
    show.given = FALSE, type = "b")
coplot(density ~ log(conc) | Run, data = DNase,
    show.given = FALSE, type = "b")
## fit a representative run
fm1 <- nls(density ~ SSlogis( log(conc), Asym, xmid, scal ),
            data = DNase, subset = Run == 1)
## compare with a four-parameter logistic
fm2 <- nls(density ~ SSfpl( log(conc), A, B, xmid, scal ),
            data = DNase, subset = Run == 1)
summary(fm2)
anova(fm1, fm2)
```

---

**esoph**

*Smoking, Alcohol and (O)esophageal Cancer*

**Description**

Data from a case-control study of (o)esophageal cancer in Ille-et-Vilaine, France.

**Usage**

esoph
Format

A data frame with records for 88 age/alcohol/tobacco combinations.

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>[.1]</td>
<td>&quot;agegp&quot; Age group</td>
<td>1 25–34 years</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 35–44</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3 45–54</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4 55–64</td>
</tr>
<tr>
<td></td>
<td></td>
<td>5 65–74</td>
</tr>
<tr>
<td></td>
<td></td>
<td>6 75+</td>
</tr>
<tr>
<td>[.2]</td>
<td>&quot;alcgp&quot; Alcohol consumption</td>
<td>1 0–39 gm/day</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 40–79</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3 80–119</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4 120+</td>
</tr>
<tr>
<td>[.3]</td>
<td>&quot;tobgp&quot; Tobacco consumption</td>
<td>1 10–9 gm/day</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 10–19</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3 20–29</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4 30+</td>
</tr>
<tr>
<td>[.4]</td>
<td>&quot;ncases&quot; Number of cases</td>
<td></td>
</tr>
<tr>
<td>[.5]</td>
<td>&quot;ncontrols&quot; Number of controls</td>
<td></td>
</tr>
</tbody>
</table>

Author(s)

Thomas Lumley

Source


Examples

```r
require(stats)
require(graphics) # for mosaicplot
summary(esoph)
## effects of alcohol, tobacco and interaction, age-adjusted
model1 <- glm(cbind(ncases, ncontrols) ~ agegp + tobgp * alcgp,
               data = esoph, family = binomial())
anova(model1)
## Try a linear effect of alcohol and tobacco
model2 <- glm(cbind(ncases, ncontrols) ~ agegp + unclass(tobgp)+ unclass(alcgp),
               data = esoph, family = binomial())
summary(model2)
## Re-arrange data for a mosaic plot
ttt <- table(esoph$agegp, esoph$alcgp, esoph$tobgp)
o <- with(esoph, order(tobgp, alcgp, agegp))
ttt[ttt == 1] <- esoph$ncases[o]
ttl <- table(esoph$agegp, esoph$alcgp, esoph$tobgp)
ttl[ttl == 1] <- esoph$ncontrols[o]
t <- array(c(ttt, ttl), c(dim(ttt),2),
c(dimnames(ttt), list(c("Cancer", "control"))))
mosaicplot(tt, main = "esoph data set", color = TRUE)
```
**Description**

Conversion rates between the various Euro currencies.

**Usage**

```r
euro
euro.cross
```

**Format**

`euro` is a named vector of length 11, `euro.cross` a matrix of size 11 by 11, with dimnames.

**Details**

The data set `euro` contains the value of 1 Euro in all currencies participating in the European monetary union (Austrian Schilling ATS, Belgian Franc BEF, German Mark DEM, Spanish Peseta ESP, Finnish Markka FIM, French Franc FRF, Irish Punt IEP, Italian Lira ITL, Luxembourg Franc LUF, Dutch Guilder NLG and Portuguese Escudo PTE). These conversion rates were fixed by the European Union on December 31, 1998. To convert old prices to Euro prices, divide by the respective rate and round to 2 digits.

The data set `euro.cross` contains conversion rates between the various Euro currencies, i.e., the result of `outer(1/euro, euro)`.

**Examples**

```r
cbind(euro)
## These relations hold:
euro == signif(euro, 6)  # [6 digit precision in Euro's definition]
all(euro.cross == outer(1/euro, euro))
## Convert 20 Euro to Belgian Franc
20 * euro["BEF"]
## Convert 20 Austrian Schilling to Euro
20 / euro["ATS"]
## Convert 20 Spanish Pesetas to Italian Lira
20 * euro.cross["ESP", "ITL"]
require(graphics)
dotchart(euro,
    main = "euro data: 1 Euro in currency unit")
dotchart(1/euro,
    main = "euro data: 1 currency unit in Euros")
dotchart(log(euro, 10),
    main = "euro data: log10(1 Euro in currency unit)")```
**eurodist**  
*Distances Between European Cities and Between US Cities*

**Description**

The `eurodist` gives the road distances (in km) between 21 cities in Europe. The data are taken from a table in *The Cambridge Encyclopaedia*.  
`UScitiesD` gives “straight line” distances between 10 cities in the US.

**Usage**

```r
eurodist
UScitiesD
```

**Format**

`dist` objects based on 21 and 10 objects, respectively. (You must have the `stats` package loaded to have the methods for this kind of object available).

**Source**

The US cities distances were provided by Pierre Legendre.

---

**EuStockMarkets**  
*Daily Closing Prices of Major European Stock Indices, 1991–1998*

**Description**

Contains the daily closing prices of major European stock indices: Germany DAX (Ibis), Switzerland SMI, France CAC, and UK FTSE. The data are sampled in business time, i.e., weekends and holidays are omitted.

**Usage**

```r
EuStockMarkets
```

**Format**

A multivariate time series with 1860 observations on 4 variables. The object is of class "mts".

**Source**

The data were kindly provided by Erste Bank AG, Vienna, Austria.
Description

Waiting time between eruptions and the duration of the eruption for the Old Faithful geyser in Yellowstone National Park, Wyoming, USA.

Usage

faithful

Format

A data frame with 272 observations on 2 variables.

<table>
<thead>
<tr>
<th>[,1]</th>
<th>eruptions</th>
<th>numeric</th>
<th>Eruption time in mins</th>
</tr>
</thead>
<tbody>
<tr>
<td>[,2]</td>
<td>waiting</td>
<td>numeric</td>
<td>Waiting time to next eruption (in mins)</td>
</tr>
</tbody>
</table>

Details

A closer look at faithful$eruptions reveals that these are heavily rounded times originally in seconds, where multiples of 5 are more frequent than expected under non-human measurement. For a better version of the eruption times, see the example below.

There are many versions of this dataset around: Azzalini and Bowman (1990) use a more complete version.

Source

W. Härdle.

References


See Also

geyer in package MASS for the Azzalini–Bowman version.

Examples

```r
require(stats); require(graphics)
f.tit <- "faithful data: Eruptions of Old Faithful"
ne60 <- round(e60 <- 60 * faithful$eruptions)
all.equal(e60, ne60) # relative diff. ~ 1/10000
table(zapsmall(abs(e60 - ne60))) # 0, 0.02 or 0.04
faithful$better.eruptions <- ne60 / 60
te <- table(ne60)
```
te[te >= 4]  # (too) many multiples of 5!
plot(names(te), te, type = "h", main = f.tit, xlab = "Eruption time (sec)"

plot(faithful[, -3], main = f.tit,
  xlab = "Eruption time (min)",
  ylab = "Waiting time to next eruption (min)"
lines(lowess(faithful$eruptions, faithful$waiting, f = 2/3, iter = 3),
  col = "red")

---

Formaldehyde

Determination of Formaldehyde

Description

These data are from a chemical experiment to prepare a standard curve for the determination of formaldehyde by the addition of chromatropic acid and concentrated sulphuric acid and the reading of the resulting purple color on a spectrophotometer.

Usage

Formaldehyde

Format

A data frame with 6 observations on 2 variables.

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>.[,1]</td>
<td>carb</td>
<td>numeric</td>
</tr>
<tr>
<td>.[,2]</td>
<td>optden</td>
<td>numeric</td>
</tr>
</tbody>
</table>

Source


References


Examples

require(stats); require(graphics)
plot(optden ~ carb, data = Formaldehyde,
  xlab = "Carbohydrate (ml)", ylab = "Optical Density",
  main = "Formaldehyde data", col = 4, las = 1)
abline(fm1 <- lm(optden ~ carb, data = Formaldehyde))
summary(fm1)
par <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0))
plot(fm1)
par(par)
Description

Freeny’s data on quarterly revenue and explanatory variables.

Usage

freeny
freeny.x
freeny.y

Format

There are three ‘freeny’ data sets.
freeny.y is a time series with 39 observations on quarterly revenue from (1962.2Q) to (1971.4Q).
freeny.x is a matrix of explanatory variables. The columns are freeny.y lagged 1 quarter, price index, income level, and market potential.

Finally, freeny is a data frame with variables y, lag.quarterly.revenue, price.index, income.level, and market.potential obtained from the above two data objects.

Source


References


Examples

```r
require(stats); require(graphics)
summary(freeny)
pairs(freeny, main = "freeny data")
# gives warning: freeny$y has class "ts"

summary(fm1 <- lm(y ~ ., data = freeny))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
         mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)
```
Description

Distribution of hair and eye color and sex in 592 statistics students.

Usage

HairEyeColor

Format

A 3-dimensional array resulting from cross-tabulating 592 observations on 3 variables. The variables and their levels are as follows:

<table>
<thead>
<tr>
<th>No</th>
<th>Name</th>
<th>Levels</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Hair</td>
<td>Black, Brown, Red, Blond</td>
</tr>
<tr>
<td>2</td>
<td>Eye</td>
<td>Brown, Blue, Hazel, Green</td>
</tr>
<tr>
<td>3</td>
<td>Sex</td>
<td>Male, Female</td>
</tr>
</tbody>
</table>

Details

The Hair × Eye table comes from a survey of students at the University of Delaware reported by Snee (1974). The split by Sex was added by Friendly (1992a) for didactic purposes.

This data set is useful for illustrating various techniques for the analysis of contingency tables, such as the standard chi-squared test or, more generally, log-linear modelling, and graphical methods such as mosaic plots, sieve diagrams or association plots.

Source

http://www.datavis.ca/sas/vcd/catdata/haireye.sas

Snee (1974) gives the two-way table aggregated over Sex. The Sex split of the ‘Brown hair, Brown eye’ cell was changed to agree with that used by Friendly (2000).

References


See Also

chisq.test, loglin, mosaicplot
Examples

```r
require(graphics)
## Full mosaic
mosaicplot(HairEyeColor)
## Aggregate over sex (as in Snee's original data)
x <- apply(HairEyeColor, c(1, 2), sum)
x
mosaicplot(x, main = "Relation between hair and eye color")
```

Description

A correlation matrix of eight physical measurements on 305 girls between ages seven and seventeen.

Usage

Harman23.cor

Source


Examples

```r
require(stats)
(Harman23.FA <- factanal(factors = 1, covmat = Harman23.cor))
for(factors in 2:4) print(update(Harman23.FA, factors = factors))
```

Description

A correlation matrix of 24 psychological tests given to 145 seventh and eight-grade children in a Chicago suburb by Holzinger and Swineford.

Usage

Harman74.cor

Source

Examples

```r
require(stats)
(Harman74.FA <- factanal(factors = 1, covmat = Harman74.cor))
for(factors in 2:5) print(update(Harman74.FA, factors = factors))
Harman74.FA <- factanal(factors = 5, covmat = Harman74.cor,
rotation = "promax")
print(Harman74.FA$loadings, sort = TRUE)
```

Description

The Indometh data frame has 66 rows and 3 columns of data on the pharmacokinetics of indometacin (or, older spelling, ‘indomethacin’).

Usage

Indometh

Format

An object of class c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame") containing the following columns:

- **Subject** an ordered factor with containing the subject codes. The ordering is according to increasing maximum response.
- **time** a numeric vector of times at which blood samples were drawn (hr).
- **conc** a numeric vector of plasma concentrations of indometacin (mcg/ml).

Details

Each of the six subjects were given an intravenous injection of indometacin.

This dataset was originally part of package nlme, and that has methods (including for [, as.data.frame, plot and print) for its grouped-data classes.

Source


See Also

`SSbiexp` for models fitted to this dataset.
Infertility after Spontaneous and Induced Abortion

Description

This is a matched case-control study dating from before the availability of conditional logistic regression.

Usage

infert

Format

1. Education 0 = 0-5 years
   1 = 6-11 years
   2 = 12+ years
2. age age in years of case
3. parity count
4. number of prior induced abortions 0 = 0
   1 = 1
   2 = 2 or more
5. case status 1 = case
   0 = control
6. number of prior spontaneous abortions 0 = 0
   1 = 1
   2 = 2 or more
7. matched set number 1-83
8. stratum number 1-63

Note

One case with two prior spontaneous abortions and two prior induced abortions is omitted.

Source


Examples

require(stats)
model1 <- glm(case ~ spontaneous+induced, data = infert, family = binomial())
summary(model1)
## adjusted for other potential confounders:
summary(model2 <- glm(case ~ age+parity+education+spontaneous+induced,
data = infert, family = binomial()))
## Really should be analysed by conditional logistic regression
## which is in the survival package
if(require(survival)){


InsectSprays <- clogit(case ~ spontaneous+induced+strata(stratum), data = infert)
print(summary(model3))
detach()  # survival (conflicts)

InsectSprays

**Effectiveness of Insect Sprays**

**Description**

The counts of insects in agricultural experimental units treated with different insecticides.

**Usage**

InsectSprays

**Format**

A data frame with 72 observations on 2 variables.

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>[.1]</td>
<td>count</td>
<td>numeric</td>
</tr>
<tr>
<td>[.2]</td>
<td>spray</td>
<td>factor</td>
</tr>
</tbody>
</table>

*Insect count*

*The type of spray*

**Source**


**References**


**Examples**

```r
require(stats); require(graphics)
boxplot(count ~ spray, data = InsectSprays,
       xlab = "Type of spray", ylab = "Insect count",
       main = "InsectSprays data", varwidth = TRUE, col = "lightgray")
fm1 <- aov(count ~ spray, data = InsectSprays)
summary(fm1)
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0))
plot(fm1)
fm2 <- aov(sqrt(count) ~ spray, data = InsectSprays)
summary(fm2)
plot(fm2)
par(opar)
```
Description
This famous (Fisher’s or Anderson’s) iris data set gives the measurements in centimeters of the variables sepal length and width and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are Iris setosa, versicolor, and virginica.

Usage
iris
iris3

Format
iris is a data frame with 150 cases (rows) and 5 variables (columns) named Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, and Species.
iris3 gives the same data arranged as a 3-dimensional array of size 50 by 4 by 3, as represented by S-PLUS. The first dimension gives the case number within the species subsample, the second the measurements with names Sepal L., Sepal W., Petal L., and Petal W., and the third the species.

Source

References

See Also
matplot some examples of which use iris.

Examples
dn13 <- dimnames(iris3)
ii <- data.frame(matrix(aperm(iris3, c(1,3,2)), ncol = 4, 
   dimnames = list(NULL, sub(" L.", ".Length", 
    sub(" W.", ".Width", dn13[[2]])))))
Species = gl(3, 50, labels = sub("S", "s", sub("V", "v", sub("V", "v", dn3[[3]]))))
all.equal(ii, iris) # TRUE
### islands

**Areas of the World’s Major Landmasses**

**Description**

The areas in thousands of square miles of the landmasses which exceed 10,000 square miles.

**Usage**

islands

**Format**

A named vector of length 48.

**Source**


**References**


**Examples**

```r
require(graphics)
dotchart(log(islands, 10),
   main = "islands data: log10(area) (log10(sq. miles))")
dotchart(log(islands[order(islands)], 10),
   main = "islands data: log10(area) (log10(sq. miles))")
```

---

### JohnsonJohnson

**Quarterly Earnings per Johnson & Johnson Share**

**Description**

Quarterly earnings (dollars) per Johnson & Johnson share 1960–80.

**Usage**

JohnsonJohnson

**Format**

A quarterly time series

**Source**

Examples

```r
require(stats); require(graphics)
JJ <- log10(JohnsonJohnson)
plot(JJ)
## This example gives a possible-non-convergence warning on some
## platforms, but does seem to converge on x86 Linux and Windows.
(fit <- StructTS(JJ, type = "BSM"))
tsdia(fit)
sm <- tsSmooth(fit)
plot(cbind(JJ, sm[, 1], sm[, 3]-0.5), plot.type = "single",
     col = c("black", "green", "blue"))
abline(h = -0.5, col = "grey60")
monthplot(fit)
```

LakeHuron

**Level of Lake Huron 1875–1972**

Description

Annual measurements of the level, in feet, of Lake Huron 1875–1972.

Usage

LakeHuron

Format

A time series of length 98.

Source


lh

**Luteinizing Hormone in Blood Samples**

Description

A regular time series giving the luteinizing hormone in blood samples at 10 mins intervals from a human female, 48 samples.

Usage

lh

Source

LifeCycleSavings  

**Description**


**Usage**

LifeCycleSavings

**Format**

A data frame with 50 observations on 5 variables.

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>sr</td>
<td>numeric</td>
<td>aggregate personal savings</td>
</tr>
<tr>
<td>2</td>
<td>pop15</td>
<td>numeric</td>
<td>% of population under 15</td>
</tr>
<tr>
<td>3</td>
<td>pop75</td>
<td>numeric</td>
<td>% of population over 75</td>
</tr>
<tr>
<td>4</td>
<td>dpi</td>
<td>numeric</td>
<td>real per-capita disposable income</td>
</tr>
<tr>
<td>5</td>
<td>ddpi</td>
<td>numeric</td>
<td>% growth rate of dpi</td>
</tr>
</tbody>
</table>

**Details**

Under the life-cycle savings hypothesis as developed by Franco Modigliani, the savings ratio (aggregate personal saving divided by disposable income) is explained by per-capita disposable income, the percentage rate of change in per-capita disposable income, and two demographic variables: the percentage of population less than 15 years old and the percentage of the population over 75 years old. The data are averaged over the decade 1960–1970 to remove the business cycle or other short-term fluctuations.

**Source**

The data were obtained from Belsley, Kuh and Welsch (1980). They in turn obtained the data from Sterling (1977).

**References**


**Examples**

```r
require(stats); require(graphics)
pairs(LifeCycleSavings, panel = panel.smooth, main = "LifeCycleSavings data")
fml <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)
summary(fml)
```
Description

The Loblolly data frame has 84 rows and 3 columns of records of the growth of Loblolly pine trees.

Usage

Loblolly

Format

An object of class c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame") containing the following columns:

- **height** a numeric vector of tree heights (ft).
- **age** a numeric vector of tree ages (yr).
- **Seed** an ordered factor indicating the seed source for the tree. The ordering is according to increasing maximum height.

Details

This dataset was originally part of package nlme, and that has methods (including for [, as.data.frame, plot and print) for its grouped-data classes.

Source


Examples

```r
require(stats); require(graphics)
plot(height ~ age, data = Loblolly, subset = Seed == 329,
    xlab = "Tree age (yr)", las = 1,
    ylab = "Tree height (ft)",
    main = "Loblolly data and fitted curve (Seed 329 only)"
)
fm1 <- nls(height ~ SSasymp(age, Asym, R0, lrc),
    data = Loblolly, subset = Seed == 329)
age <- seq(0, 30, length.out = 101)
lines(age, predict(fm1, list(age = age)))
```
longley

Longley's Economic Regression Data

Description
A macroeconomic data set which provides a well-known example for a highly collinear regression.

Usage
longley

Format
A data frame with 7 economical variables, observed yearly from 1947 to 1962 \((n = 16)\).

- **GNP.deflator**  GNP implicit price deflator \((1954 = 100)\)
- **GNP**  Gross National Product.
- **Unemployed**  number of unemployed.
- **Armed.Forces**  number of people in the armed forces.
- **Population**  ‘noninstitutionalized’ population \(\geq 14\) years of age.
- **Year**  the year (time).
- **Employed**  number of people employed.

The regression \(\text{lm}(\text{Employed} \sim .)\) is known to be highly collinear.

Source

References

Examples
```r
require(stats); require(graphics)
## give the data set in the form it is used in S-PLUS:
longley.x <- data.matrix(longley[, 1:6])
longley.y <- longley[, "Employed"]
pairs(longley, main = "longley data")
summary(fm1 <- lm(Employed ~ ., data = longley))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
          mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)
```
** lynx  

* Annual Canadian Lynx trappings 1821–1934 *

** Description **

Annual numbers of lynx trappings for 1821–1934 in Canada. Taken from Brockwell & Davis (1991), this appears to be the series considered by Campbell & Walker (1977).

** Usage **

[ lynx ]

** Source **


** References **


** morley  

* Michelson Speed of Light Data *

** Description **

A classical data of Michelson (but not this one with Morley) on measurements done in 1879 on the speed of light. The data consists of five experiments, each consisting of 20 consecutive ‘runs’. The response is the speed of light measurement, suitably coded (km/sec, with 299000 subtracted).

** Usage **

[ morley ]

** Format **

A data frame with 100 observations on the following 3 variables.

- **Expt** The experiment number, from 1 to 5.
- **Run** The run number within each experiment.
- **Speed** Speed-of-light measurement.

** Details **

The data is here viewed as a randomized block experiment with ‘experiment’ and ‘run’ as the factors. ‘run’ may also be considered a quantitative variate to account for linear (or polynomial) changes in the measurement over the course of a single experiment.
Note

This is the same dataset as michelson in package MASS.

Source

A. A. Michelson (1882) Experimental determination of the velocity of light made at the United States Naval Academy, Annapolis. Astronomic Papers 1 135–8. U.S. Nautical Almanac Office. (See Table 24.)

Examples

```r
require(stats); require(graphics)
michelson <- transform(morley,
                        Expt = factor(Expt), Run = factor(Run))
xtabs(~ Expt + Run, data = michelson) # 5 x 20 balanced (two-way)
plot(Speed ~ Expt, data = michelson,
     main = "Speed of Light Data", xlab = "Experiment No.")
fm <- aov(Speed ~ Run + Expt, data = michelson)
summary(fm)
fm0 <- update(fm, . ~ . - Run)
anova(fm0, fm)
```

### mtcars

**Motor Trend Car Road Tests**

**Description**

The data was extracted from the 1974 Motor Trend US magazine, and comprises fuel consumption and 10 aspects of automobile design and performance for 32 automobiles (1973–74 models).

**Usage**

```r
mtcars
```

**Format**

A data frame with 32 observations on 11 (numeric) variables.

```r
[,1] mpg Miles/(US) gallon
[,2] cyl Number of cylinders
[,3] disp Displacement (cu.in.)
[,4] hp Gross horsepower
[,5] drat Rear axle ratio
[,6] wt Weight (1000 lbs)
[,7] qsec 1/4 mile time
[,8] vs Engine (0 = V-shaped, 1 = straight)
[,9] am Transmission (0 = automatic, 1 = manual)
[,10] gear Number of forward gears
```
nhtemp

[.11] carb Number of carburetors

Notes

Henderson and Velleman (1981) comment in a footnote to Table 1: ‘Hocking [original transcriber]’s noncrucial coding of the Mazda’s rotary engine as a straight six-cylinder engine and the Porsche’s flat engine as a V engine, as well as the inclusion of the diesel Mercedes 240D, have been retained to enable direct comparisons to be made with previous analyses.’

Source


Examples

```r
require(graphics)
pairs(mtcars, main = "mtcars data", gap = 1/4)
coplot(mpg ~ disp | as.factor(cyl), data = mtcars,
panel = panel.smooth, rows = 1)
## possibly more meaningful, e.g., for summary() or bivariate plots:
mtcars2 <- within(mtcars, {
  vs <- factor(vs, labels = c("V", "S"))
  am <- factor(am, labels = c("automatic", "manual"))
  cyl <- ordered(cyl)
  gear <- ordered(gear)
  carb <- ordered(carb)
})
summary(mtcars2)
```

nhtemp

Average Yearly Temperatures in New Haven

Description

The mean annual temperature in degrees Fahrenheit in New Haven, Connecticut, from 1912 to 1971.

Usage

nhtemp

Format

A time series of 60 observations.

Source


References

**Nile Flow of the River Nile**

**Description**

Measurements of the annual flow of the river Nile at Aswan (formerly Assuan), 1871–1970, in $10^8 m^3$, “with apparent changepoint near 1898” (Cobb(1978), Table 1, p.249).

**Usage**

Nile

**Format**

A time series of length 100.

**Source**


**References**


**Examples**

```r
require(stats); require(graphics)
par(mfrow = c(2, 2))
plot(Nile)
acf(Nile)
pacf(Nile)
ar(Nile) # selects order 2
cpgram(ar(Nile)$resid)
par(mfrow = c(1, 1))
arima(Nile, c(2, 0, 0))

## Now consider missing values, following Durbin & Koopman
NileNA <- Nile
NileNA[c(21:40, 61:80)] <- NA
arima(NileNA, c(2, 0, 0))
plot(NileNA)
pred <-
  predict(arima(window(NileNA, 1871, 1890), c(2, 0, 0)), n.ahead = 20)
lines(pred$pred, lty = 3, col = "red")
```
Average Monthly Temperatures at Nottingham, 1920–1939

Description
A time series object containing average air temperatures at Nottingham Castle in degrees Fahrenheit for 20 years.

Usage
nottem

Source

Examples
```r
require(stats); require(graphics)
nott <- window(nottem, end = c(1936,12))
fit <- arima(nott, order = c(1,0,0), list(order = c(2,1,0), period = 12))
nott.fore <- predict(fit, n.ahead = 36)
plot(nott, nott.fore$pred, nott.fore$pred+2*nott.fore$se, nott.fore$pred-2*nott.fore$se, gpars = list(col = c(1,1,2,2)))
```
**npk**

*Classical N, P, K Factorial Experiment*

**Description**

A classical N, P, K (nitrogen, phosphate, potassium) factorial experiment on the growth of peas conducted on 6 blocks. Each half of a fractional factorial design confounding the NPK interaction was used on 3 of the plots.

**Usage**

npk

**Format**

The npk data frame has 24 rows and 5 columns:

- block: which block (label 1 to 6).
- N: indicator (0/1) for the application of nitrogen.
- P: indicator (0/1) for the application of phosphate.
- K: indicator (0/1) for the application of potassium.
- yield: Yield of peas, in pounds/plot (the plots were (1/70) acre).

**Source**


**References**


**Examples**

```r
options(contrasts = c("contr.sum", "contr.poly"))
npk.aov <- aov(yield ~ block + N+P+K, npk)
npk.aov
summary(npk.aov)
coef(npk.aov)
options(contrasts = c("contr.treatment", "contr.poly"))
npk.aov1 <- aov(yield ~ block + N + K, data = npk)
summary.lm(npk.aov1)
se.contrast(npk.aov1, list(N=="0", N=="1"), data = npk)
model.tables(npk.aov1, type = "means", se = TRUE)
```
occupationalStatus

Description

Cross-classification of a sample of British males according to each subject's occupational status and his father's occupational status.

Usage

occupationalStatus

Format

A table of counts, with classifying factors origin (father's occupational status; levels 1:8) and destination (son's occupational status; levels 1:8).

Source


The data set has been in package gnm and been provided by the package authors.

Examples

```r
require(stats); require(graphics)
plot(occupationalStatus)

## Fit a uniform association model separating diagonal effects
Diag <- as.factor(diag(1:8))
Rscore <- scale(as.numeric(row(occupationalStatus)), scale = FALSE)
Cscore <- scale(as.numeric(col(occupationalStatus)), scale = FALSE)
modUnif <- glm(Freq ~ origin + destination + Diag + Rscore:Cscore,
               family = poisson, data = occupationalStatus)

summary(modUnif)
plot(modUnif) # 4 plots, with warning about h_ii ~ 1
```

Orange

Description

The Orange data frame has 35 rows and 3 columns of records of the growth of orange trees.

Usage

Orange
OrchardSprays

Description

An experiment was conducted to assess the potency of various constituents of orchard sprays in repelling honeybees, using a Latin square design.

Usage

OrchardSprays
Format

A data frame with 64 observations on 4 variables.

<table>
<thead>
<tr>
<th>.1</th>
<th>rowpos</th>
<th>numeric</th>
<th>Row of the design</th>
</tr>
</thead>
<tbody>
<tr>
<td>.2</td>
<td>colpos</td>
<td>numeric</td>
<td>Column of the design</td>
</tr>
<tr>
<td>.3</td>
<td>treatment</td>
<td>factor</td>
<td>Treatment level</td>
</tr>
<tr>
<td>.4</td>
<td>decrease</td>
<td>numeric</td>
<td>Response</td>
</tr>
</tbody>
</table>

Details

Individual cells of dry comb were filled with measured amounts of lime sulphur emulsion in sucrose solution. Seven different concentrations of lime sulphur ranging from a concentration of 1/100 to 1/1,562,500 in successive factors of 1/5 were used as well as a solution containing no lime sulphur. The responses for the different solutions were obtained by releasing 100 bees into the chamber for two hours, and then measuring the decrease in volume of the solutions in the various cells.

An $8 \times 8$ Latin square design was used and the treatments were coded as follows:

- A: highest level of lime sulphur
- B: next highest level of lime sulphur
- .
- .
- G: lowest level of lime sulphur
- H: no lime sulphur

Source


References


Examples

```r
require(graphics)
pairs(OrchardSprays, main = "OrchardSprays data")
```

---

**PlantGrowth**

*Results from an Experiment on Plant Growth*

Description

Results from an experiment to compare yields (as measured by dried weight of plants) obtained under a control and two different treatment conditions.

Usage

PlantGrowth
### Format

A data frame of 30 cases on 2 variables.

```
[, 1]   weight  numeric
[, 2]   group   factor
```

The levels of `group` are ‘ctrl’, ‘trt1’, and ‘trt2’.

### Source


### Examples

```r
## One factor ANOVA example from Dobson's book, cf. Table 7.4:
require(stats); require(graphics)
boxplot(weight ~ group, data = PlantGrowth, main = "PlantGrowth data",
ylab = "Dried weight of plants", col = "lightgray",
       notch = TRUE, varwidth = TRUE)
anova(lm(weight ~ group, data = PlantGrowth))
```

---

**precip**

### Description

The average amount of precipitation (rainfall) in inches for each of 70 United States (and Puerto Rico) cities.

### Usage

```
precip
```

### Format

A named vector of length 70.

### Note

The dataset version up to Nov.16, 2016 had a typo in "Cincinnati"’s name. The examples show how to recreate that version.

### Source


### References

presidents

Examples

```r
require(graphics)
dotchart(precip[order(precip)], main = "precip data")
title(sub = "Average annual precipitation (in.)")
```

```r
## Old ("wrong") version of dataset (just name change):
precip.O <- local({
  p <- precip; names(p)[names(p) == "Cincinnati"] <- "Cincinati" ; p })
stopifnot(all(precip == precip.O),
  match("Cincinnati", names(precip)) == 46,
  identical(names(precip)[46], names(precip.O)[46]))
```

---

presidents  Quarterly Approval Ratings of US Presidents

Description

The (approximately) quarterly approval rating for the President of the United States from the first quarter of 1945 to the last quarter of 1974.

Usage

presidents

Format

A time series of 120 values.

Details

The data are actually a fudged version of the approval ratings. See McNeil’s book for details.

Source

The Gallup Organisation.

References


Examples

```r
require(stats); require(graphics)
plot(presidents, las = 1, ylab = "Approval rating (%)",
  main = "presidents data")
```
Vapor Pressure of Mercury as a Function of Temperature

Description
Data on the relation between temperature in degrees Celsius and vapor pressure of mercury in millimeters (of mercury).

Usage
pressure

Format
A data frame with 19 observations on 2 variables.

```
[, 1] temperature numeric temperature (deg C)
[, 2] pressure numeric pressure (mm)
```

Source

References

Examples
```
require(graphics)
plot(pressure, xlab = "Temperature (deg C)",
     ylab = "Pressure (mm of Hg)",
     main = "pressure data: Vapor Pressure of Mercury")
plot(pressure, xlab = "Temperature (deg C)", log = "y",
     ylab = "Pressure (mm of Hg)",
     main = "pressure data: Vapor Pressure of Mercury")
```

Puromycin

Reaction Velocity of an Enzymatic Reaction

Description
The Puromycin data frame has 23 rows and 3 columns of the reaction velocity versus substrate concentration in an enzymatic reaction involving untreated cells or cells treated with Puromycin.

Usage
Puromycin
Puromycin

Format

This data frame contains the following columns:

- **conc**: a numeric vector of substrate concentrations (ppm)
- **rate**: a numeric vector of instantaneous reaction rates (counts/min/min)
- **state**: a factor with levels treated untreated

Details

Data on the velocity of an enzymatic reaction were obtained by Treloar (1974). The number of counts per minute of radioactive product from the reaction was measured as a function of substrate concentration in parts per million (ppm) and from these counts the initial rate (or velocity) of the reaction was calculated (counts/min/min). The experiment was conducted once with the enzyme treated with Puromycin, and once with the enzyme untreated.

Source


See Also

- [SSmicmen](#) for other models fitted to this dataset.

Examples

```r
require(stats); require(graphics)

plot(rate ~ conc, data = Puromycin, las = 1,
     xlab = "Substrate concentration (ppm)",
     ylab = "Reaction velocity (counts/min/min)",
     pch = as.integer(Puromycin$state),
     col = as.integer(Puromycin$state),
     main = "Puromycin data and fitted Michaelis-Menten curves")

## simplest form of fitting the Michaelis-Menten model to these data
fm1 <- nls(rate ~ Vm * conc/(K + conc), data = Puromycin,
           subset = state == "treated",
           start = c(Vm = 200, K = 0.05))
fm2 <- nls(rate ~ Vm * conc/(K + conc), data = Puromycin,
           subset = state == "untreated",
           start = c(Vm = 160, K = 0.05))
summary(fm1)
summary(fm2)

## add fitted lines to the plot
conc <- seq(0, 1.2, length.out = 101)
lines(conc, predict(fm1, list(conc = conc)), lty = 1, col = 1)
lines(conc, predict(fm2, list(conc = conc)), lty = 2, col = 2)
legend(0.8, 120, levels(Puromycin$state),
       col = 1:2, lty = 1:2, pch = 1:2)

## using partial linearity
fm3 <- nls(rate ~ conc/(K + conc), data = Puromycin,}
```
The data set give the locations of 1000 seismic events of MB > 4.0. The events occurred in a cube near Fiji since 1964.

Usage

quakes

Format

A data frame with 1000 observations on 5 variables.

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>lat</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>long</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>depth</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>mag</td>
<td>numeric</td>
</tr>
<tr>
<td></td>
<td>stations</td>
<td>numeric</td>
</tr>
</tbody>
</table>

Details

There are two clear planes of seismic activity. One is a major plate junction; the other is the Tonga trench off New Zealand. These data constitute a subsample from a larger dataset of containing 5000 observations.

Source

This is one of the Harvard PRIM-H project data sets. They in turn obtained it from Dr. John Woodhouse, Dept. of Geophysics, Harvard University.

Examples

```r
require(graphics)
pairs(quakes, main = "Fiji Earthquakes, N = 1000", cex.main = 1.2, pch = ".")
```
**Description**

400 triples of successive random numbers were taken from the VAX FORTRAN function RANDU running under VMS 1.5.

**Usage**

```r
randu
```

**Format**

A data frame with 400 observations on 3 variables named `x`, `y` and `z` which give the first, second and third random number in the triple.

**Details**

In three dimensional displays it is evident that the triples fall on 15 parallel planes in 3-space. This can be shown theoretically to be true for all triples from the RANDU generator.

These particular 400 triples start 5 apart in the sequence, that is they are \(((U[5i+1], U[5i+2], U[5i+3]), i= 0, \ldots, 399)\), and they are rounded to 6 decimal places.

Under VMS versions 2.0 and higher, this problem has been fixed.

**Source**

David Donoho

**Examples**

```r
## We could re-generate the dataset by the following R code
seed <- as.double(1)
RANDU <- function() {
  seed <<- ((2^16 + 3) * seed) %% (2^31)
  seed/(2^31)
}
for(i in 1:400) {
  U <- c(RANDU(), RANDU(), RANDU(), RANDU(), RANDU())
  print(round(U[1:3], 6))
}
```
**rivers**  
*Lengths of Major North American Rivers*

**Description**

This data set gives the lengths (in miles) of 141 “major” rivers in North America, as compiled by the US Geological Survey.

**Usage**

`rivers`

**Format**

A vector containing 141 observations.

**Source**


**References**


---

**rock**  
*Measurements on Petroleum Rock Samples*

**Description**

Measurements on 48 rock samples from a petroleum reservoir.

**Usage**

`rock`

**Format**

A data frame with 48 rows and 4 numeric columns.

<table>
<thead>
<tr>
<th>.1</th>
<th>area</th>
<th>area of pores space, in pixels out of 256 by 256</th>
</tr>
</thead>
<tbody>
<tr>
<td>.2</td>
<td>peri</td>
<td>perimeter in pixels</td>
</tr>
<tr>
<td>.3</td>
<td>shape</td>
<td>perimeter/sqrt(area)</td>
</tr>
<tr>
<td>.4</td>
<td>perm</td>
<td>permeability in milli-Darcies</td>
</tr>
</tbody>
</table>

**Details**

Twelve core samples from petroleum reservoirs were sampled by 4 cross-sections. Each core sample was measured for permeability, and each cross-section has total area of pores, total perimeter of pores, and shape.

**Source**

Data from BP Research, image analysis by Ronit Katz, U. Oxford.
Student’s Sleep Data

Description

Data which show the effect of two soporific drugs (increase in hours of sleep compared to control) on 10 patients.

Usage

sleep

Format

A data frame with 20 observations on 3 variables.

<table>
<thead>
<tr>
<th></th>
<th>extra</th>
<th>group</th>
<th>ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>numeric</td>
<td>factor</td>
<td>factor</td>
</tr>
<tr>
<td>2</td>
<td>increase in hours of sleep</td>
<td>drug given</td>
<td>patient ID</td>
</tr>
</tbody>
</table>

Details

The `group` variable name may be misleading about the data: They represent measurements on 10 persons, not in groups.

Source


References


Examples

```r
require(stats)
## Student’s paired t-test
with(sleep, 
  t.test(extra[group == 1],
         extra[group == 2], paired = TRUE))

## The sleep prolongations*
sleep1 <- with(sleep, extra[group == 2] - extra[group == 1])
summary(sleep1)
stripchart(sleep1, method = "stack", xlab = "hours",
           main = "Sleep prolongation (n = 10)")
boxplot(sleep1, horizontal = TRUE, add = TRUE,
        at = .6, pars = list(boxwex = 0.5, staplewex = 0.25))
```
stackloss  | Brownlee’s Stack Loss Plant Data

**Description**
Operational data of a plant for the oxidation of ammonia to nitric acid.

**Usage**

- stackloss
- stack.x
- stack.loss

**Format**

stackloss is a data frame with 21 observations on 4 variables.

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Air Flow</td>
</tr>
<tr>
<td>2</td>
<td>Water Temp</td>
</tr>
<tr>
<td>3</td>
<td>Acid Conc.</td>
</tr>
<tr>
<td>4</td>
<td>stack.loss</td>
</tr>
</tbody>
</table>

For compatibility with S-PLUS, the data sets stack.x, a matrix with the first three (independent) variables of the data frame, and stack.loss, the numeric vector giving the fourth (dependent) variable, are provided as well.

**Details**

“Obtained from 21 days of operation of a plant for the oxidation of ammonia (NH₃) to nitric acid (HNO₃). The nitric oxides produced are absorbed in a countercurrent absorption tower”. (Brownlee, cited by Dodge, slightly reformatted by MM.)

Air Flow represents the rate of operation of the plant. Water Temp is the temperature of cooling water circulated through coils in the absorption tower. Acid Conc. is the concentration of the acid circulating, minus 50, times 10: that is, 89 corresponds to 58.9 per cent acid. stack.loss (the dependent variable) is 10 times the percentage of the ingoing ammonia to the plant that escapes from the absorption column unabsorbed; that is, an (inverse) measure of the over-all efficiency of the plant.

**Source**

**References**


Examples

```r
require(stats)
summary(lm(stack <- lm(stack.loss ~ stack.x))
```

---

**state**  

**US State Facts and Figures**

**Description**

Data sets related to the 50 states of the United States of America.

**Usage**

- `state.abb`
- `state.area`
- `state.center`
- `state.division`
- `state.name`
- `state.region`
- `state.x77`

**Details**

R currently contains the following “state” data sets. Note that all data are arranged according to alphabetical order of the state names.

- `state.abb`: character vector of 2-letter abbreviations for the state names.
- `state.area`: numeric vector of state areas (in square miles).
- `state.center`: list with components named `x` and `y` giving the approximate geographic center of each state in negative longitude and latitude. Alaska and Hawaii are placed just off the West Coast. See ‘Examples’ on how to “correct”.
- `state.division`: `factor` giving state divisions (New England, Middle Atlantic, South Atlantic, East South Central, West South Central, East North Central, West North Central, Mountain, and Pacific).
- `state.name`: character vector giving the full state names.
- `state.region`: `factor` giving the region (Northeast, South, North Central, West) that each state belongs to.
- `state.x77`: matrix with 50 rows and 8 columns giving the following statistics in the respective columns.
  - Population: population estimate as of July 1, 1975
  - Illiteracy: illiteracy (1970, percent of population)
  - Life Exp: life expectancy in years (1969–71)
  - Murder: murder and non-negligent manslaughter rate per 100,000 population (1976)
  - HS Grad: percent high-school graduates (1970)
  - Frost: mean number of days with minimum temperature below freezing (1931–1960) in capital or large city
  - Area: land area in square miles

Note that a square mile is by definition exactly \((\text{cm}(1760 \times 3 \times 12) / 100 / 1000)^2 \text{ km}^2\), i.e., \(2.589988110336km^2\).
Source
U.S. Department of Commerce, Bureau of the Census (1977) *County and City Data Book*.

References

Examples

```r
(dst <- dxy <- data.frame(state.center, row.names=state.abb))
## Alaska and Hawaii are placed just off the West Coast (for compact map drawing):
dst[c("AK", "HI"),]
## state.center2 := version of state.center with "correct" coordinates for AK & HI:
## From https://pubs.usgs.gov/gip/Elevations-Distances/elvadist.html#Geographic%20Centers
## Alaska 63°50' N., 152°00' W., 60 miles northwest of Mount McKinley
## Hawaii 20°15' N., 156°20' W., off Maui Island
dxy["AK",] <- c(-152  , 63.83) # or c(-152.11, 65.17)
dxy["HI",] <- c(-156.33, 20.25) # or c(-156.69, 20.89)
state.center2 <- as.list(dxy)
plot(dxy, asp=1.2, pch=3, col=2)
text(state.center2, state.abb, cex=1/2, pos=4, offset=1/4)
i <- c("AK","HI")
do.call(arrows, c(setNames(c(dst[i,], dxy[i,]), c("x0","y0", "x1","y1")),
    col=adjustcolor(4, .7), length=1/8))
points(dst[i,], col=2)
if(FALSE) { # if(require("maps")) {
    map("state", interior = FALSE, add = TRUE)
    map("state", boundary = FALSE, lty = 2, add = TRUE)
}
```

---

**sunspot.month**

*Monthly Sunspot Data, from 1749 to "Present"*

---

**Description**

Monthly numbers of sunspots, as from the World Data Center, aka SIDC. This is the version of the data that will occasionally be updated when new counts become available.

**Usage**

```
sunspot.month
```

**Format**

The univariate time series `sunspot.year` and `sunspot.month` contain 289 and 2988 observations, respectively. The objects are of class "ts".
sunspot.year

Author(s)

R

Source

WDC-SILSO, Solar Influences Data Analysis Center (SIDC), Royal Observatory of Belgium, Av. Circulaire, 3, B-1180 BRUSSELS Currently at http://www.sidc.be/silso/datafiles

See Also

sunspot.month is a longer version of sunspots: the latter runs until 1983 and is kept fixed (for reproducibility as example dataset).

Examples

require(stats); require(graphics)
## Compare the monthly series
plot(sunspot.month, main="sunspot.month & sunspots [package 'datasets']", col=2)
lines(sunspots) # -> faint differences where they overlap

## Now look at the difference:
all(tsp(sunspots) [c(1,3)] == tsp(sunspot.month)[c(1,3)]) # Start & Periodicity are the same
n1 <- length(sunspots)
table(eq <- sunspots == sunspot.month[1:n1]) #> 132 are different!
i <- which(!eq)
rug(time(eq)[i])
s1 <- sunspots[i]; s2 <- sunspot.month[i]
cbind(i = i, time = time(sunspots)[i], sunspots = s1, ss.month = s2, perc.diff = round(100*2*abs(s1-s2)/(s1+s2), 1))

## How to recreate the "old" sunspot.month (R <= 3.0.3):
.sunspot.diff <- cbind(i = c(1202L, 1256L, 1258L, 1301L, 1407L, 1429L, 1452L, 1455L, 1663L, 2151L, 2329L, 2498L, 2594L, 2694L, 2819L),
res10 = c(1L, 1L, 1L, -1L, -1L, -1L, 1L, -1L, 1L, 1L, 1L, 1L, 1L, 20L, 1L))
ssm0 <- sunspot.month[1:2988]
with(as.data.frame(.sunspot.diff), ssm0[i] <<- ssm0[i] - res10/10)
sunspot.month.0 <- ts(ssm0, start = 1749, frequency = 12)

Description

Yearly Sunspot Data, 1700–1988

Yearly numbers of sunspots from 1700 to 1988 (rounded to one digit).
Note that monthly numbers are available as sunspot.month, though starting slightly later.

Usage

sunspot.year
The univariate time series sunspot.year contains 289 observations, and is of class "ts".


For monthly sunspot numbers, see sunspot.month and sunspots.

Regularly updated yearly sunspot numbers are available from WDC-SILSO, Royal Observatory of Belgium, at [http://www.sidc.be/silso/datafiles](http://www.sidc.be/silso/datafiles)

```r
utils::str(sm <- sunspots)# the monthly version we keep unchanged
utils::str(sy <- sunspot.year)
## The common time interval
(t1 <- c(max(start(sm), start(sy)), 1)) # Jan 1749
(t2 <- c(min( end(sm)[1],end(sy)[1], 12)) # Dec 1983
s.m <- window(sm, start=t1, end=t2)
 s.y <- window(sy, start=t1, end=t2[1]) # {irrelevant warning}
stopifnot(length(s.y) * 12 == length(s.m),
  ## The yearly series *is* close to the averages of the monthly one:
  all.equal(s.y, aggregate(s.m, FUN = mean), tolerance = 0.0020))
## NOTE: Strangely, correctly weighting the number of days per month
## (using 28.25 for February) is *not* closer than the simple mean:
ndays <- c(31, 28.25, rep(c(31,30, 31,30, 31), 2))
all.equal(s.y, aggregate(s.m, FUN = weighted.mean)) # 0.0013
all.equal(s.y, aggregate(s.m, FUN = weighted.mean, w = ndays)) # 0.0017
```

**Description**

Monthly mean relative sunspot numbers from 1749 to 1983. Collected at Swiss Federal Observatory, Zurich until 1960, then Tokyo Astronomical Observatory.

**Usage**

sunspots

**Format**

A time series of monthly data from 1749 to 1983.

**Source**

See Also

sunspot.month has a longer (and a bit different) series, sunspot.year is a much shorter one. See there for getting more current sunspot numbers.

Examples

require(graphics)
plot(sunspots, main = "sunspots data", xlab = "Year",
ylab = "Monthly sunspot numbers")

swiss

Swiss Fertility and Socioeconomic Indicators (1888) Data

Description

Standardized fertility measure and socio-economic indicators for each of 47 French-speaking provinces of Switzerland at about 1888.

Usage

swiss

Format

A data frame with 47 observations on 6 variables, each of which is in percent, i.e., in [0, 100].

[,1] Fertility  I_y, ‘common standardized fertility measure’
[,2] Agriculture % of males involved in agriculture as occupation
[,3] Examination % draftees receiving highest mark on army examination
[,4] Education % education beyond primary school for draftees.
[,5] Catholic % ‘catholic’ (as opposed to ‘protestant’).

All variables but ‘Fertility’ give proportions of the population.

Details

(paraphrasing Mosteller and Tukey):
Switzerland, in 1888, was entering a period known as the demographic transition; i.e., its fertility was beginning to fall from the high level typical of underdeveloped countries.
The data collected are for 47 French-speaking “provinces” at about 1888.
Here, all variables are scaled to [0, 100], where in the original, all but “Catholic” were scaled to [0, 1].

Note

Files for all 182 districts in 1888 and other years have been available at https://opr.princeton.edu/archive/pefp/switz.aspx.
They state that variables Examination and Education are averages for 1887, 1888 and 1889.
Theoph

Pharmacokinetics of Theophylline

Description

The Theoph data frame has 132 rows and 5 columns of data from an experiment on the pharmacokinetics of theophylline.

Usage

Theoph

Format

An object of class c("nfnGroupedData", "nfGroupedData", "groupedData", "data.frame") containing the following columns:

- **Subject** an ordered factor with levels 1, ..., 12 identifying the subject on whom the observation was made. The ordering is by increasing maximum concentration of theophylline observed.
- **Wt** weight of the subject (kg).
- **Dose** dose of theophylline administered orally to the subject (mg/kg).
- **Time** time since drug administration when the sample was drawn (hr).
- **conc** theophylline concentration in the sample (mg/L).
Details

Boeckmann, Sheiner and Beal (1994) report data from a study by Dr. Robert Upton of the kinetics of the anti-asthmatic drug theophylline. Twelve subjects were given oral doses of theophylline then serum concentrations were measured at 11 time points over the next 25 hours.

These data are analyzed in Davidian and Giltinan (1995) and Pinheiro and Bates (2000) using a two-compartment open pharmacokinetic model, for which a self-starting model function, SSfol, is available.

This dataset was originally part of package nlme, and that has methods (including for [], as.data.frame, plot and print) for its grouped-data classes.

Source


See Also

SSfol

Examples

require(stats); require(graphics)
coplot(conc ~ Time | Subject, data = Theoph, show.given = FALSE)
Theoph.4 <- subset(Theoph, Subject == 4)
fml <- nls(conc ~ SSfol(Dose, Time, lKe, lKa, lCl),
     data = Theoph.4)
summary(fml)
plot(conc ~ Time, data = Theoph.4,
     xlab = "Time since drug administration (hr)",
     ylab = "Theophylline concentration (mg/L)",
     main = "Observed concentrations and fitted model",
     sub = "Theophylline data - Subject 4 only",
     las = 1, col = 4)
xvals <- seq(0, par("usr")[2], length.out = 55)
lines(xvals, predict(fml, newdata = list(Time = xvals)),
     col = 4)

Titanic

Survival of passengers on the Titanic

Description

This data set provides information on the fate of passengers on the fatal maiden voyage of the ocean liner ‘Titanic’, summarized according to economic status (class), sex, age and survival.
Usage

Titanic

Format

A 4-dimensional array resulting from cross-tabulating 2201 observations on 4 variables. The variables and their levels are as follows:

<table>
<thead>
<tr>
<th>No</th>
<th>Name</th>
<th>Levels</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Class</td>
<td>1st, 2nd, 3rd, Crew</td>
</tr>
<tr>
<td>2</td>
<td>Sex</td>
<td>Male, Female</td>
</tr>
<tr>
<td>3</td>
<td>Age</td>
<td>Child, Adult</td>
</tr>
<tr>
<td>4</td>
<td>Survived</td>
<td>No, Yes</td>
</tr>
</tbody>
</table>

Details

The sinking of the Titanic is a famous event, and new books are still being published about it. Many well-known facts—from the proportions of first-class passengers to the ‘women and children first’ policy, and the fact that that policy was not entirely successful in saving the women and children in the third class—are reflected in the survival rates for various classes of passenger.

These data were originally collected by the British Board of Trade in their investigation of the sinking. Note that there is not complete agreement among primary sources as to the exact numbers on board, rescued, or lost.

Due in particular to the very successful film ‘Titanic’, the last years saw a rise in public interest in the Titanic. Very detailed data about the passengers is now available on the Internet, at sites such as Encyclopedia Titanica (https://www.encyclopedia-titanica.org/).

Source


The source provides a data set recording class, sex, age, and survival status for each person on board of the Titanic, and is based on data originally collected by the British Board of Trade and reprinted in:


Examples

```r
require(graphics)
mosaicplot(Titanic, main = "Survival on the Titanic")
## Higher survival rates in children?
apply(Titanic, c(3, 4), sum)
## Higher survival rates in females?
apply(Titanic, c(2, 4), sum)
## Use loglm() in package 'MASS' for further analysis ...
```
ToothGrowth

The Effect of Vitamin C on Tooth Growth in Guinea Pigs

Description

The response is the length of odontoblasts (cells responsible for tooth growth) in 60 guinea pigs. Each animal received one of three dose levels of vitamin C (0.5, 1, and 2 mg/day) by one of two delivery methods, orange juice or ascorbic acid (a form of vitamin C and coded as VC).

Usage

ToothGrowth

Format

A data frame with 60 observations on 3 variables.

<table>
<thead>
<tr>
<th>.1</th>
<th>.2</th>
<th>.3</th>
</tr>
</thead>
<tbody>
<tr>
<td>len</td>
<td>supp</td>
<td>dose</td>
</tr>
<tr>
<td>numeric</td>
<td>factor</td>
<td>numeric</td>
</tr>
<tr>
<td>Tooth length</td>
<td>Supplement type (VC or OJ).</td>
<td>Dose in milligrams/day</td>
</tr>
</tbody>
</table>

Source


References


Examples

```r
require(graphics)
coplot(len ~ dose | supp, data = ToothGrowth, panel = panel.smooth,
       xlab = "ToothGrowth data: length vs dose, given type of supplement")
```

treering

Yearly Treering Data, -6000–1979

Description

Contains normalized tree-ring widths in dimensionless units.

Usage

treering
trees

Format

A univariate time series with 7981 observations. The object is of class "ts". Each tree ring corresponds to one year.

Details

The data were recorded by Donald A. Graybill, 1980, from Gt Basin Bristlecone Pine 2805M, 3726-11810 in Methuselah Walk, California.

Source

Time Series Data Library: https://robjhyndman.com/TSDL/, series ’CA535.DAT’

References

For some photos of Methuselah Walk see https://web.archive.org/web/20110523225828/http://www.ltrr.arizona.edu/~hallman/sitephotos/meth.html

trees

Diameter, Height and Volume for Black Cherry Trees

Description

This data set provides measurements of the diameter, height and volume of timber in 31 felled black cherry trees. Note that the diameter (in inches) is erroneously labelled Girth in the data. It is measured at 4 ft 6 in above the ground.

Usage

trees

Format

A data frame with 31 observations on 3 variables.

[,1] Girth numeric Tree diameter (rather than girth, actually) in inches
[,2] Height numeric Height in ft
[,3] Volume numeric Volume of timber in cubic ft

Source


References

Examples

```r
require(stats); require(graphics)
pairs(trees, panel = panel.smooth, main = "trees data")
plot(Volume ~ Girth, data = trees, log = "xy")
coplot(log(Volume) ~ log(Girth) | Height, data = trees,
panel = panel.smooth)
summary(fm1 <- lm(log(Volume) ~ log(Girth), data = trees))
summary(fm2 <- update(fm1, ~ . + log(Height), data = trees))
step(fm2)
## i.e., Volume \sim c \times \text{Height} \times \text{Girth}^2 \text{ seems reasonable}
```

UCBAdmissions

### Description

Aggregate data on applicants to graduate school at Berkeley for the six largest departments in 1973 classified by admission and sex.

### Usage

UCBAdmissions

### Format

A 3-dimensional array resulting from cross-tabulating 4526 observations on 3 variables. The variables and their levels are as follows:

<table>
<thead>
<tr>
<th>No</th>
<th>Name</th>
<th>Levels</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Admit</td>
<td>Admitted, Rejected</td>
</tr>
<tr>
<td>2</td>
<td>Gender</td>
<td>Male, Female</td>
</tr>
<tr>
<td>3</td>
<td>Dept</td>
<td>A, B, C, D, E, F</td>
</tr>
</tbody>
</table>

### Details

This data set is frequently used for illustrating Simpson’s paradox, see Bickel et al (1975). At issue is whether the data show evidence of sex bias in admission practices. There were 2691 male applicants, of whom 1198 (44.5%) were admitted, compared with 1835 female applicants of whom 557 (30.4%) were admitted. This gives a sample odds ratio of 1.83, indicating that males were almost twice as likely to be admitted. In fact, graphical methods (as in the example below) or log-linear modelling show that the apparent association between admission and sex stems from differences in the tendency of males and females to apply to the individual departments (females used to apply more to departments with higher rejection rates).

This data set can also be used for illustrating methods for graphical display of categorical data, such as the general-purpose mosaicplot or the fourfoldplot for 2-by-2-by-k tables.

### References

Examples

```r
require(graphics)
## Data aggregated over departments
apply(UCBAdmissions, c(1, 2), sum)
mosaicplot(apply(UCBAdmissions, c(1, 2), sum),
          main = "Student admissions at UC Berkeley")
## Data for individual departments
opar <- par(mfrow = c(2, 3), oma = c(0, 0, 2, 0))
for(i in 1:6)
  mosaicplot(UCBAdmissions[,,i],
             xlab = "Admit", ylab = "Sex",
             main = paste("Department", LETTERS[i]))
  mtext(expression(bold("Student admissions at UC Berkeley")),
         outer = TRUE, cex = 1.5)
par(opar)
```

UKDriverDeaths

Road Casualties in Great Britain 1969–84

Description

UKDriverDeaths is a time series giving the monthly totals of car drivers in Great Britain killed or seriously injured Jan 1969 to Dec 1984. Compulsory wearing of seat belts was introduced on 31 Jan 1983.

Seatbelts is more information on the same problem.

Usage

UKDriverDeaths
Seatbelts

Format

Seatbelts is a multiple time series, with columns

- DriversKilled car drivers killed.
- drivers same as UKDriverDeaths.
- front front-seat passengers killed or seriously injured.
- rear rear-seat passengers killed or seriously injured.
- kms distance driven.
- PetrolPrice petrol price.
- VanKilled number of van (‘light goods vehicle’) drivers.
- law 0/1: was the law in effect that month?

Source


UKgas

UK Quarterly Gas Consumption

Description

Quarterly UK gas consumption from 1960Q1 to 1986Q4, in millions of therms.

Usage

UKgas

Format

A quarterly time series of length 108.

Source


Examples

## maybe str(UKgas) ; plot(UKgas) ...
UKLungDeaths  Monthly Deaths from Lung Diseases in the UK

Description

Three time series giving the monthly deaths from bronchitis, emphysema and asthma in the UK, 1974–1979, both sexes (ldeaths), males (mdeaths) and females (fdeaths).

Usage

ldeaths
fdeaths
mdeaths

Source


Examples

require(stats); require(graphics) # for time
plot(ldeaths)
plot(mdeaths, fdeaths)
## Better labels:
yr <- floor(tt <- time(mdeaths))
plot(mdeaths, fdeaths,
     xy.labels = paste(month.abb[12*(tt - yr)], yr-1900, sep = " "))

USAccDeaths  Accidental Deaths in the US 1973–1978

Description

A time series giving the monthly totals of accidental deaths in the USA. The values for the first six months of 1979 are 7798 7406 8363 8460 9217 9316.

Usage

USAccDeaths

Source

USArrests

**Description**

This data set contains statistics, in arrests per 100,000 residents for assault, murder, and rape in each of the 50 US states in 1973. Also given is the percent of the population living in urban areas.

**Usage**

USArrests

**Format**

A data frame with 50 observations on 4 variables.

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>.1</td>
<td>Murder</td>
<td>numeric</td>
<td>Murder arrests (per 100,000)</td>
</tr>
<tr>
<td>.2</td>
<td>Assault</td>
<td>numeric</td>
<td>Assault arrests (per 100,000)</td>
</tr>
<tr>
<td>.3</td>
<td>UrbanPop</td>
<td>numeric</td>
<td>Percent urban population</td>
</tr>
<tr>
<td>.4</td>
<td>Rape</td>
<td>numeric</td>
<td>Rape arrests (per 100,000)</td>
</tr>
</tbody>
</table>

**Note**

USArrests contains the data as in McNeil’s monograph. For the UrbanPop percentages, a review of the table (No. 21) in the Statistical Abstracts 1975 reveals a transcription error for Maryland (and that McNeil used the same “round to even” rule that R’s `round()` uses), as found by Daniel S Coven (Arizona).

See the example below on how to correct the error and improve accuracy for the ‘<n>.5’ percentages.

**Source**


**References**


**See Also**

The `state` data sets.

**Examples**

```r
summary(USArrests)

require(graphics)
pairs(USArrests, panel = panel.smooth, main = "USArrests data")
```

## Difference between 'USArrests' and its correction
USArrests["Maryland", "UrbanPop"] # 67 -- the transcription error
UA.C <- USArrests
UA.C["Maryland", "UrbanPop"] <- 76.6

## also +/- 0.5 to restore the original <n>.5 percentages
s5u <- c("Colorado", "Florida", "Mississippi", "Wyoming")
s5d <- c("Nebraska", "Pennsylvania")
UA.C[s5u, "UrbanPop"] <- UA.C[s5u, "UrbanPop"] + 0.5
UA.C[s5d, "UrbanPop"] <- UA.C[s5d, "UrbanPop"] - 0.5

## ==> UA.C is now a *C*orrected version of USArrests

### USJudgeRatings

**Lawyers’ Ratings of State Judges in the US Superior Court**

**Description**

Lawyers’ ratings of state judges in the US Superior Court.

**Usage**

USJudgeRatings

**Format**

A data frame containing 43 observations on 12 numeric variables.

[1] CONT Number of contacts of lawyer with judge.
[8] FAMI Familiarity with law.

**Source**

New Haven Register, 14 January, 1977 (from John Hartigan).

**Examples**

```
require(graphics)
pairs(USJudgeRatings, main = "USJudgeRatings data")
```
USPersonalExpenditure  Personal Expenditure Data

Description
This data set consists of United States personal expenditures (in billions of dollars) in the categories; food and tobacco, household operation, medical and health, personal care, and private education for the years 1940, 1945, 1950, 1955 and 1960.

Usage
USPersonalExpenditure

Format
A matrix with 5 rows and 5 columns.

Source

References

Examples
```r
require(stats) # for medpolish
USPersonalExpenditure
medpolish(log10(USPersonalExpenditure))
```

uspop  Populations Recorded by the US Census

Description
This data set gives the population of the United States (in millions) as recorded by the decennial census for the period 1790–1970.

Usage
uspop

Format
A time series of 19 values.

Source
**Examples**

```r
require(graphics)
plot(uspop, log = "y", main = "uspop data", xlab = "Year",
     ylab = "U.S. Population (millions)"
```

---

**VADeaths**  
*Death Rates in Virginia (1940)*

**Description**

Death rates per 1000 in Virginia in 1940.

**Usage**

VADeaths

**Format**

A matrix with 5 rows and 4 columns.

**Details**

The death rates are measured per 1000 population per year. They are cross-classified by age group (rows) and population group (columns). The age groups are: 50–54, 55–59, 60–64, 65–69, 70–74 and the population groups are Rural/Male, Rural/Female, Urban/Male and Urban/Female.

This provides a rather nice 3-way analysis of variance example.

**Source**


**References**


**Examples**

```r
require(stats); require(graphics)
n <- length(dr <- c(VADeaths))
nam <- names(VADeaths)
d.VAD <- data.frame(
  Drate = dr,
  age = rep(ordered(rownames(VADeaths)), length.out = n),
  gender = gl(2, 5, n, labels = c("M", "F")),
  site = gl(2, 10, labels = c("rural", "urban")))
coplot(Drate ~ as.numeric(age) | gender * site, data = d.VAD,
      panel = panel.smooth, xlab = "VADeaths data - Given: gender")
summary(aov.VAD <- aov(Drate ~ .^2, data = d.VAD))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0))
plot(aov.VAD)
par(opar)
```
volcano

Topographic Information on Auckland’s Maunga Whau Volcano

Description

Maunga Whau (Mt Eden) is one of about 50 volcanos in the Auckland volcanic field. This data set gives topographic information for Maunga Whau on a 10m by 10m grid.

Usage

volcano

Format

A matrix with 87 rows and 61 columns, rows corresponding to grid lines running east to west and columns to grid lines running south to north.

Source

Digitized from a topographic map by Ross Ihaka. These data should not be regarded as accurate.

See Also

filled.contour for a nice plot.

Examples

```r
require(grDevices); require(graphics)
filled.contour(volcano, color.palette = terrain.colors, asp = 1)
title(main = "volcano data: filled contour map")
```

warpbreaks

The Number of Breaks in Yarn during Weaving

Description

This data set gives the number of warp breaks per loom, where a loom corresponds to a fixed length of yarn.

Usage

warpbreaks

Format

A data frame with 54 observations on 3 variables.

```
[,1] breaks numeric The number of breaks
[,2] wool factor The type of wool (A or B)
[,3] tension factor The level of tension (L, M, H)
```

There are measurements on 9 looms for each of the six types of warp (AL, AM, AH, BL, BM, BH).
Source


References


See Also

*xtabs* for ways to display these data as a table.

Examples

```r
require(stats); require(graphics)
summary(warpbreaks)
opar <- par(mfrow = c(1, 2), oma = c(0, 0, 1.1, 0))
plot(breaks ~ tension, data = warpbreaks, col = "lightgray",
     varwidth = TRUE, subset = wool == "A", main = "Wool A")
plot(breaks ~ tension, data = warpbreaks, col = "lightgray",
     varwidth = TRUE, subset = wool == "B", main = "Wool B")
mtext("warpbreaks data", side = 3, outer = TRUE)
par(opar)
summary(fm1 <- lm(breaks ~ wool*tension, data = warpbreaks))
anova(fm1)
```

---

**women**

*Average Heights and Weights for American Women*

Description

This data set gives the average heights and weights for American women aged 30–39.

Usage

`women`

Format

A data frame with 15 observations on 2 variables.

<table>
<thead>
<tr>
<th></th>
<th>height</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>numeric</td>
<td>numeric</td>
</tr>
</tbody>
</table>

Details

The data set appears to have been taken from the American Society of Actuaries *Build and Blood Pressure Study* for some (unknown to us) earlier year.

The World Almanac notes: “The figures represent weights in ordinary indoor clothing and shoes, and heights with shoes”.
WorldPhones

Source


References


Examples

```r
require(graphics)
plot(women, xlab = "Height (in)", ylab = "Weight (lb)",
     main = "women data: American women aged 30-39")
```

---

**WorldPhones**

**The World's Telephones**

Description

The number of telephones in various regions of the world (in thousands).

Usage

WorldPhones

Format

A matrix with 7 rows and 8 columns. The columns of the matrix give the figures for a given region, and the rows the figures for a year.

The regions are: North America, Europe, Asia, South America, Oceania, Africa, Central America.


Source


References


Examples

```r
require(graphics)
matplot(rownames(WorldPhones), WorldPhones, type = "b", log = "y",
        xlab = "Year", ylab = "Number of telephones (1000's)"
        main = "World phones data: log scale for response")
legend(1951.5, 80000, colnames(WorldPhones), col = 1:6, lty = 1:5,
       pch = rep(21, 7))
```

WWWusage

Internet Usage per Minute

Description

A time series of the numbers of users connected to the Internet through a server every minute.

Usage

WWWusage

Format

A time series of length 100.

Source


References


Examples

```r
require(graphics)
work <- diff(WWWusage)
par(mfrow = c(2, 1)); plot(WWWusage); plot(work)
## Not run:
require(stats)
aics <- matrix(, 6, 6, dimnames = list(p = 0:5, q = 0:5))
for(q in 1:5) aics[1, 1+q] <- arima(WWWusage, c(0, 1, q),
  optim.control = list(maxit = 500))$aic
for(p in 1:5)
  for(q in 0:5) aics[1+p, 1+q] <- arima(WWWusage, c(p, 1, q),
    optim.control = list(maxit = 500))$aic
round(aics - min(aics, na.rm = TRUE), 2)
## End(Not run)
```
Chapter 4

The grDevices package

grDevices-package  The R Graphics Devices and Support for Colours and Fonts

Description

Graphics devices and support for base and grid graphics

Details

This package contains functions which support both base and grid graphics.
For a complete list of functions, use library(help = "grDevices").

Author(s)

R Core Team and contributors worldwide
Maintainer: R Core Team <R-core@r-project.org>

adjustcolor  Adjust Colors in One or More Directions Conveniently.

Description

Adjust or modify a vector of colors by “turning knobs” on one or more coordinates in \((r, g, b, \alpha)\) space, typically by up or down scaling them.

Usage

adjustcolor(col, alpha.f = 1, red.f = 1, green.f = 1, blue.f = 1, offset = c(0, 0, 0, 0), transform = diag(c(red.f, green.f, blue.f, alpha.f)))
Adjust color

Arguments

- `col`: vector of colors, in any format that `col2rgb()` accepts
- `alpha.f`: factor modifying the opacity alpha; typically in [0,1]
- `red.f`, `green.f`, `blue.f`: factors modifying the “red-”, “green-” or “blue-”ness of the colors, respectively.
- `offset`: numeric vector of length 4 to offset \( x := c(r, g, b, \alpha) \), where \( x \) is the \([0, 1]-\)scaled result of `col2rgb(col, alpha=TRUE)`.
- `transform`: a 4x4 numeric matrix applied to \( x + offset \).

Value

A color vector of the same length as `col`, effectively the result of `rgb()`.

See Also

`rgb`, `col2rgb`. For more sophisticated color constructions: `convertColor`

Examples

```r
## Illustrative examples:
opal <- palette("default")
stopifnot(identical(adjustcolor(1:8, 0.75),
                      adjustcolor(palette(), 0.75)))
cbind(palette(), adjustcolor(1:8, 0.75))

## alpha = 1/2 * previous alpha --> opaque colors
x <- palette(adjustcolor(palette(), 0.5))
sines <- outer(1:20, 1:4, function(x, y) sin(x / 20 * pi * y))
matplot(sines, type = "b", pch = 21:23, col = 2:5, bg = 2:5,
        main = "Using an 'opaque ('translucent') color palette")
x. <- adjustcolor(x, offset = c(0.5, 0.5, 0.5, 0), # <- "more white"
                   transform = diag(c(.7, .7, .7, .6)))
cbind(x, x.)

op <- par(bg = adjustcolor("goldenrod", offset = -rep(.4, 4)), xpd = NA)
plot(0:9, 0:9, type = "n", axes = FALSE, xlab = "", ylab = "",
     main = "adjustcolor() -> translucent")
text(1:8, labels = paste0(x,"++"), col = x., cex = 8)
par(op)

## and
(M <- cbind( rbind( matrix(1/3, 3, 3), 0), c(0, 0, 0, 1)))
adjustcolor(x, transform = M)

## revert to previous palette: active
palette(opal)
```
Coerce an Object for Graphics Annotation

Description

Coerce an R object into a form suitable for graphics annotation.

Usage

as.graphicsAnnot(x)

Arguments

x

an R object

Details

Expressions, calls and names (as used by plotmath) are passed through unchanged. All other objects with an explicit class (as determined by is.object) are coerced by as.character to character vectors.

All the graphics and grid functions which use this coerce calls and names to expressions internally.

Value

A language object or a character vector.

Create a Raster Object

Description

Functions to create a raster object (representing a bitmap image) and coerce other objects to a raster object.

Usage

is.raster(x)
as.raster(x, ...)

## S3 method for class 'matrix'
as.raster(x, max = 1, ...)
## S3 method for class 'array'
as.raster(x, max = 1, ...)
## S3 method for class 'logical'
as.raster(x, max = 1, ...)
## S3 method for class 'numeric'
as.raster(x, max = 1, ...)
## S3 method for class 'character'
as.raster(x, max = 1, ...)
## S3 method for class 'raw'
as.raster(x, max = 255L, ...)
Arguments

- **x**: any R object.
- **max**: number giving the maximum of the color values range.
- **...**: further arguments passed to or from other methods.

Details

An object of class "raster" is a matrix of colour values as given by `rgb` representing a bitmap image.

It is not expected that the user will need to call these functions directly; functions to render bitmap images in graphics packages will make use of the `as.raster()` function to generate a raster object from their input.

The `as.raster()` function is (S3) generic so methods can be written to convert other R objects to a raster object.

The default implementation for numeric matrices interprets scalar values on black-to-white scale.

Raster objects can be subsetted like a matrix and it is possible to assign to a subset of a raster object.

There is a method for converting a raster object to a `matrix` (of colour strings).

Raster objects can be compared for equality or inequality (with each other or with a colour string).

There is a `is.na` method which returns a logical matrix of the same dimensions as the raster object.

Note that NA values are interpreted as the fully transparent colour by some (but not all) graphics devices.

Value

- For `as.raster()`, a raster object.
- For `is.raster()`, a logical indicating whether x is a raster object.

Note

Raster images are internally represented row-first, which can cause confusion when trying to manipulate a raster object. The recommended approach is to coerce a raster to a matrix, perform the manipulation, then convert back to a raster.

Examples

```r
# A red gradient
as.raster(matrix(hcl(0, 80, seq(50, 80, 10)),
                 nrow = 4, ncol = 5))

# Vectors are 1-column matrices ...
# character vectors are color names ...
as.raster(hcl(0, 80, seq(50, 80, 10)))
# numeric vectors are greyscale ...
as.raster(1:5, max = 5)
# logical vectors are black and white ...
as.raster(1:10 %% 2 == 0)

# ... unless nrow/ncol are supplied ...
as.raster(1:10 %% 2 == 0, nrow = 1)

# Matrix can also be logical or numeric (or raw) ...
```
axisTicks  Compute Pretty Axis Tick Scales

Description

Compute pretty axis scales and tick mark locations, the same way as traditional R graphics do it. This is interesting particularly for log scale axes.

Usage

axisTicks(usr, log, exp = NULL, nint = 5)
.axisPars(usr, log = FALSE, nintLog = 5)

Arguments

usr numeric vector of length 2, with c(min, max) axis extents.
log logical indicating if a log scale is (thought to be) in use.
exp numeric vector of length 3, c(mi, ma, n.), with identical meaning to
par("?exp") (where ? is x or y), namely “pretty” axis extents, and an integer
code n..
nint, nintLog positive integer value indicating (approximately) the desired number of intervals. nintLog is used only for the case log = TRUE.

Details

axisTicks(usr, *) calls .axisPars(usr, ..) to set exp when that is missing or NULL.

Apart from that, axisTicks() just calls the C function CreateAtVector() in
"<Rsrc>/src/main/plot.c" which is also called by the base graphics package function
axis(side, *) when its argument at is not specified.

Since R 4.1.0, the underlying C CreateAtVector() has been tuned to provide a considerably more balanced (symmetric) set of tick locations.
boxplot.stats

Box Plot Statistics

Description

This function is typically called by another function to gather the statistics necessary for producing box plots, but may be invoked separately.

Usage

boxplot.stats(x, coef = 1.5, do.conf = TRUE, do.out = TRUE)

Arguments

x

a numeric vector for which the boxplot will be constructed (NAs and NaNs are allowed and omitted).
coef this determines how far the plot ‘whiskers’ extend out from the box. If coef is positive, the whiskers extend to the most extreme data point which is no more than coef times the length of the box away from the box. A value of zero causes the whiskers to extend to the data extremes (and no outliers be returned).

do.conf, do.out
logicals; if FALSE, the conf or out component respectively will be empty in the result.

Details
The two ‘hinges’ are versions of the first and third quartile, i.e., close to quantile(x, c(1,3)/4). The hinges equal the quartiles for odd n (where n <- length(x)) and differ for even n. Whereas the quartiles only equal observations for n %% 4 == 1 (n ≡ 1 mod 4), the hinges do so additionally for n %% 4 == 2 (n ≡ 2 mod 4), and are in the middle of two observations otherwise.

The notches (if requested) extend to +/-1.58 IQR/sqrt(n). This seems to be based on the same calculations as the formula with 1.57 in Chambers et al (1983, p. 62), given in McGill et al (1978, p. 16). They are based on asymptotic normality of the median and roughly equal sample sizes for the two medians being compared, and are said to be rather insensitive to the underlying distributions of the samples. The idea appears to be to give roughly a 95% confidence interval for the difference in two medians.

Value
List with named components as follows:

stats a vector of length 5, containing the extreme of the lower whisker, the lower ‘hinge’, the median, the upper ‘hinge’ and the extreme of the upper whisker.
n the number of non-NA observations in the sample.
conf the lower and upper extremes of the ‘notch’ (if(do.conf)). See the details.
out the values of any data points which lie beyond the extremes of the whiskers (if(do.out)).

Note that $stats and $conf are sorted in increasing order, unlike S, and that $n and $out include any +/- Inf values.

References


See Also
fivenum, boxplot, bxp.
Examples

```r
require(stats)
x <- c(1:100, 1000)
(b1 <- boxplot.stats(x))
(b2 <- boxplot.stats(x, do.conf = FALSE, do.out = FALSE))
stopifnot(b1 $ stats == b2 $ stats) # do.out = FALSE is still robust
boxplot.stats(x, coef = 3, do.conf = FALSE)
## no outlier treatment:
boxplot.stats(x, coef = 0)

boxplot.stats(c(x, NA)) # slight change : n is 101
(r <- boxplot.stats(c(x, -1:1/0)))
stopifnot(r$out == c(1000, -Inf, Inf))
```

bringToTop Assign Focus to a Window

Description

bringToTop brings the specified screen device’s window to the front of the window stack (and gives it focus). With first argument -1 it brings the console to the top.

If stay = TRUE, the window is designated as a topmost window, i.e., it will stay on top of any regular window. stay may only be used when Rgui is run in SDI mode. This corresponds to the “Stay on top” popup menu item in Rgui.

Usage

```r
bringToTop(which = dev.cur(), stay = FALSE)
```

Arguments

- `which` a device number, or -1.
- `stay` whether to make the window stay on top.

See Also

`msgWindow`, `windows`
Description

Graphics devices for SVG, PDF and PostScript graphics files using the cairo graphics API.

Usage

```r
csv(filename = if(onefile) "Rplots.svg" else "Rplot%03d.svg",
    width = 7, height = 7, pointsize = 12,
    onefile = FALSE, family = "sans", bg = "white",
    antialias = c("default", "none", "gray", "subpixel"),
    symbolfamily)

cairo_pdf(filename = if(onefile) "Rplots.pdf" else "Rplot%03d.pdf",
    width = 7, height = 7, pointsize = 12,
    onefile = FALSE, family = "sans", bg = "white",
    antialias = c("default", "none", "gray", "subpixel"),
    fallback_resolution = 300, symbolfamily)

cairo_ps(filename = if(onefile) "Rplots.ps" else "Rplot%03d.ps",
    width = 7, height = 7, pointsize = 12,
    onefile = FALSE, family = "sans", bg = "white",
    antialias = c("default", "none", "gray", "subpixel"),
    fallback_resolution = 300, symbolfamily)
```

Arguments

- **filename**
  - the name of the output file. The page number is substituted if a C integer format is included in the character string, as in the default. (Depending on the platform, the result must be less than PATH_MAX characters long, and may be truncated if not. See `postscript` for further details.) Tilde expansion is performed where supported by the platform.

- **width**
  - the width of the device in inches.

- **height**
  - the height of the device in inches.

- **pointsize**
  - the default pointsize of plotted text (in big points).

- **onefile**
  - should all plots appear in one file or in separate files?

- **family**
  - one of the device-independent font families, "sans", "serif" and "mono", or a character string specify a font family to be searched for in a system-dependent way.
  
  On unix-alikes (incl. Mac), see the ‘Cairo fonts’ section in the help for `X11`.

- **bg**
  - the initial background colour: can be overridden by setting `par("bg")`.

- **antialias**
  - string, the type of anti-aliasing (if any) to be used; defaults to "default".

- **fallback_resolution**
  - numeric: the resolution in dpi used when falling back to bitmap output. Prior to R 3.3.0 this depended on the cairo implementation but was commonly 300.

- **symbolfamily**
  - a length-one character string that specifies the font family to be used as the "symbol" font (e.g., for `plotmath` output).
Details

SVG (Scalar Vector Graphics) is a W3C standard for vector graphics. See https://www.w3.org/Graphics/SVG/. The output from svg is SVG version 1.1 for onefile = FALSE (the default), otherwise SVG 1.2. (Few SVG viewers are capable of displaying multi-page SVG files.) Note that unlike postscript and pdf, cairo_pdf and cairo_ps sometimes record bitmaps and not vector graphics. On the other hand, they can (on suitable platforms) include a much wider range of UTF-8 glyphs, and embed the fonts used.

The output produced by cairo_ps(onefile = FALSE) will be encapsulated postscript on a platform with cairo >= 1.6.

R can be compiled without support for any of these devices: this will be reported if you attempt to use them on a system where they are not supported. They all require cairo version 1.2 or later.

If you plot more than one page on one of these devices and do not include something like %d for the sequence number in file (or set onefile = TRUE) the file will contain the last page plotted.

There is full support of semi-transparency, but using this is one of the things liable to trigger bitmap output (and will always do so for cairo_ps).

Value

A plot device is opened: nothing is returned to the R interpreter.

Anti-aliasing

Anti-aliasing is applied to both graphics and fonts. It is generally preferable for lines and text, but can lead to undesirable effects for fills, e.g. for image plots, and so is never used for fills. antialias = "default" is in principle platform-dependent, but seems most often equivalent to antialias = "gray".

Conventions

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

• The default device size is in pixels (svg) or inches.
• Font sizes are in big points.
• The default font family is Helvetica.
• Line widths are multiples of 1/96 inch.
• Circle radii have a minimum of 1/72 inch.
• Colours are interpreted by the viewing application.

Warning

Support for all these devices are optional, so in packages they should be used conditionally after checking capabilities("cairo").

Note

In principle these devices are independent of X11 (as is seen by their presence on Windows). But on a Unix-alike the cairo libraries may be distributed as part of the X11 system and hence that (for example, on x86_64 macOS, XQuartz) may need to be installed.
cairoSymbolFont

See Also

Devices, dev.print.pdf, postscript
capabilities to see if cairo is supported.

cairoSymbolFont  Specify a Symbol Font

Description

Specify a symbol font for a Cairo-based graphics device. This function provides the opportunity to
specify whether the font supports Private Use Area code points.

Usage

cairoSymbolFont(family, usePUA = TRUE)

Arguments

family  A character vector giving the symbol font family name.
usePUA  Does the font support Private Use Area code points?

Details

On Cairo-based graphics devices, when drawing with a symbol font (e.g., plotmath), Adobe Symbol
Encoding characters are converted to UTF-8 code points. This conversion can use Private Use Area
code points or not. It is useful to be able to specify this option because some fonts (e.g., the
OpenSymbol font that is included in LibreOffice) have glyphs mapped to the Private Use Area and
some fonts (e.g., Nimbus Sans L, the URW Fonts equivalent of Helvetica) do not.

Value

An object of class "CairoSymbolFont".

See Also

cairo_pdf.

Examples

## Not run:
## If a font uses PUA, we can just specify the font name ... 
cairo_pdf(symbolfamily="OpenSymbol")
dev.off()
## ... or equivalently ...
cairo_pdf(symbolfamily=cairoSymbolFont("OpenSymbol"))
dev.off()

## If a font does not use PUA, we must indicate that ...
cairo_pdf(symbolfamily=cairoSymbolFont("Nimbus Sans", usePUA=FALSE))
dev.off()

## End(Not run)
check.options  Set Options with Consistency Checks

Description

Utility function for setting options with some consistency checks. The attributes of the new settings in new are checked for consistency with the model (often default) list in name.opt.

Usage

check.options(new, name.opt, reset = FALSE, assign.opt = FALSE, envir = .GlobalEnv, check.attributes = c("mode", "length"), override.check = FALSE)

Arguments

new        a named list
name.opt   character with the name of R object containing the default list.
reset      logical; if TRUE, reset the options from name.opt. If there is more than one R object with name name.opt, remove the first one in the search() path.
assign.opt logical; if TRUE, assign the ...
envir      the environment used for get and assign.
check.attributes character containing the attributes which check.options should check.
override.check logical vector of length length(new) (or 1 which entails recycling). For those new[i] where override.check[i] == TRUE, the checks are overridden and the changes made anyway.

Value

A list of components with the same names as the one called name.opt. The values of the components are changed from the new list, as long as these pass the checks (when these are not overridden according to override.check).

Note

Option "names" is exempt from all the checks or warnings, as in the application it can be NULL or a variable-length character vector.

Author(s)

Martin Maechler

See Also

ps.options and pdf.options, which use check.options.
Examples

(L1 <- list(a = 1:3, b = pi, ch = "CH"))
check.options(list(a = 0:2), name.opt = "L1")
check.options(NULL, reset = TRUE, name.opt = "L1")

chull

Compute Convex Hull of a Set of Points

Description

Computes the subset of points which lie on the convex hull of the set of points specified.

Usage

chull(x, y = NULL)

Arguments

x, y coordinate vectors of points. This can be specified as two vectors x and y, a 2-column matrix x, a list x with two components, etc, see xy.coords.

Details

xy.coords is used to interpret the specification of the points. Infinite, missing and NaN values are not allowed.

The algorithm is that given by Eddy (1977).

Value

An integer vector giving the indices of the unique points lying on the convex hull, in clockwise order. (The first will be returned for duplicate points.)

References


See Also

xy.coords, polygon
Examples

```r
X <- matrix(stats::rnorm(2000), ncol = 2)
chull(X)
## Not run:
# Example usage from graphics package
plot(X, cex = 0.5)
htpts <- chull(X)
htpts <- c(htpts, hpts[1])
lines(X[htpts, ])
## End(Not run)
```

#### cm

**Unit Transformation**

Translates from inches to cm (centimeters).

**Usage**

```r
cm(x)
```

**Arguments**

- `x`: numeric vector

**Examples**

```r
cm(1)  # = 2.54
```

```r
## Translate *from* cm *to* inches:
10 / cm(1) # -> 10cm are 3.937 inches
```

#### col2rgb

**Color to RGB Conversion**

R color to RGB (red/green/blue) conversion.

**Usage**

```r
col2rgb(col, alpha = FALSE)
```

**Arguments**

- `col`: vector of any of the three kinds of R color specifications, i.e., either a color name (as listed by `colors()`), a hexadecimal string of the form "#rrggbb" or "#rrggbbaa" (see `rgb`), or a positive integer i meaning `palette()[i]`.
- `alpha`: logical value indicating whether the alpha channel (opacity) values should be returned.
Details

NA (as integer or character) and "NA" mean transparent, which can also be specified as "transparent".

Values of col not of one of these types are coerced: real vectors are coerced to integer and other types to character. (factors are coerced to character: in all other cases the class is ignored when doing the coercion.)

Zero and negative values of col are an error.

Value

An integer matrix with three or four (for alpha = TRUE) rows and number of columns the length of col. If col has names these are used as the column names of the return value.

Author(s)

Martin Maechler and the R core team.

See Also

rgb, colors, palette, etc.

The newer, more flexible interface, convertColor().

Examples

col2rgb("peachpuff")

col2rgb(c(blu = "royalblue", reddish = "tomato")) # note: colnames

col2rgb(1:8) # the ones from the palette() (if the default)

col2rgb(paste0("gold", 1:4))

col2rgb("#08a0ff")

## all three kinds of color specifications:
col2rgb(c(red = "red", hex = "#abedef"))
col2rgb(c(palette = 1:3))

##-- NON-INTRODUCTORY examples --
grC <- col2rgb(paste0("gray", 0:100))
table(print(diff(grC["red",]))) # '2' or '3': almost equidistant

# The 'named' grays are in between ("slate gray" is not gray, strictly)
col2rgb(c(g66 = "gray66", darkg = "dark gray", g67 = "gray67",
g74 = "gray74", gray = "gray", g75 = "gray75",
g82 = "gray82", light = "light gray", g83 = "gray83"))

crgb <- col2rgb(cc <- colors())
colnames(crgb) <- cc
t(crgb) # The whole table

ccodes <- c(256^(2:0) %*% crgb) # = internal codes

# How many names are 'aliases' of each other:
table(tcc <- table(ccodes))

length(unique(sort(ccodes))) # 502

# All the multiply named colors:
mult <- uc[tcc >= 2]
c1 <- lapply(mult, function(m) cc[ccodes == m])
names(c1) <- apply(col2rgb(sapply(c1, function(x)x[1])), 2, function(n)paste(n, collapse = ","))
utils::str(c1)
## Not run:
if(require(xgobi)) { ## Look at the color cube dynamically :
tc <- t(crgb[, !duplicated(ccodes)])
table(is.gray <- tc[,1] == tc[,2] & tc[,2] == tc[,3]) # (397, 105)
xgobi(tc, color = c("gold", "gray")[1 + is.gray])
}
## End(Not run)

colorRamp

**Color interpolation**

Description

These functions return functions that interpolate a set of given colors to create new color palettes (like `topo.colors`) and color ramps, functions that map the interval \([0, 1]\) to colors (like `grey`).

Usage

```r
colorRamp(colors, bias = 1, space = c("rgb", "Lab"),
          interpolate = c("linear", "spline"), alpha = FALSE)
colorRampPalette(colors, ...)
```

Arguments

- `colors`: colors to interpolate; must be a valid argument to `col2rgb()`.
- `bias`: a positive number. Higher values give more widely spaced colors at the high end.
- `space`: a character string; interpolation in RGB or CIE Lab color spaces.
- `interpolate`: use spline or linear interpolation.
- `alpha`: logical: should alpha channel (opacity) values be returned? It is an error to give a true value if `space` is specified.
- `...`: arguments to pass to `colorRamp`.

Details

The CIE Lab color space is approximately perceptually uniform, and so gives smoother and more uniform color ramps. On the other hand, palettes that vary from one hue to another via white may have a more symmetrical appearance in RGB space.

The conversion formulas in this function do not appear to be completely accurate and the color ramp may not reach the extreme values in Lab space. Future changes in the R color model may change the colors produced with `space = "Lab"`. 
**colorRamp**

Value

colorRamp returns a function with argument a vector of values between 0 and 1 that are mapped to a numeric matrix of RGB color values with one row per color and 3 or 4 columns.

colorRampPalette returns a function that takes an integer argument (the required number of colors) and returns a character vector of colors (see rgb) interpolating the given sequence (similar to heat.colors or terrain.colors).

See Also

Good starting points for interpolation are the “sequential” and “diverging” ColorBrewer palettes in the RColorBrewer package.
splinefun or approxfun are used for interpolation.

Examples

## Both return a *function* :
colorRamp(c("red", "green"))( (0:4)/4 ) ## (x) , x in [0,1]
colorRampPalette(c("blue", "red"))( 4 ) ## (n)
## a ramp in opacity of blue values
colorRampPalette(c(rgb(0,0,1,1), rgb(0,0,1,0)), alpha = TRUE)(8)

require(graphics)
## Here space="rgb" gives palettes that vary only in saturation, ## as intended.
## With space="Lab" the steps are more uniform, but the hues
## are slightly purple.
filled.contour(volcano,
color.palette =
colorRampPalette(c("red", "white", "blue")),
asp = 1)
filled.contour(volcano,
color.palette =
colorRampPalette(c("red", "white", "blue"),
    space = "Lab"),
asp = 1)

## Interpolating a 'sequential' ColorBrewer palette
YlOrBr <- c("#FFFFD4", "#FED98E", "#FE9929", "#D95F0E", "#993404")
filled.contour(volcano,
color.palette = colorRampPalette(YlOrBr, space = "Lab"),
asp = 1)
filled.contour(volcano,
color.palette = colorRampPalette(YlOrBr, space = "Lab",
    bias = 0.5),
asp = 1)

## 'jet.colors' is "as in Matlab"
## (and hurting the eyes by over-saturation)
jet.colors <-
colorRampPalette(c("#00007F", "blue", "#007FFF", "cyan",
    "#7FFFFFF", "yellow", "#FF7F00", "red", "#7F0000"))
filled.contour(volcano, color.palette = jet.colors, asp = 1)

## space="Lab" helps when colors don't form a natural sequence
m <- outer(1:20, 1:20, function(x,y) sin(sqrt(x*y)/3))
rgb.palette <- colorRampPalette(c("red", "orange", "blue"),
    space = "rgb")
Lab.palette <- colorRampPalette(c("red", "orange", "blue"),
    space = "Lab")
filled.contour(m, col = rgb.palette(20))
filled.contour(m, col = Lab.palette(20))

colors

<table>
<thead>
<tr>
<th>Color Names</th>
<th>Description</th>
</tr>
</thead>
</table>

Returns the built-in color names which R knows about.

Usage

colors (distinct = FALSE)
colours(distinct = FALSE)

Arguments

distinct logical indicating if the colors returned should all be distinct; e.g., "snow" and "snow1" are effectively the same point in the \((0 : 255)^3\) RGB space.

Details

These color names can be used with a col= specification in graphics functions.

An even wider variety of colors can be created with primitives rgb, hsv and hcl, or the derived rainbow, heat.colors, etc.

"transparent" is not a color and so not listed, but it is accepted as a color specification.

Value

A character vector containing all the built-in color names.

See Also

palette for setting the ‘palette’ of colors for par(col=<num>); rgb, hsv, hcl, gray; rainbow for a nice example; and heat.colors, topo.colors for images.
col2rgb for translating to RGB numbers and extended examples.

Examples

c1 <- colors()
length(c1); c1[1:20]

length(c1. <- colors(TRUE))
# only 502 of the 657 named ones

# ------- Show all named colors and more:
demo("colors")
# -------
Description

Calculate contour lines for a given set of data.

Usage

```r
contourLines(x = seq(0, 1, length.out = nrow(z)),
             y = seq(0, 1, length.out = ncol(z)),
             z, nlevels = 10,
             levels = pretty(range(z, na.rm = TRUE), nlevels))
```

Arguments

- **x, y** locations of grid lines at which the values in z are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If x is a list, its components `x$x` and `x$y` are used for x and y, respectively. If the list has component z this is used for z.
- **z** a matrix containing the values to be plotted (NAs are allowed). Note that x can be used instead of z for convenience.
- **nlevels** number of contour levels desired if levels is not supplied.
- **levels** numeric vector of levels at which to draw contour lines.

Details

contourLines draws nothing, but returns a set of contour lines.

There is currently no documentation about the algorithm. The source code is in `R_HOME/src/main/plot3d.c`.

Value

A list of contours, each itself a list with elements:

- **level** The contour level.
- **x** The x-coordinates of the contour.
- **y** The y-coordinates of the contour.

See Also

- `options("max.contour.segments")` for the maximal complexity of a single contour line.
- `contour`: Its ‘Examples’ demonstrate how `contourLines()` can be drawn and are the same (as those from `contour()`).
Examples

```r
x <- 10*(1:nrow(volcano))
y <- 10*(1:ncol(volcano))
cl <- contourLines(x, y, volcano)
## summarize the sizes of each the contour lines :
cbind(lev = vapply(cl, `[[`, .5, "level"),
n = vapply(cl, function(l) length(l$x), 1))
```

```r
z <- outer(-9:25, -9:25)
pretty(range(z), 10) # -300 -200 ... 600 700
utils::str(c2 <- contourLines(z))
# no segments for {-300, 700};
# 2 segments for {-200, -100, 0}
# 1 segment for 100:600
```

---

**convertColor**

*Convert between Colour Spaces*

**Description**

Convert colours between their representations in standard colour spaces.

**Usage**

```r
convertColor(color, from, to, from.ref.white, to.ref.white,
    scale.in = 1, scale.out = 1, clip = TRUE)
```

**Arguments**

- `color` A matrix whose rows specify colors. The function will also accept a data frame, but will silently convert to a matrix internally.
- `from, to` Input and output color spaces. See ‘Details’ below.
- `from.ref.white, to.ref.white` Reference whites or NULL if these are built in to the definition, as for RGB spaces. D65 is the default, see ‘Details’ for others.
- `scale.in, scale.out` Input is divided by scale.in, output is multiplied by scale.out. Use NULL to suppress scaling when input or output is not numeric.
- `clip` If TRUE, truncate RGB output to [0,1], FALSE return out-of-range RGB, NA set out of range colors to NaN.

**Details**

Color spaces are specified by objects of class `colorConverter`, created by `colorConverter` or `make.rgb`. Built-in color spaces may be referenced by strings: "XYZ", "sRGB", "Apple RGB", "CIE RGB", "Lab", "Luv". The converters for these colour spaces are in the object `colorspaces`.

The "sRGB" color space is that used by standard PC monitors. "Apple RGB" is used by Apple monitors. "Lab" and "Luv" are approximately perceptually uniform spaces standardized by the Commission Internationale d’Eclairage. XYZ is a 1931 CIE standard capable of representing all visible colors (and then some), but not in a perceptually uniform way.
The Lab and Luv spaces describe colors of objects, and so require the specification of a reference ‘white light’ color. Illuminant D65 is a standard indirect daylight, Illuminant D50 is close to direct sunlight, and Illuminant A is the light from a standard incandescent bulb. Other standard CIE illuminants supported are B, C, E and D55. RGB colour spaces are defined relative to a particular reference white, and can be only approximately translated to other reference whites. The von Kries chromatic adaptation algorithm is used for this. Prior to R 3.6, color conversions involving color spaces created with `make.rgb` were carried out assuming a D65 illuminant, irrespective of the actual illuminant used in the creation of the color space. This affected the built-in "CIE RGB" color space.

The RGB color spaces are specific to a particular class of display. An RGB space cannot represent all colors, and the clip option controls what is done to out-of-range colors.

For the named color spaces `color` must be a matrix of values in the from color space: in particular opaque colors.

Value

A 3-column matrix whose rows specify the colors.

References


See Also

`col2rgb` and `colors` for ways to specify colors in graphics.

`make.rgb` for specifying other colour spaces.

Examples

```r
## The displayable colors from four planes of Lab space
ab <- expand.grid(a = (-10:15)*10,
                  b = (-15:10)*10)
require(graphics); require(stats) # for na.omit
par(mfrow = c(2, 2), mar = .1+c(3, 3, 3, .5), mgp = c(2, .8, 0))
Lab <- cbind(L = 20, ab)
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
colored <- attr(na.omit(srgb), "na.action")
srgb[colored, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
      xlab = "a", ylab = "b", main = "Lab: L=20")
Lab <- cbind(L = 40, ab)
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
colored <- attr(na.omit(srgb), "na.action")
srgb[colored, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
      xlab = "a", ylab = "b", main = "Lab: L=40")
Lab <- cbind(L = 60, ab)
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
```
densCols <- attr(na.omit(srgb), "na.action")
srgb[clipped, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
      xlab = "a", ylab = "b", main = "Lab: L=60")

Lab <- cbind(L = 80, ab)
srgb <- convertColor(Lab, from = "Lab", to = "sRGB", clip = NA)
clipped <- attr(na.omit(srgb), "na.action")
srgb[clipped, ] <- 0
cols <- rgb(srgb[, 1], srgb[, 2], srgb[, 3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol = 26), col = cols,
      xlab = "a", ylab = "b", main = "Lab: L=80")
cols <- t(col2rgb(palette())); rownames(cols) <- palette(); cols
zapsmall(lab <- convertColor(cols, from = "sRGB", to = "Lab", scale.in = 255))
stopifnot(all.equal(cols, # converting back.. getting the original:
                 round(convertColor(lab, from = "Lab", to = "sRGB", scale.out = 255)),
                 check.attributes = FALSE))

densCols

Colors for Smooth Density Plots

densCols produces a vector containing colors which encode the local densities at each point in a scatterplot.

Usage

densCols(x, y = NULL, nbin = 128, bandwidth,
          colramp = colorRampPalette(blues9[-(1:3)]))
blues9

Arguments

  x, y    the x and y arguments provide the x and y coordinates of the points. Any reasonable way of defining the coordinates is acceptable. See the function xy.coords for details. If supplied separately, they must be of the same length.

  nbin    numeric vector of length one (for both directions) or two (for x and y separately) specifying the number of equally spaced grid points for the density estimation; directly used as gridsize in bkde2D().

  bandwidth    numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. bandwidth is subsequently passed to function bkde2D.

  colramp    function accepting an integer n as an argument and returning n colors.

Details

densCols computes and returns the set of colors that will be used in plotting, calling bkde2D(*, bandwidth, gridsize = nbin, ...) from package KernSmooth.

blues9 is a set of 9 color shades of blue used as the default in plotting.
Value

densCols returns a vector of length \( \text{nrow}(x) \) that contains colors to be used in a subsequent scatterplot. Each color represents the local density around the corresponding point.

Author(s)

Florian Hahne at FHCRC, originally

See Also

bkde2D from package KernSmooth; further, smoothScatter() (package graphics) which builds on the same computations as densCols.

Examples

```r
x1 <- matrix(rnorm(1e3), ncol = 2)
x2 <- matrix(rnorm(1e3, mean = 3, sd = 1.5), ncol = 2)
x <- rbind(x1, x2)
dcols <- densCols(x)
graphics::plot(x, col = dcols, pch = 20, main = "n = 1000")
```

---

**dev**  

Control Multiple Devices

Description

These functions provide control over multiple graphics devices.

Usage

```r
dev.cur()
dev.list()
dev.next(which = dev.cur())
dev.prev(which = dev.cur())
dev.off(which = dev.cur())
dev.set(which = dev.next())
dev.new(..., noRStudioGD = FALSE)
graphics.off()
```

Arguments

- `which`  
  An integer specifying a device number.
- `...`  
  arguments to be passed to the device selected.
- `noRStudioGD`  
  Do not use the RStudio graphics device even if specified as the default device: it does not accept arguments such as width and height.
Details

Only one device is the ‘active’ device: this is the device in which all graphics operations occur. There is a "null device" which is always open but is really a placeholder: any attempt to use it will open a new device specified by `getOption("device")`.

Devices are associated with a name (e.g., "X11" or "postscript") and a number in the range 1 to 63; the "null device" is always device 1. Once a device has been opened the null device is not considered as a possible active device. There is a list of open devices, and this is considered as a circular list not including the null device. dev.next and dev.prev select the next open device in the appropriate direction, unless no device is open.

`dev.off` shuts down the specified (by default the current) device. If the current device is shut down and any other devices are open, the next open device is made current. It is an error to attempt to shut down device 1. `graphics.off()` shuts down all open graphics devices. Normal termination of a session runs the internal equivalent of `graphics.off()`.

`dev.set` makes the specified device the active device. If there is no device with that number, it is equivalent to `dev.next`. If which = 1 it opens a new device and selects that.

`dev.new` opens a new device. Normally R will open a new device automatically when needed, but this enables you to open further devices in a platform-independent way. (For which device is used see `getOption("device")`.) Note that care is needed with file-based devices such as pdf and postscript and in that case file names such as ‘Rplots.pdf’, ‘Rplots1.pdf’, ...., ‘Rplots999.pdf’ are tried in turn. Only named arguments are passed to the device, and then only if they match the argument list of the device. Even so, care is needed with the interpretation of e.g. width, and for the standard bitmap devices units = "in", res = 72 is forced if neither is supplied but both width and height are.

Value

`dev.cur` returns a length-one named integer vector giving the number and name of the active device, or 1, the null device, if none is active.

`dev.list` returns the numbers of all open devices, except device 1, the null device. This is a numeric vector with a `names` attribute giving the device names, or `NULL` is there is no open device. `dev.next` and `dev.prev` return the number and name of the next / previous device in the list of devices. This will be the null device if and only if there are no open devices.

`dev.off` returns the number and name of the new active device (after the specified device has been shut down).

`dev.set` returns the number and name of the new active device.

`dev.new` returns the return value of the device opened, usually invisible `NULL`.

See Also

Devices, such as postscript, etc.

layout and its links for setting up plotting regions on the current device.

Examples

```R
## Not run: ## Unix-specific example
x11()
plot(1:10)
x11()
plot(rnorm(10))
dev.set(dev.prev())
```
dev.capabilities

abline(0, 1) # through the 1:10 points
dev.set(dev.next())
abline(h = 0, col = "gray") # for the residual plot
dev.set(dev.prev())
dev.off(); dev.off() # close the two X devices

## End(Not run)

dev.capabilities

Query Capabilities of the Current Graphics Device

Description

Query the capabilities of the current graphics device.

Usage

dev.capabilities(what = NULL)

Arguments

what a character vector partially matching the names of the components listed in section ‘Value’, or NULL which lists all available capabilities.

Details

The capabilities have to be specified by the author of the graphics device, unless they can be deduced from missing hooks. Thus they will often by returned as NA, and may reflect the maximal capabilities of the underlying device where several output formats are supported by one device.

Most recent devices support semi-transparent colours provided the graphics format does (which PostScript does not). On the other hand, relatively few graphics formats support (fully or semi-) transparent backgrounds: generally the latter is found only in PDF and PNG plots.

Value

A named list with some or all of the following components, any of which may take value NA:

semiTransparency logical: Does the device support semi-transparent colours?
transparentBackground character: Does the device support (semi)-transparent backgrounds? Possible values are "no", "fully" (only full transparency) and "semi" (semi-transparent background colours are supported).
rasterImage character: To what extent does the device support raster images as used by rasterImage and grid.raster? Possible values "no", "yes" and "non-missing" (support only for arrays without any missing values).
capture logical: Does the current device support raster capture as used by grid.cap?
locator logical: Does the current device support locator and identify?
events character: Which events can be generated on this device? Currently this will be a subset of c("MouseDown", "MouseMove", "MouseUp", "Keybd"), but other events may be supported in the future.
patterns character: Does the device support pattern fills? One or more of c("LinearGradient", "RadialGradient", "TilingPattern") May also be FALSE.

clippingPaths logical: Does the device support clipping paths?

masks character: Does the device support masks? One or more of c("alpha", "luminance") May also be FALSE.

compositing character: Does the device support compositing operators? There are many possible operators and devices may support any subset. For example the pdf device supports a set of “blend modes” whereas Cairo-based devices support Porter-Duff operators as well. May also be FALSE.

transformations logical: Does the devices support affine transformations ?

paths logical: Does the device support stroking and filling paths?

glyphs logical: Does the device support rendering glyphs?

See Also
See `getGraphicsEvent` for details on interactive events.

Examples

```r
dev.capabilities()
```

Description

dev.capture captures the current contents of a graphics device as a raster (bitmap) image.

Usage

```r
dev.capture(native = FALSE)
```

Arguments

- `native` Logical. If FALSE the result is a matrix of R color names, if TRUE the output is returned as a nativeRaster object which is more efficient for plotting, but not portable.

Details

Not all devices support capture of the output as raster bitmaps. Typically, only image-based devices do and even not all of them.

Value

NULL if the device does not support capture, otherwise a matrix of color names (for native = FALSE) or a nativeRaster object (for native = TRUE).
### dev.flush

**Hold or Flush Output on an On-Screen Graphics Device.**

**Description**

This gives a way to hold/flush output on certain on-screen devices, and is ignored by other devices.

**Usage**

```r
dev.hold(level = 1L)
dev.flush(level = 1L)
```

**Arguments**

- `level`: Integer `>= 0`. The amount by which to change the hold level. Negative values will be silently replaced by zero.

**Details**

Devices which implement this maintain a stack of hold levels: calling `dev.hold` increases the level and `dev.flush` decreases it. Calling `dev.hold` when the hold level is zero increases the hold level and inhibits graphics display. When calling `dev.flush` clears all pending holds the screen display is refreshed and normal operation is resumed.

This is implemented for the cairo-based X11 types with buffering. When the hold level is positive the ‘watch’ cursor is set on the device’s window.

It is available on the quartz device on macOS.

This is implemented for the windows device with buffering selected (the default). When the hold level is positive the ‘busy’ cursor is set on the device’s window.

**Value**

The current level after the change, invisibly. This is 0 on devices where hold levels are not supported.

### dev.interactive

**Is the Current Graphics Device Interactive?**

**Description**

Test if the current graphics device (or that which would be opened) is interactive.

**Usage**

```r
dev.interactive(orNone = FALSE)
deviceIsInteractive(name = NULL)
```
Arguments

- `orNone` logical; if TRUE, the function also returns TRUE when `.Device` == "null device" and `getOption("device")` is among the known interactive devices.
- `name` one or more device names as a character vector, or NULL to give the existing list.

Details

The X11 (Unix), windows (Windows) and quartz (macOS, on-screen types only) are regarded as interactive, together with JavaGD (from the package of the same name) and CairoWin and CairoX11 (from package Cairo). Packages can add their devices to the list by calling `deviceIsInteractive`.

Value

dev.interactive() returns a logical, TRUE if and only if an interactive (screen) device is in use.
deviceIsInteractive returns the updated list of known interactive devices, invisibly unless name = NULL.

See Also

- `Devices` for the available devices on your platform.

Examples

dev.interactive()
print(deviceIsInteractive(NULL))

Find Size of Device Surface

dev.size

Description

Find the dimensions of the device surface of the current device.

Usage

dev.size(units = c("in", "cm", "px"))

Arguments

- `units` the units in which to return the value – inches, cm, or pixels (device units).

Value

A two-element numeric vector giving width and height of the current device; a new device is opened if there is none, similarly to `dev.new()`.

See Also

The size information in inches can be obtained by `par("din")`, but this provides a way to access it independent of the graphics sub-system in use. Note that `par("din")` is only updated when a new plot is started, whereas `dev.size` tracks the size as an on-screen device is resized.
Examples

dev.size("cm")

Copy Graphics Between Multiple Devices

Description

dev.copy copies the graphics contents of the current device to the device specified by which or to a new device which has been created by the function specified by device (it is an error to specify both which and device). (If recording is off on the current device, there are no contents to copy: this will result in no plot or an empty plot.) The device copied to becomes the current device.
dev.print copies the graphics contents of the current device to a new device which has been created by the function specified by device and then shuts the new device.
dev.copy2eps is similar to dev.print but produces an EPSF output file in portrait orientation (horizontal = FALSE). dev.copy2pdf is the analogue for PDF output.
dev.control allows the user to control the recording of graphics operations in a device. If displaylist is "inhibit" ("enable") then recording is turned off (on). It is only safe to change this at the beginning of a plot (just before or just after a new page). Initially recording is on for screen devices, and off for print devices.

Usage

dev.copy(device, ..., which = dev.next())
dev.print(device = postscript, ...)
dev.copy2eps(...)
dev.copy2pdf(..., out.type = "pdf")
dev.control(displaylist = c("inhibit", "enable"))

Arguments

device A device function (e.g., x11, postscript,...)
... Arguments to the device function above: for dev.copy2eps arguments to postscript and for dev.copy2pdf, arguments to pdf. For dev.print, this includes which and by default any postscript arguments.
which A device number specifying the device to copy to.
out.type The name of the output device: can be "pdf", or "quartz" (some macOS builds) or "cairo" (Windows and some Unix-alikes, see cairo_pdf).
displaylist A character string: the only valid values are "inhibit" and "enable".

details

Note that these functions copy the device region and not a plot: the background colour of the device surface is part of what is copied. Most screen devices default to a transparent background, which is probably not what is needed when copying to a device such as png.

For dev.copy2eps and dev.copy2pdf, width and height are taken from the current device unless otherwise specified. If just one of width and height is specified, the other is adjusted to preserve the aspect ratio of the device being copied. The default file name is Rplot.eps or Rplot.pdf, and can be overridden by specifying a file argument.
Copying to devices such as postscript and pdf which need font families pre-specified needs extra care – R is unaware of which families were used in a plot and so they will need to manually specified by the fonts argument passed as part of .... Similarly, if the device to be copied from was opened with a family argument, a suitable family argument will need to be included in ....

The default for dev.print is to produce and print a postscript copy. This will not work unless options("printcmd") is set suitably and you have a PostScript printing system: see postscript for how to set this up. Windows users may prefer to use dev.print(win.print).

dev.print is most useful for producing a postscript print (its default) when the following applies. Unless file is specified, the plot will be printed. Unless width, height and pointsize are specified the plot dimensions will be taken from the current device, shrunk if necessary to fit on the paper. (pointsize is rescaled if the plot is shrunk.) If horizontal is not specified and the plot can be printed at full size by switching its value this is done instead of shrinking the plot region.

If dev.print is used with a specified device (even postscript) it sets the width and height in the same way as dev.copy2eps. This will not be appropriate unless the device specifies dimensions in inches, in particular not for png, jpeg, tiff and bmp unless units = "inches" is specified.

Value

dev.copy returns the name and number of the device which has been copied to.

dev.print, dev.copy2eps and dev.copy2pdf return the name and number of the device which has been copied from.

Note

Most devices (including all screen devices) have a display list which records all of the graphics operations that occur in the device. dev.copy copies graphics contents by copying the display list from one device to another device. Also, automatic redrawing of graphics contents following the resizing of a device depends on the contents of the display list.

After the command dev.control("inhibit"), graphics operations are not recorded in the display list so that dev.copy and dev.print will not copy anything and the contents of a device will not be redrawn automatically if the device is resized.

The recording of graphics operations is relatively expensive in terms of memory so the command dev.control("inhibit") can be useful if memory usage is an issue.

See Also

dev.cur and other dev.xxx functions.

Examples

```r
## Not run:
x11() # on a Unix-alike
plot(rnorm(10), main = "Plot 1")
dev.copy(device = x11)
mtext("Copy 1", 3)
dev.print(width = 6, height = 6, horizontal = FALSE) # prints it
dev.off(dev.prev())
dev.off()
## End(Not run)
```
Description

bitmap generates a graphics file. dev2bitmap copies the current graphics device to a file in a
graphics format.

Usage

bitmap(file, type = "png16m", height = 7, width = 7, res = 72,
       units = "in", pointsize, taa = NA, gaa = NA, ...)

dev2bitmap(file, type = "png16m", height = 7, width = 7, res = 72,
           units = "in", pointsize, ...,
           method = c("postscript", "pdf"), taa = NA, gaa = NA)

Arguments

file The output file name, with an appropriate extension.
type The type of bitmap.
width, height Dimensions of the display region.
res Resolution, in dots per inch.
units The units in which height and width are given. Can be in (inches), px (pixels),
cm or mm.
pointsize The pointsize to be used for text: defaults to something reasonable given the
       width and height
... Other parameters passed to postscript or pdf.
method Should the plot be done by postscript or pdf?
taa, gaa Number of bits of antialiasing for text and for graphics respectively. Usually 4
       (for best effect) or 2. Not supported on all types.

Details

dev2bitmap works by copying the current device to a postscript or pdf device, and post-
processing the output file using ghostscript. bitmap works in the same way using a postscript
device and post-processing the output as ‘printing’.

You will need ghostscript: the full path to the executable can be set by the environment variable
R_GSCMD. If this is unset, a GhostScript executable will be looked for by name on your path: on
a Unix alike “gs” is used, and on Windows the setting of the environment variable GSC is used,
otherwise commands "gswi64c.exe" then "gswin32c.exe" are tried.

The types available will depend on the version of ghostscript, but are likely to include
"jpeg","jpegcmyk","jpeggray","tifffcrle","tifffg3","tifffg32d","tifffg4","tifffgray",
"tifffzw","tifffpack","tifff2nc","tifff4nc","tifff32nc" "png16"."png16m"."png256",
"png48"."pngmono"."pnggray"."pngalpha"."bmp16"."bmp16m"."bmp256"."bmp32b",
"bmpgray"."bmpmono".

The default type, "png16m", supports 24-bit colour and anti-aliasing. Type "png256" uses a
palette of 256 colours and could give a more compact representation. Monochrome graphs can
use "pngmono", or "pnggray" if anti-aliasing is desired. Plots with a transparent background and varying degrees of transparency should use "pngalpha".

Note that for a colour TIFF image you probably want "tiff24nc", which is 8-bit per channel RGB (the most common TIFF format). None of the listed TIFF types support transparency. "tiff32nc" uses 8-bit per channel CMYK, which printers might require.

For formats which contain a single image, a file specification like Rplots%03d.png can be used: this is interpreted by Ghostscript.

For dev2bitmap if just one of width and height is specified, the other is chosen to preserve the aspect ratio of the device being copied. The main reason to prefer method = "pdf" over the default would be to allow semi-transparent colours to be used.

For graphics parameters such as "cra" that need to work in pixels, the default resolution of 72dpi is always used.

On Windows only, paths for file and R_GSCMD which contain spaces are mapped to short names via shortPathName.

Value
None.

Conventions
This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual. These devices follow the underlying device, so when viewed at the stated res:

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is (for the standard Ghostscript setup) URW Nimbus Sans.
- Line widths are as a multiple of 1/96 inch, with no minimum.
- Circle of any radius are allowed.
- Colours are interpreted by the viewing/printing application.

Note
On Windows, Use of bitmap will leave a temporary file (with file name starting Rbit).

Although using type = "pdfwrite" will work for simple plots, it is not recommended. Either use pdf to produce PDF directly, or call ps2pdf -dAutoRotatePages=/None on the output of postscript: that command is optimized to do the conversion to PDF in ways that these functions are not.

See Also
savePlot, which for windows and X11(type = "cairo") provides a simple way to record a PNG record of the current plot.

postscript, pdf, png, jpeg, tiff and bmp.

To display an array of data, see image.
devAskNewPage

Prompt before New Page

devAskNewPage

Description
This function can be used to control (for the current device) whether the user is prompted before starting a new page of output.

Usage
devAskNewPage(ask = NULL)

Arguments
ask NULL or a logical value. If TRUE, the user will in future be prompted before a new page of output is started.

Details
If the current device is the null device, this will open a graphics device.
The default argument just returns the current setting and does not change it.
The default value when a device is opened is taken from the setting of options("device.ask.default").
The precise circumstances when the user will be asked to confirm a new page depend on the graphics subsystem. Obviously this needs to be an interactive session. In addition 'recording' needs to be in operation, so only when the display list is enabled (see dev.control) which it usually is only on a screen device.

Value
The current prompt setting before any new setting is applied. Invisibly if ask is logical.

See Also
plot.new, grid.newpage

Devices
List of Graphical Devices

Description
The following graphics devices are currently available:

windows: On Windows only, the graphics device for Windows (on screen, to printer and to Windows metafile).
pdf: Write PDF graphics commands to a file.
postscript: Writes PostScript graphics commands to a file.
xfig: Device for XFig graphics file format.
bitmap: bitmap pseudo-device via Ghostscript (if available).

pictex: Writes TeX/PicTeX graphics commands to a file (of historical interest only).

The following devices will be functional if \texttt{R} was compiled to use them (they exist but will return with a warning on other systems):

\texttt{cairo_pdf}, \texttt{cairo_ps}: PDF and PostScript devices based on cairo graphics.
\texttt{svg}: SVG device based on cairo graphics
\texttt{png}: PNG bitmap device
\texttt{jpeg}: JPEG bitmap device
\texttt{bmp}: BMP bitmap device
\texttt{tiff}: TIFF bitmap device

On Unix-alikes (including macOS) only:

\texttt{x11}: The graphics device for the X11 windowing system
\texttt{quartz}: The graphics device for the macOS native Quartz 2d graphics system. (This is only functional on macOS where it can be used from the \texttt{R.app} GUI and from the command line: but it will display on the local screen even for a remote session.)

Details

If no device is open, calling any high-level graphics function will cause a device to be opened. Which device is determined by \texttt{options("device")} which is initially set as the most appropriate for each platform: a screen device for most interactive use and \texttt{pdf} (or the setting of \texttt{R_DEFAULT_DEVICE}) otherwise. The exception is interactive use under Unix if no screen device is known to be available, when \texttt{pdf()} is used.

It is possible for an \texttt{R} package (or an \texttt{R} front-end such as RStudio) to provide further graphics devices and several packages on CRAN do so. These include devices outputting SVG (\texttt{svglite} and PGF/TiKZ (\texttt{tikzDevice}, TeX-based graphics, see https://pgf.sourceforge.net/).

See Also

The individual help files for further information on any of the devices listed here;

\texttt{windows.options}, \texttt{x11.options}, \texttt{quartz.options}, \texttt{ps.options} and \texttt{pdf.options} for how to customize devices.
\texttt{dev.interactive}, \texttt{dev.cur}, \texttt{dev.print}, \texttt{graphics.off}, \texttt{image}, \texttt{dev2bitmap}.

On Unix-alikes only: \texttt{capabilities} to see if \texttt{x11}, \texttt{jpeg}, \texttt{png}, \texttt{tiff}, \texttt{quartz} and the cairo-based devices are available.

Examples

```r
## Not run:
## open the default screen device on this platform if no device is
## open
if(dev.cur() == 1) dev.new()
## End(Not run)
```
Description

Runs Ghostscript to process a PDF or PostScript file and embed all fonts in the file.
Use `embedGlyphs()` if you have drawn typeset glyphs (see `glyphInfo`), which is only relevant for PDF files.

Usage

```r
eMBEDFonts(file, format, outfile = file,
          fontpaths = character(), options = character())
```

```r
embedGlyphs(file, glyphInfo, outfile = file, options = character())
```

Arguments

- `file` a character string giving the name of the original file.
- `format` the format for the new file (with fonts embedded) given as the name of a ghostscript output device. If not specified, it is guessed from the suffix of `file`.
- `outfile` the name of the new file (with fonts embedded).
- `fontpaths` a character vector giving directories that Ghostscript will search for fonts.
- `options` a character vector containing further options to Ghostscript.
- `glyphInfo` typeset glyph information produced by `glyphInfo()`.

Details

This function is not necessary if you just use the standard default fonts for PostScript and PDF output.

If you use a special font, this function is useful for embedding that font in your PostScript or PDF document so that it can be shared with others without them having to install your special font (provided the font licence allows this).

If the special font is not installed for Ghostscript, you will need to tell Ghostscript where the font is, using something like `options="-sFONTPATH=path/to/font"`.

You will need `ghostscript`: the full path to the executable can be set by the environment variable R_GSCMD. If this is unset, a GhostScript executable will be looked for by name on your path: on a Unix alike “gs” is used, and on Windows the setting of the environment variable GSC is used, otherwise commands “gswi64c.exe” then “gswin32c.exe” are tried.

The format is by default ”ps2write”, when the original file has a .ps or .eps suffix, or ”pdf2write” when the original file has a .pdf suffix. For versions of Ghostscript before 9.10, `format = "pswrite"` or `format = "epswrite"` can be used; as from 9.14 `format = "eps2write"` is also available. If an invalid device is given, the error message will list the available devices.

Note that Ghostscript may do font substitution, so the font embedded may differ from that specified in the original file.

Some other options which can be useful (see your Ghostscript documentation) are ‘-dMaxSubsetPct=100’, ‘-dSubsetFonts=true’ and ‘-dEmbedAllFonts=true’.
extendrange

Value

The shell command used to invoke Ghostscript is returned invisibly. This may be useful for debugging purposes as you can run the command by hand in a shell to look for problems.

See Also

postscriptFonts, Devices.


extendrange  Extend a Numerical Range by a Small Percentage

Description

Extends a numerical range by a small percentage, i.e., fraction, on both sides.

Usage

extendrange(x, r = range(x, na.rm = TRUE), f = 0.05)

Arguments

x numeric vector; not used if r is specified.

r numeric vector of length 2; defaults to the range of x.

f positive number(s) specifying the fraction by which the range should be extended. If longer than one, f[1] is used on the left, and f[2] on the right.

Value

A numeric vector of length 2, r + c(-f1,f2) * diff(r), where f1 is f[1] and f2 is f[2] or f if it is of length one.

See Also

range; pretty which can be considered a sophisticated extension of extendrange.

Examples

x <- 1:5
(r <- range(x)) # 1 5
extendrange(x) # 0.8 5.2
extendrange(x, f = 0.01) # 0.96 5.04

## extend more to the right:
extendrange(x, f=c(.01,.03)) # 0.96 5.12

## Use 'r' if you have it already:
stopifnot(identical(extendrange(r = r), extendrange(x)))
getGraphicsEvent

Wait for a mouse or keyboard event from a graphics window

Description

This function waits for input from a graphics window in the form of a mouse or keyboard event.

Usage

getGraphicsEvent(prompt = "Waiting for input",
    onMouseDown = NULL, onMouseMove = NULL,
    onMouseUp = NULL, onKeybd = NULL,
    onIdle = NULL,
    consolePrompt = prompt)

setGraphicsEventHandlers(which = dev.cur(), ...)

setGraphicsEventEnv(which = dev.cur())

Arguments

prompt prompt to be displayed to the user in the graphics window

onMouseDown a function to respond to mouse clicks

onMouseMove a function to respond to mouse movement

onMouseUp a function to respond to mouse button releases

onKeybd a function to respond to key presses

onIdle a function to call when no events are pending

consolePrompt prompt to be displayed to the user in the console

which which graphics device does the call apply to?

... items including handlers to be placed in the event environment

env an environment to be used as the event environment

Details

These functions allow user input from some graphics devices (currently only the windows(), X11(type = "Xlib") and X11(type = "cairo") screen displays in base R). Event handlers may be installed to respond to events involving the mouse or keyboard.

The functions are related as follows. If any of the first six arguments to getGraphicsEvent are given, then it uses those in a call to setGraphicsEventHandlers to replace any existing handlers in the current device. This is for compatibility with pre-2.12.0 R versions. The current normal way to set up event handlers is to set them using setGraphicsEventHandlers or setGraphicsEventEnv on one or more graphics devices, and then use getGraphicsEvent() with no arguments to retrieve event data. getGraphicsEventEnv() may be used to save the event environment for use later.

The names of the arguments in getGraphicsEvent are special. When handling events, the graphics system will look through the event environment for functions named onMouseDown, onMouseMove, onMouseUp, onKeybd, and onIdle, and use them as event handlers. It will use prompt for a label on the graphics device. Two other special names are which, which will identify the graphics device,
and result, where the result of the last event handler will be stored before being returned by getGraphicsEvent().

The mouse event handlers should be functions with header function(buttons, x, y). The coordinates x and y will be passed to mouse event handlers in device independent coordinates (i.e., the lower left corner of the window is (0,0), the upper right is (1,1)). The buttons argument will be a vector listing the buttons that are pressed at the time of the event, with 0 for left, 1 for middle, and 2 for right.

The keyboard event handler should be a function with header function(key). A single character vector will be passed to this handler, corresponding to the key press. Shift and other modifier keys will have been processed, so shift-a will be passed as "A". The following special keys may also be passed to the handler:

- Control keys, passed as "Ctrl-A", etc.
- Navigation keys, passed as one of "Left", "Up", "Right", "Down", "PgUp", "PgDn", "End", "Home"
- Edit keys, passed as one of "Ins", "Del"
- Function keys, passed as one of "F1", "F2", ...

The idle event handler onIdle should be a function with no arguments. If the function is undefined or NULL, then R will typically call a system function which (efficiently) waits for the next event to appear on a filehandle. Otherwise, the idle event handler will be called whenever the event queue of the graphics device was found to be empty, i.e. in an infinite loop. This feature is intended to allow animations to respond to user input, and could be CPU-intensive. Currently, onIdle is only implemented for X11() devices.

Note that calling Sys.sleep() is not recommended within an idle handler - Sys.sleep() removes pending graphics events in order to allow users to move, close, or resize windows while it is executing. Events such as mouse and keyboard events occurring during Sys.sleep() are lost, and currently do not trigger the event handlers registered via getGraphicsEvent or setGraphicsEventHandlers.

The event handlers are standard R functions, and will be executed as though called from the event environment.

In an interactive session, events will be processed until

- one of the event handlers returns a non-NULL value which will be returned as the value of getGraphicsEvent, or
- the user interrupts the function from the console.

Value

When run interactively, getGraphicsEvent returns a non-NULL value returned from one of the event handlers. In a non-interactive session, getGraphicsEvent will return NULL immediately. It will also return NULL if the user closes the last window that has graphics handlers.

getGraphicsEventEnv returns the current event environment for the graphics device, or NULL if none has been set.

setGraphicsEventEnv and setGraphicsEventHandlers return the previous event environment for the graphics device.

Author(s)

Duncan Murdoch
getGraphicsEvent

Examples

# This currently only works on the Windows, X11(type = "Xlib"), and # X11(type = "cairo") screen devices...
## Not run:
savepar <- par(ask = FALSE)
dragplot <- function(..., xlim = NULL, ylim = NULL, xaxs = "r", yaxs = "r") {
  plot(..., xlim = xlim, ylim = ylim, xaxs = xaxs, yaxs = yaxs)
  startx <- NULL
  starty <- NULL
  prevx <- NULL
  prevy <- NULL
  usr <- NULL
  devset <- function()
    if (dev.cur() != eventEnv$which) dev.set(eventEnv$which)

dragmousedown <- function(buttons, x, y) {
  startx <<- x
  starty <<- y
  prevx <<- 0
  prevy <<- 0
  devset()
  usr <<- par("usr")
  eventEnv$onMouseMove <- dragmousemove
  NULL
}
dragmousemove <- function(buttons, x, y) {
  devset()
  deltax <- diff(grconvertX(c(startx, x), "ndc", "user"))
  deltay <- diff(grconvertY(c(starty, y), "ndc", "user"))
  if (abs(deltax-prevx) + abs(deltay-prevy) > 0) {
    plot(..., xlim = usr[1:2]-deltax, xaxs = "i",
         ylim = usr[3:4]-deltay, yaxs = "i")
    prevx <<- deltax
    prevy <<- deltay
  }
  NULL
}

mouseup <- function(buttons, x, y) {
  eventEnv$onMouseMove <- NULL
}

keydown <- function(key) {
  if (key == "q") return(invisible(1))
  eventEnv$onMouseMove <- NULL
  NULL
}

setGraphicsEventHandlers(prompt = "Click and drag, hit q to quit",
onMouseDown = dragmousedown,
onMouseMove = dragmousemove,
onMouseUp = mouseup,
onKeybd = keydown)
eventEnv <- getGraphicsEventEnv()
Describe a Set of Typeset Glyphs.

Create an object that contains information about typeset glyphs. This includes glyph identifiers, glyph locations, font and colour information, and metric information.

Usage

glyphInfo(id, x, y, font, size, fontList, 
  width, height, hAnchor, vAnchor, 
  col=NA)

glyphFont(file, index, family, weight, style, PSname=NA)

glyphFontList(...)

glyphAnchor(value, label)

glyphWidth(w, label="width", left="left")

glyphHeight(h, label="height", bottom="bottom")

glyphWidthLeft(w, label)

glyphHeightBottom(h, label)

glyphJust(just, ...)

## S3 method for class 'GlyphJust'

glyphJust(just, ...)

## S3 method for class 'character'

glyphJust(just, ...)

## S3 method for class 'numeric'

glyphJust(just, which=NULL, ...)

Arguments

- **id**
  - Numeric vector of glyph identifiers (index of glyph within font file).

- **x, y**
  - Numeric locations of glyphs in (big) points (1/72 inches).

- **font**
  - Integer index into fontList.

- **size**
  - Numeric size of glyphs (in points).

- **fontList**
  - List of glyph fonts, as generated by glyphFont().

- **width**
  - Overall width of glyphs. Can be a single numeric value, but can also be the result from a call to glyphWidth().

- **height**
  - Overall height of glyphs. Can be a single numeric value, but can also be the result from a call to glyphHeight().

- **hAnchor**
  - Horizontal anchors for justifying glyphs relative to the (x, y) location. Can be a single numeric value (against which to "left" justify), but can also be result from a call to glyphAnchor().
glyphInfo

vAnchor  | Vertical anchors for justifying glyphs relative to the \((x, y)\) location. Can be a single numeric value (against which to "bottom" justify), but can also be result from a call to `glyphAnchor()`.

col      | An R colour value for each glyph. Can be NA.

file     | Character path to font file.

index    | Numeric index of font within font file.

family   | Character name of font family.

weight   | Numeric weight of glyphs (400 is normal, 700 is bold).

style    | Character style of glyphs ("normal", "italic", or "oblique").

PSname   | The PostScript name for each font. Can be NA.

value, w, h | A numeric value.

label, left, bottom | A character value.

just     | A justification value. Either a character value like "left" or a numeric value like 0.

which    | When \(x\) is numeric, a character value identifying which width metric the numeric value is relative to.

... | Further arguments passed to other methods.

Details

Multiple anchors can be specified so as to allow different character-based justifications of the glyphs relative to the \((x, y)\) location. Horizontal anchors with labels "left", "centre", and "right" are required. It is possible to specify a single numeric \(h\)Anchor, which is treated as the "left" anchor, or a single anchor with label "left", in which case the other required anchors will be calculated based on the required width of the glyphs (see below). Vertical anchors with labels "bottom", "centre", and "top" are required. It is possible to specify a single numeric \(v\)Anchor, which is treated as the "bottom" anchor, or a single anchor with label "bottom", in which case the other required anchors will be calculated based on the required height of the glyphs (see below). An example of a non-required anchor is a vertical anchor with the label "baseline" so that the glyphs can be placed with their baseline at the \(y\) location.

Multiple widths and heights can be specified so as to allow different numeric-based justifications of the glyphs relative to the \((x, y)\) location, e.g., 0 for left-justification and 1 for right-justification, but with any value in between or even outside those limits also possible. A width with label "width", relative to the "left" horizontal anchor, is required, but if a single numeric value is given, that is assumed to be the required width. A height with label "height", relative to the "bottom" vertical anchor is required, but if a single numeric value is given, that is assumed to be the required height. An example of a non-required width is a "tight" width that is relative to a "left-bearing" horizontal anchor, so that the glyphs can be justified relative to a bounding box around the glyph ink, rather than a bounding box that includes left and right bearings.

glyphWidthLeft() and glyphWidthHeight() provide an API for code that needs to access the relevant anchors for width and height metrics.

Value

The result from `glyphInfo()` is an "RGlyphInfo" object, essentially a data frame with each row containing id, location, font, and colour for a glyph. The metric information (widths and anchors) are stored as attributes of the data frame.

glyphAnchor(), glyphWidth(), and glyphHeight() return values that can be used to specify width, height, \(h\)Anchor, and \(v\)Anchor values to `glyphInfo()`.
Warning

Any glyph with NA in any of id, x, y, or size is silently dropped.

Description

Create a vector of colors from a vector of gray levels.

Usage

\begin{verbatim}
gray(level, alpha)
grey(level, alpha)
\end{verbatim}

Arguments

- **level**: a vector of desired gray levels between 0 and 1; zero indicates "black" and one indicates "white".
- **alpha**: the opacity, if specified.

Details

The values returned by `gray` can be used with a `col=` specification in graphics functions or in `par`. `grey` is an alias for `gray`.

Value

A vector of colors of the same length as `level`.

See Also

`rainbow`, `hsv`, `hcl`, `rgb`.

Examples

\begin{verbatim}
gray(0:8 / 8)
\end{verbatim}
Description

Create a vector of \( n \) gamma-corrected gray colors.

Usage

\[
\text{gray.colors}(n, \text{start} = 0.3, \text{end} = 0.9, \text{gamma} = 2.2, \text{alpha}, \text{rev} = \text{FALSE})
\]

Arguments

- **n**: the number of gray colors (\( \geq 1 \)) to be in the palette.
- **start**: starting gray level in the palette (should be between 0 and 1 where zero indicates "black" and one indicates "white").
- **end**: ending gray level in the palette.
- **gamma**: the gamma correction.
- **alpha**: the opacity, if specified.
- **rev**: logical indicating whether the ordering of the colors should be reversed.

Details

The function `gray.colors` chooses a series of \( n \) gamma-corrected gray levels between `start` and `end`: \( \text{seq(start}^{\text{gamma}}, \text{end}^{\text{gamma}}, \text{length} = n)^(1/\text{gamma}) \). The returned palette contains the corresponding gray colors. This palette is used in `barplot.default`.

`grey.colors` is an alias for `gray.colors`.

Value

A vector of \( n \) gray colors.

See Also

- `gray`, `rainbow`, `palette`.

Examples

```r
require(graphics)
pie(rep(1, 12), col = gray.colors(12))
barplot(1:12, col = gray.colors(12))
```
Description

Report versions of third-party graphics software available on the current platform for R’s graphics.

Usage

grSoftVersion()

Value

A named character vector containing at least the elements

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cairo</td>
<td>the version of cairographics in use, or &quot;&quot; if cairographics is not available.</td>
</tr>
<tr>
<td>cairoFT</td>
<td>the FreeType/FontConfig versions if cairographics is using those libraries directly (not via pango); otherwise, &quot;&quot;. Earlier versions of R returned &quot;yes&quot; rather than the versions. The FontConfig version is determined when R is built.</td>
</tr>
<tr>
<td>pango</td>
<td>the version of pango in use, or &quot;&quot; if pango is not available.</td>
</tr>
</tbody>
</table>

It may also contain the versions of third-party software used by the standard (on Windows), or X11-based (on Unix-alikes) bitmap devices:

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>libpng</td>
<td>the version of libpng in use, or &quot;&quot; if not available.</td>
</tr>
<tr>
<td>jpeg</td>
<td>the version of the JPEG headers used for compilation, or &quot;&quot; if JPEG support was not compiled in.</td>
</tr>
<tr>
<td>libtiff</td>
<td>the version of libtiff in use, or &quot;&quot; if not available.</td>
</tr>
</tbody>
</table>

It is conceivable but unlikely that the cairo-based bitmap devices will use different versions linked via cairographics, especially png(type = "cairo-png").

On macOS, if available, the Quartz-based devices will use the system versions of these libraries rather than those reported here.

Unless otherwise stated the reported version is that of the (possibly dynamically-linked) library in use at runtime.

Note that libjpeg-turbo as used on some Linux distributions reports its version as "6.2", the IJG version from which it forked.

See Also

extSoftVersion for versions of non-graphics software.

Examples

grSoftVersion()
Description

Create a vector of colors from vectors specifying hue, chroma and luminance.

Usage

hcl(h = 0, c = 35, l = 85, alpha, fixup = TRUE)

Arguments

h
  The hue of the color specified as an angle in the range [0,360]. 0 yields red, 120 yields green 240 yields blue, etc.

c
  The chroma of the color. The upper bound for chroma depends on hue and luminance.

l
  A value in the range [0,100] giving the luminance of the colour. For a given combination of hue and chroma, only a subset of this range is possible.

alpha
  numeric vector of values in the range [0,1] for alpha transparency channel (0 means transparent and 1 means opaque).

fixup
  a logical value which indicates whether the resulting RGB values should be corrected to ensure that a real color results. if fixup is FALSE RGB components lying outside the range [0,1] will result in an NA value.

Details

This function corresponds to polar coordinates in the CIE-LUV color space. Steps of equal size in this space correspond to approximately equal perceptual changes in color. Thus, hcl can be thought of as a perceptually based version of hsv.

The function is primarily intended as a way of computing colors for filling areas in plots where area corresponds to a numerical value (pie charts, bar charts, mosaic plots, histograms, etc). Choosing colors which have equal chroma and luminance provides a way of minimising the irradiation illusion which would otherwise produce a misleading impression of how large the areas are.

The default values of chroma and luminance make it possible to generate a full range of hues and have a relatively pleasant pastel appearance.

The RGB values produced by this function correspond to the sRGB color space used on most PC computer displays. There are other packages which provide more general color space facilities. Semi-transparent colors (0 < alpha < 1) are supported only on some devices: see rgb.

Value

A vector of character strings which can be used as color specifications by R graphics functions.

Missing or infinite values of any of h, c, l result in NA: such values of alpha are taken as 1 (opaque).

Note

At present there is no guarantee that the colours rendered by R graphics devices will correspond to their sRGB description. It is planned to adopt sRGB as the standard R color description in future.
Author(s)
Ross Ihaka

References

See Also
hsv, rgb.

Examples

```r
require(graphics)

# The Foley and Van Dam PhD Data.
csd <- matrix(c( 4,2,4,6, 4,3,1,4, 4,7,7,1, 0,7,3,2, 4,5,3,2, 5,4,2,2, 3,1,3,0, 4,4,6,7, 1,10,8,7, 1,5,3,2, 1,5,2,1, 4,1,4,3, 0,3,0,6, 2,1,5,5), nrow = 4)

cspdhd <- function(colors)
  barplot(csd, col = colors, ylim = c(0,30),
          names.arg = 72:85, xlab = "Year", ylab = "Students",
          legend.text = c("Winter", "Spring", "Summer", "Fall"),
          main = "Computer Science PhD Graduates", las = 1)

cspdh(c("blue", "green", "yellow", "orange"))

cspdh(hcl(h = c(30, 120, 210, 300)))

cspdh(hcl(h = c(30, 120, 210, 300),
          c = 20, l = 90, fixup = FALSE))

cspdh(hcl(h = seq(60, 240, length.out = 4)))

cspdh(hcl(h = seq(210, 60, length.out = 4)))

cspdh(hcl(h = seq(120, 0, length.out = 4) + 150))

cspdh(hcl(h = seq(120, 0, length.out = 4) - 30))
```

# Single Color
hist(stats::rnorm(1000), col = hcl(240))

## Exploring the hcl() color space (in its mapping to R's sRGB colors):
demo(hclColors)

---

**Hershey**

**Hershey Vector Fonts in R**

**Description**

If the family graphical parameter (see `par`) has been set to one of the Hershey fonts (see ‘Details’) Hershey vector fonts are used to render text. When using the `text` and `contour` functions Hershey fonts may be selected via the `vfont` argument, which is a character vector of length 2 (see ‘Details’ for valid values). This allows Cyrillic to be selected, which is not available via the font families.

**Usage**

Hershey

**Details**

The Hershey fonts have two advantages:

1. vector fonts describe each character in terms of a set of points; R renders the character by joining up the points with straight lines. This intimate knowledge of the outline of each character means that R can arbitrarily transform the characters, which can mean that the vector fonts look better for rotated text.

2. this implementation was adapted from the GNU libplot library which provides support for non-ASCII and non-English fonts. This means that it is possible, for example, to produce weird plotting symbols and Japanese characters.

**Drawback:**
You cannot use mathematical expressions (`plotmath`) with Hershey fonts.

The Hershey characters are organised into a set of fonts. A particular font is selected by specifying one of the following font families via `par(family)` and specifying the desired font face (plain, bold, italic, bold-italic) via `par(font)`.

<table>
<thead>
<tr>
<th>family</th>
<th>faces available</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;HersheySerif&quot;</td>
<td>plain, bold, italic, bold-italic</td>
</tr>
<tr>
<td>&quot;HersheySans&quot;</td>
<td>plain, bold, italic, bold-italic</td>
</tr>
<tr>
<td>&quot;HersheyScript&quot;</td>
<td>plain, bold</td>
</tr>
<tr>
<td>&quot;HersheyGothicEnglish&quot;</td>
<td>plain</td>
</tr>
<tr>
<td>&quot;HersheyGothicGerman&quot;</td>
<td>plain</td>
</tr>
<tr>
<td>&quot;HersheyGothicItalian&quot;</td>
<td>plain</td>
</tr>
<tr>
<td>&quot;HersheySymbol&quot;</td>
<td>plain, bold, italic, bold-italic</td>
</tr>
<tr>
<td>&quot;HersheySansSymbol&quot;</td>
<td>plain, italic</td>
</tr>
</tbody>
</table>
In the vfont specification for the text and contour functions, the Hershey font is specified by a typeface (e.g., serif or sans serif) and a fontindex or 'style' (e.g., plain or italic). The first element of vfont specifies the typeface and the second element specifies the fontindex. The first table produced by demo(Hershey) shows the character a produced by each of the different fonts.

The available typeface and fontindex values are available as list components of the variable Hershey. The allowed pairs for (typeface, fontindex) are:

<table>
<thead>
<tr>
<th>Typeface</th>
<th>Fontindex</th>
</tr>
</thead>
<tbody>
<tr>
<td>serif</td>
<td>plain</td>
</tr>
<tr>
<td>serif</td>
<td>italic</td>
</tr>
<tr>
<td>serif</td>
<td>bold</td>
</tr>
<tr>
<td>serif</td>
<td>bold italic</td>
</tr>
<tr>
<td>serif</td>
<td>cyrillic</td>
</tr>
<tr>
<td>serif</td>
<td>oblique cyrillic</td>
</tr>
<tr>
<td>serif</td>
<td>EUC</td>
</tr>
<tr>
<td>sans serif</td>
<td>plain</td>
</tr>
<tr>
<td>sans serif</td>
<td>italic</td>
</tr>
<tr>
<td>sans serif</td>
<td>bold</td>
</tr>
<tr>
<td>sans serif</td>
<td>bold italic</td>
</tr>
<tr>
<td>script</td>
<td>plain</td>
</tr>
<tr>
<td>script</td>
<td>italic</td>
</tr>
<tr>
<td>script</td>
<td>bold</td>
</tr>
<tr>
<td>gothic english</td>
<td>plain</td>
</tr>
<tr>
<td>gothic german</td>
<td>plain</td>
</tr>
<tr>
<td>gothic italian</td>
<td>plain</td>
</tr>
<tr>
<td>serif symbol</td>
<td>plain</td>
</tr>
<tr>
<td>serif symbol</td>
<td>italic</td>
</tr>
<tr>
<td>serif symbol</td>
<td>bold</td>
</tr>
<tr>
<td>serif symbol</td>
<td>bold italic</td>
</tr>
<tr>
<td>sans serif symbol</td>
<td>plain</td>
</tr>
<tr>
<td>sans serif symbol</td>
<td>italic</td>
</tr>
</tbody>
</table>

and the indices of these are available as Hershey$allowed.

**Escape sequences:** The string to be drawn can include escape sequences, which all begin with a ‘\’. When R encounters a ‘\’, rather than drawing the ‘\’, it treats the subsequent character(s) as a coded description of what to draw.

One useful escape sequence (in the current context) is of the form: ‘\123’. The three digits following the ‘\’ specify an octal code for a character. For example, the octal code for p is 160 so the strings ”p” and ”\160” are equivalent. This is useful for producing characters when there is not an appropriate key on your keyboard.

The other useful escape sequences all begin with ‘\ \’. These are described below. Remember that backslashes have to be doubled in R character strings, so they need to be entered with four backslashes.

**Symbols:** an entire string of Greek symbols can be produced by selecting the HersheySymbol or HersheySansSymbol family or the Serif Symbol or Sans Serif Symbol typeface. To allow Greek symbols to be embedded in a string which uses a non-symbol typeface, there are a set of symbol escape sequences of the form ‘\ab’. For example, the escape sequence ‘\*a’ produces a Greek alpha. The second table in demo(Hershey) shows all of the symbol escape sequences and the symbols that they produce.

**ISO Latin-1:** further escape sequences of the form ‘\ab’ are provided for producing ISO Latin-1 characters. Another option is to use the appropriate octal code. The (non-ASCII) ISO Latin-1
characters are in the range 241...377. For example, \366 produces the character o with an umlaut. The third table in demo(Hershey) shows all of the ISO Latin-1 escape sequences. These characters can be used directly. (Characters not in Latin-1 are replaced by a dot.) Several characters are missing, c-cedilla has no cedilla and ‘sharp s’ (‘U+00DF’, also known as ‘esszet’) is rendered as ss.

**Special Characters:** a set of characters are provided which do not fall into any standard font. These can only be accessed by escape sequence. For example, \LI produces the zodiac sign for Libra, and \JU produces the astronomical sign for Jupiter. The fourth table in demo(Hershey) shows all of the special character escape sequences.

**Cyrillic Characters:** cyrillic characters are implemented according to the K018-R encoding, and can be used directly in such a locale using the Serif typeface and Cyrillic (or Oblique Cyrillic) fontindex. Alternatively they can be specified via an octal code in the range 300 to 337 for lower case characters or 340 to 377 for upper case characters. The fifth table in demo(Hershey) shows the octal codes for the available Cyrillic characters.

Cyrillic has to be selected via a ("serif", fontindex) pair rather than via a font family.

**Japanese Characters:** 83 Hiragana, 86 Katakana, and 603 Kanji characters are implemented according to the EUC-JP (Extended Unix Code) encoding. Each character is identified by a unique hexadecimal code. The Hiragana characters are in the range 0x2421 to 0x2473, Katakana are in the range 0x2521 to 0x2576, and Kanji are (scattered about) in the range 0x3021 to 0x6d55.

When using the Serif typeface and EUC fontindex, these characters can be produced by a pair of octal codes. Given the hexadecimal code (e.g., 0x2421), take the first two digits and add 0x80 and do the same to the second two digits (e.g., 0x21 and 0x24 become 0xa4 and 0xa1), then convert both to octal (e.g., 0x4a and 0xa1 become 244 and 241). For example, the first Hiragana character is produced by \244\241.

It is also possible to use the hexadecimal code directly. This works for all non-EUC fonts by specifying an escape sequence of the form \#J1234. For example, the first Hiragana character is produced by \#J2421.

The Kanji characters may be specified in a third way, using the so-called "Nelson Index", by specifying an escape sequence of the form \#N1234. For example, the (obsolete) Kanji for ‘one’ is produced by \#N0001.

demo(Japanese) shows the available Japanese characters.

**Raw Hershey Glyphs:** all of the characters in the Hershey fonts are stored in a large array. Some characters are not accessible in any of the Hershey fonts. These characters can only be accessed via an escape sequence of the form \#H1234. For example, the fleur-de-lys is produced by \#H8746. The sixth and seventh tables of demo(Hershey) shows all of the available raw glyphs.

References


See Also

demo(Hershey), par, text, contour.

Japanese for the Japanese characters in the Hershey fonts.

Examples

Hershey

## for tables of examples, see demo(Hershey)
hsv

HSV Color Specification

Description

Create a vector of colors from vectors specifying hue, saturation and value.

Usage

hsv(h = 1, s = 1, v = 1, alpha)

Arguments

h, s, v
numeric vectors of values in the range \([0, 1]\) for ‘hue’, ‘saturation’ and ‘value’ to be combined to form a vector of colors. Values in shorter arguments are recycled.

alpha
numeric vector of values in the range \([0, 1]\) for alpha transparency channel (0 means transparent and 1 means opaque).

Details

Semi-transparent colors \((0 < \alpha < 1)\) are supported only on some devices: see rgb.

Value

This function creates a vector of colors corresponding to the given values in HSV space. The values returned by hsv can be used with a col= specification in graphics functions or in par.

See Also

hcl for a perceptually based version of hsv(), rgb and rgb2hsv for RGB to HSV conversion; rainbow, gray.

Examples

```r
require(graphics)

hsv(.5,.5,.5)

## Red tones:
n <- 20; y <- -sin(3*pi*((1:n)-1/2)/n)
op <- par(mar = rep(1.5, 4))
plot(y, axes = FALSE, frame.plot = TRUE,
     xlab = "", ylab = "", pch = 21, cex = 30,
     bg = rainbow(n, start = .85, end = .1),
     main = "Red tones")
par(op)
```
Description

The implementation of Hershey vector fonts provides a large number of Japanese characters (Hira-gana, Katakana, and Kanji).

Details

Without keyboard support for typing Japanese characters, the only way to produce these characters is to use special escape sequences: see Hershey.

For example, the Hiragana character for the sound "ka" is produced by `\#J242b` and the Katakana character for this sound is produced by `\#J252b`. The Kanji ideograph for "one" is produced by `\#J306c` or `\#N0001`.

The output from `demo(Japanese)` shows tables of the escape sequences for the available Japanese characters.

References

https://www.gnu.org/software/plotutils/plotutils.html

See Also

demo(Japanese), Hershey, text

Examples

```r
require(graphics)
plot(1:9, type = "n", axes = FALSE, frame.plot = TRUE, ylab = "", main = "example(Japanese)", xlab = "using Hershey fonts")
par(cex = 3)
Vf <- c("serif", "plain")
text(4, 2, "\#J244b\#J245b\#J2473", vfont = Vf)
text(4, 4, "\#J2538\#J2563\#J2573", vfont = Vf)
text(4, 6, "\#J467c\#J4b5c", vfont = Vf)
text(4, 8, "Japan", vfont = Vf)
par(cex = 1)
text(8, 2, "Hiragana")
text(8, 4, "Katakana")
text(8, 6, "Kanji")
text(8, 8, "English")
```
make.rgb  

Create colour spaces

Description

These functions specify colour spaces for use in `convertColor`.

Usage

```r
make.rgb(red, green, blue, name = NULL, white = "D65",
gamma = 2.2)
```

```r
colorConverter(toXYZ, fromXYZ, name, white = NULL, vectorized = FALSE)
```

Arguments

- `red`, `green`, `blue`: Chromaticity (xy or xyY) of RGB primaries
- `name`: Name for the colour space
- `white`: Character string specifying the reference white (see ‘Details’.)
- `gamma`: Display gamma (nonlinearity). A positive number or the string "sRGB"
- `fromXYZ`: Function to convert from XYZ tristimulus coordinates to this space
- `toXYZ`: Function to convert from this space to XYZ tristimulus coordinates.
- `vectorized`: Whether `fromXYZ` and `toXYZ` are vectorized internally to handle input color matrices.

Details

An RGB colour space is defined by the chromaticities of the red, green and blue primaries. These are given as vectors of length 2 or 3 in xyY coordinates (the Y component is not used and may be omitted). The chromaticities are defined relative to a reference white, which must be one of the CIE standard illuminants: "A", "B", "C", "D50", "D55", "D60", "E" (usually "D65").

The display gamma is most commonly 2.2, though 1.8 is used for Apple RGB. The sRGB standard specifies a more complicated function that is close to a gamma of 2.2; `gamma = "sRGB"` uses this function.

Colour spaces other than RGB can be specified directly by giving conversions to and from XYZ tristimulus coordinates. The functions should take two arguments. The first is a vector giving the coordinates for one colour. The second argument is the reference white. If a specific reference white is included in the definition of the colour space (as for the RGB spaces) this second argument should be ignored and may be `...`.

As of R 3.6.0 the built in color converters along with `convertColor` were vectorized to process three column color matrices in one call, instead of row by row via `apply`. In order to maintain backwards compatibility, `colorConverter` wraps `fromXYZ` and `toXYZ` in a `apply` loop in case they do not also support matrix inputs. If the `fromXYZ` and `toXYZ` functions you are using operate correctly on the whole color matrix at once instead of row by row, you can set `vectorized=TRUE` for a performance improvement.

Value

An object of class `colorConverter`
References


See Also

convertColor

Examples

```r
(pal <- make.rgb(red = c(0.6400, 0.3300),
green = c(0.2900, 0.6000),
blue = c(0.1500, 0.0600),
name = "PAL/SECAM RGB"))

## converter for sRGB in #rrggbb format
hexcolor <- colorConverter(toXYZ = function(hex, ...) {
  rgb <- t(col2rgb(hex))/255
  colorspace$sRGB$toXYZ(rgb, ...),
fromXYZ = function(xyz, ...) {
  rgb <- colorspace$sRGB$fromXYZ(xyz, ...)
  rgb <- round(rgb, 5)
  if (min(rgb) < 0 || max(rgb) > 1)
    as.character(NA)
  else rgb(rgb[1], rgb[2], rgb[3]),
white = "D65", name = "#rrggbb")

(cols <- t(col2rgb(palette())))
zapsmall(luv <- convertColor(cols, from = "sRGB", to = "Luv", scale.in = 255))
(hex <- convertColor(luv, from = "Luv", to = hexcolor, scale.out = NULL))

## must make hex a matrix before using it
(cc <- round(convertColor(as.matrix(hex), from = hexcolor, to = "sRGB", scale.in = NULL, scale.out = 255)))
stopifnot(cc == cols)

## Internally vectorized version of hexcolor, notice the use
## of `vectorized = TRUE`:
hexcolorv <- colorConverter(toXYZ = function(hex, ...) {
  rgb <- t(col2rgb(hex))/255
  colorspace$sRGB$toXYZ(rgb, ...),
fromXYZ = function(xyz, ...) {
  rgb <- colorspace$sRGB$fromXYZ(xyz, ...)
  rgb <- round(rgb, 5)
  oob <- pmin(rgb[,1],rgb[,2],rgb[,3]) < 0 | pmax(rgb[,1],rgb[,2],rgb[,3]) > 0
  res <- rep(NA_character_, nrow(rgb))
  res[!oob] <- rgb(rgb[!oob,,drop=FALSE]),
white = "D65", name = "#rrggbb",
vectorized=TRUE)
(ccv <- round(convertColor(as.matrix(hex), from = hexcolor, to = "sRGB", scale.in = NULL, scale.out = 255)))
stopifnot(ccv == cols)
```
**msgWindow**  
*Manipulate a Window*

**Description**

msgWindow sends a message to manipulate the specified screen device’s window. With argument `which = -1` it applies to the GUI console (which only accepts the first three actions).

**Usage**

```r
msgWindow(type = c("minimize", "restore", "maximize",  
    "hide", "recordOn", "recordOff"),  
    which = dev.cur())
```

**Arguments**

- `type` action to be taken.
- `which` a device number, or -1.

**See Also**

bringToTop, windows

---

**n2mfrow**  
*Compute Default 'mfrow' From Number of Plots*

**Description**

Easy setup for plotting multiple figures (in a rectangular layout) on one page. This computes a sensible default for `par(mfrow)`.

**Usage**

```r
n2mfrow(nr.plots, asp = 1)
```

**Arguments**

- `nr.plots` integer; the number of plot figures you’ll want to draw.
- `asp` positive number; the target aspect ratio (columns / rows) in the output. Was implicitly hardwired to 1; because of that and back compatibility, there is a somewhat discontinuous behavior when varying asp around 1, for `nr.plots <= 12`.

**Value**

A length-two integer vector (`nr`, `nc`) giving the positive number of rows and columns, fulfilling `nr * nc >= nr.plots`, and currently, for `asp = 1`, `nr >= nc >= 1`. 
Conceptually, this is a quadratic integer optimization problem, with inequality constraints \( nr \geq 1 \), \( nc \geq 1 \), and \( nr \cdot plots \geq nr \cdot nc \) (and possibly \( nr \geq asp \cdot nc \)), and two objective functions which would have to be combined via a tuning weight, say \( w \), to, e.g., \( (nr \cdot plots - nr \cdot nc) + w|nr/nc - asp| \).

The current algorithm is simple and not trying to solve one of these optimization problems.

**Author(s)**

Martin Maechler; suggestion of \( asp \) by Michael Chirico.

**See Also**

par, layout.

**Examples**

```r
require(graphics)

n2mfrow(8) # 3 x 3

n <- 5 ; x <- seq(-2, 2, length.out = 51)
## suppose now that 'n' is not known (inside function)
op <- par(mfrow = n2mfrow(n))
for (j in 1:n)
  plot(x, x^j, main = substitute(x^ exp, list(exp = j)), type = "l",
    col = "blue")

sapply(1:14, n2mfrow)
sapply(1:14, n2mfrow, asp=16/9)
```

---

**nclass**  
**Compute the Number of Classes for a Histogram**

**Description**

Compute the number of classes for a histogram, notably `hist()`.

**Usage**

```r
nclass.Sturges(x)
nclass.scott(x)
nclass.FD(x, digits = 5)
```

**Arguments**

- `x` a data vector.
- `digits` number of *significant* digits to keep when rounding \( x \) before the IQR computation; see ‘Details’ below.
**Details**

`nclass.Sturges` uses Sturges' formula, implicitly basing bin sizes on the range of the data.

`nclass.scott` uses Scott's choice for a normal distribution based on the estimate of the standard error, unless that is zero where it returns 1.

`nclass.FD` uses the Freedman-Diaconis choice based on the inter-quartile range \( \text{IQR}(\text{signif}(x, \text{digits})) \) unless that's zero where it uses increasingly more extreme symmetric quantiles up to \( (1,511)/512 \) and if that difference is still zero, reverts to using Scott's choice. The default of \( \text{digits} = 5 \) was chosen after a few experiments, but may be too low for some situations, see PR#17274.

**Value**

The suggested number of classes.

**References**


**See Also**

`hist` and `truehist` (package `MASS`); `dpih` (package `KernSmooth`) for a plugin bandwidth proposed by Wand(1995).

**Examples**

```r
set.seed(1)
x <- stats::rnorm(1111)
nclass.Sturges(x)

## Compare them:
NC <- function(x) c(Sturges = nclass.Sturges(x),
                      Scott = nclass.scott(x), FD = nclass.FD(x))
NC(x)
onePt <- rep(1, 11)
NC(onePt) # no longer gives NaN
```
palette  

Set or View the Graphics Palette

Description
View or manipulate the color palette which is used when col= has a numeric index and supporting functions.

Usage
```r
palette(value)
palette.pals()
palette.colors(n = NULL, palette = "Okabe-Ito", alpha, recycle = FALSE)
```

Arguments
- **value**: an optional character vector specifying a new palette (see Details).
- **n**: the number of colors to select from a palette. The default `NULL` selects all colors of the given palette.
- **palette**: a valid palette name (one of `palette.pals()`). The name is matched to the list of available palettes, ignoring upper vs. lower case, spaces, dashes, etc. in the matching.
- **alpha**: an alpha-transparency level in the range [0,1] (0 means transparent and 1 means opaque).
- **recycle**: logical indicating what happens in case `n > length(palette(.))`. By default (`recycle = FALSE`), the result is as for `n = NULL`, but with a warning.

Details
The `palette()` function gets or sets the current palette, the `palette.pals()` function lists the available predefined palettes, and the `palette.colors()` function selects colors from the predefined palettes.

The color palette and referring to colors by number (see e.g. `par`) was provided for compatibility with S. R extends and improves on the available set of palettes.

If `value` has length 1, it is taken to be the name of a built-in color palette. The available palette names are returned by `palette.pals()`. It is also possible to specify "default".

If `value` has length greater than 1 it is assumed to contain a description of the colors which are to make up the new palette. The maximum size for a palette is 1024 entries.

If `value` is omitted, no change is made to the current palette.

There is only one palette setting for all devices in an R session. If the palette is changed, the new palette applies to all subsequent plotting.

The current palette also applies to re-plotting (for example if an on-screen device is resized or `dev.copy` or `replayPlot` is used). The palette is recorded on the displaylist at the start of each page and when it is changed.
Value

`palette()` returns a character vector giving the colors from the palette which was in effect. This is invisible unless the argument is omitted.

`palette.pals()` returns a character vector giving the names of predefined palettes.

`palette.colors()` returns a vector of R colors.

See Also

`colors` for the vector of built-in named colors; `hsv`, `gray`, `hcl.colors`, ... to construct colors.

`adjustcolor`, e.g., for tweaking existing palettes; `colorRamp` to interpolate colors, making custom palettes; `col2rgb` for translating colors to RGB 3-vectors.

Examples

```r
require(graphics)
palette()  # obtain the current palette
palette("R3"); palette()  # old default palette
palette("ggplot2")  # ggplot2-style palette
palette()

palette(hcl.colors(8, "viridis"))

(palettedata(gray(seq(0, .9,length.out = 25))))  # gray scales; print old palette
matplot(outer(1:100, 1:30), type = "l", lty = 1, lwd = 2, col = 1:30,
        main = "Gray Scales Palette",
        sub = "palette(gray(seq(0, .9, len=25)))")
palette("default")  # reset back to the default

## on a device where alpha transparency is supported,
## use 'alpha = 0.3' transparency with the default palette :
mycols <- adjustcolor(palette(), alpha.f = 0.3)
opal <- palette(mycols)
x <- rnorm(1000); xy <- cbind(x, 3*x + rnorm(1000))
plot (xy, lwd = 2,
      main = "Alpha-Transparency Palette\nalpha = 0.3")
xy[,1] <- -xy[,1]
points(xy, col = 8, pch = 16, cex = 1.5)
palette("default")

## List available built-in palettes
palette.pals()

## Demonstrate the colors 1:8 in different palettes using a custom matplot()
sinplot <- function(main=NULL) {
  x <- outer(
    seq(-pi, pi, length.out = 50),
    seq(0, pi, length.out = 8),
    function(x, y) sin(x - y)
  )
  matplot(x, type = "l", lwd = 4, lty = 1, col = 1:8, ylab = "", main=main)
}
sinplot("default palette")
palette("R3"); sinplot("R3")
```
Palettes

palette("Okabe-Ito"); sinplot("Okabe-Ito")
palette("Tableau"); sinplot("Tableau")
palette("default") # reset

## color swatches for palette.colors()
palette.swatch <- function(palette = palette.pals(), n = 8, nrow = 8,
                          border = "black", cex = 1, ...)
  {
    cols <- sapply(palette, palette.colors, n = n, recycle = TRUE)
    ncol <- ncol(cols)
    nswatch <- min(ncol, nrow)
    op <- par(mar = rep(0.1, 4),
             mfrow = c(1, min(5, ceiling(ncol/nrow))),
             cex = cex, ...)
    on.exit(par(op))
    while (length(palette)) {
      subset <- seq_len(min(nrow, ncol(cols)))
      plot.new()
      plot.window(c(0, n), c(0.25, nrow + 0.25))
      y <- rev(subset)
      text(0, y + 0.1, palette[subset], adj = c(0, 0))
      y <- rep(y, each = n)
      rect(rep(0:(n-1), n), y, rep(1:n, n), y - 0.5,
           col = cols[, subset], border = border)
      palette <- palette[-subset]
      cols <- cols[, -subset, drop = FALSE]
    }
  }
palette.swatch()
palette.swatch(n = 26) # show full "Alphabet"; recycle most others

Palettes

<table>
<thead>
<tr>
<th>Color Palettes</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Create a vector of n contiguous colors.</td>
</tr>
</tbody>
</table>

Usage

hcl.colors(n, palette = "viridis", alpha = NULL, rev = FALSE, fixup = TRUE)
hcl.pals(type = NULL)

rainbow(n, s = 1, v = 1, start = 0, end = max(1, n - 1)/n,
        alpha, rev = FALSE)
heat.colors(n, alpha, rev = FALSE)
terrain.colors(n, alpha, rev = FALSE)
topo.colors(n, alpha, rev = FALSE)
cm.colors(n, alpha, rev = FALSE)
Arguments

n             the number of colors (≥ 1) to be in the palette.
palette       a valid palette name (one of hcl.pals()). The name is matched to the list of
              available palettes, ignoring upper vs. lower case, spaces, dashes, etc. in the
              matching.
alpha         an alpha-transparency level in the range [0,1] (0 means transparent and 1 means
              opaque), see argument alpha in hsv and hcl, respectively.
              A missing, i.e., not explicitly specified alpha is equivalent to alpha = NULL,
              which does not add opacity codes (“FF”) to the individual color hex codes.
rev           logical indicating whether the ordering of the colors should be reversed.
fixup         logical indicating whether the resulting color should be corrected to RGB coordi-
              nates in [0,1], see hcl.
type          the type of palettes to list: “qualitative”, “sequential”, “diverging”, or
              “divergingx”. NULL lists all palettes.
s, v          the ‘saturation’ and ‘value’ to be used to complete the HSV color descriptions.
start         the (corrected) hue in [0,1] at which the rainbow begins.
end           the (corrected) hue in [0,1] at which the rainbow ends.

Details

All of these functions (except the helper function hcl.pals) create a vector of n contiguous colors,
either based on the HSV color space (rainbow, heat, terrain, topography, and cyan-magenta colors)
or the perceptually-based HCL color space.

HSV (hue-saturation-value) is a simple transformation of the RGB (red-green-blue) space which
was therefore a convenient choice for color palettes in many software systems (see also hsv).
However, HSV colors capture the perceptual properties hue, colorfulness/saturation/chroma, and
lightness/brightness/luminance/value only poorly and consequently the corresponding palettes are
typically not a good choice for statistical graphics and data visualization.

In contrast, HCL (hue-chroma-luminance) colors are much more suitable for capturing human color
perception (see also hcl) and better color palettes can be derived based on HCL coordinates. Con-
ceptually, three types of palettes are often distinguished:

• Qualitative: For coding categorical information, i.e., where no particular ordering of cate-
gories is available and every color should receive the same perceptual weight.
• Sequential: For coding ordered/numeric information, i.e., where colors go from high to low
  (or vice versa).
• Diverging: Designed for coding numeric information around a central neutral value, i.e.,
  where colors diverge from neutral to two extremes.

The hcl.colors function provides a basic and lean implementation of the pre-specified palettes
in the colorspace package. In addition to the types above, the functions distinguish “diverging”
palettes where the two arms are restricted to be rather balanced as opposed to flexible “divergingx”
palettes that combine two sequential palettes without any restrictions. The latter group also includes
the cividis palette as it is based on two different hues (blue and yellow) but it is actually a sequential
palette (going from dark to light).

The names of all available HCL palettes can be queried with the hcl.pals function and they are also
visualized by color swatches in the examples. Many of the palettes closely approximate palettes of
the same name from various other packages (including RColorBrewer, rcartocolor, viridis, scico,
among others).
The default HCL palette is the widely used viridis palette which is a sequential palette with relatively high chroma throughout so that it also works reasonably well as a qualitative palette. However, while viridis is a rather robust default palette, more suitable HCL palettes are available for most visualizations.

For example, "Dark 3" works well for shading points or lines in up to five groups, "YlGnBu" is a sequential palette similar to "viridis" but with aligned chroma/luminance, and "Green-Brown" or "Blue-Red 3" are colorblind-safe diverging palettes.

Further qualitative palettes are provided in the palette.colors function. While the qualitative palettes in hcl.colors are always based on the same combination of chroma and luminance, the palette.colors vary in chroma and luminance up to a certain degree. The advantage of fixing chroma/luminance is that the perceptual weight of the resulting colors is more balanced. The advantage of allowing variation is that more distinguishable colors can be obtained, especially for viewers with color vision deficiencies.

Note that the rainbow function implements the (in-)famous rainbow (or jet) color palette that was used very frequently in many software packages but has been widely criticized for its many perceptual problems. It is specified by a start and end hue with red = 0, yellow = \frac{1}{6}, green = \frac{2}{6}, cyan = \frac{3}{6}, blue = \frac{4}{6}, and magenta = \frac{5}{6}. However, these are very flashy and unbalanced with respect to both chroma and luminance which can lead to various optical illusions. Also, the hues that are equispaced in RGB space tend to cluster at the red, green, and blue primaries. Therefore, it is recommended to use a suitable palette from hcl.colors instead of rainbow.

Value

A character vector cv containing either palette names (for hcl.pals) or n hex color codes (for all other functions). The latter can be used either to create a user-defined color palette for subsequent graphics by palette(cv), a col = specification in graphics functions or in par.

References


See Also
colors, palette, gray.colors, hsv, hcl, rgb, gray and col2rgb for translating to RGB numbers.

Examples

require("graphics")

# color wheels in RGB/HSV and HCL space
par(mfrow = c(2, 2))


Palettes

```r
pie(rep(1, 12), col = rainbow(12), main = "RGB/HSV")
pie(rep(1, 12), col = hcl.colors(12, "Set 2"), main = "HCL")
par(mfrow = c(1, 1))

## color swatches for RGB/HSV palettes
demo.pal <-
    function(n, border = if (n < 32) "light gray" else NA,
             main = paste("color palettes; n=", n),
             ch.col = c("rainbow(n, start=.7, end=.1)", "heat.colors(n)",
                        "terrain.colors(n)", "topo.colors(n)",
                        "cm.colors(n)")) {
    nt <- length(ch.col)
i <- 1:n; j <- n / nt; d <- j/6; dy <- 2*d
    plot(i, i+d, type = "n", yaxt = "n", ylab = ", main = main)
    for (k in 1:nt) {
        rect(i-.5, (k-1)*j+ dy, i+.4, k*j,
             col = eval(str2lang(ch.col[k])), border = border)
        text(2*j, k * j + dy/4, ch.col[k])
    }
    demo.pal(16)

## color swatches for HCL palettes
hcl.swatch <- function(type = NULL, n = 5, nrow = 11,
                        border = if (n < 15) "black" else NA) {
    palette <- hcl.pals(type)
    cols <- sapply(palette, hcl.colors, n = n)
    ncol <- ncol(cols)
    nswatch <- min(ncol, nrow)
    par(mar = rep(0.1, 4),
         mfrow = c(1, min(5, ceiling(ncol/nrow))),
         pin = c(1, 0.5 * nswatch),
         cex = 0.7)
    while (length(palette)) {
        subset <- 1:min(nrow, ncol(cols))
        plot.new()
        plot.window(c(0, n), c(0, nrow + 1))
        text(0, rev(subset) + 0.1, palette[subset], adj = c(0, 0))
        y <- rep(subset, each = n)
        rect(rep(0:(n-1), n), rev(y), rep(1:n, n), rev(y) - 0.5,
             col = cols[, subset], border = border)
        palette <- palette[-subset]
        cols <- cols[, -subset, drop = FALSE]
    }
    par(mfrow = c(1, 1), mar = c(5.1, 4.1, 4.1, 2.1), cex = 1)
}
hcl.swatch()
hcl.swatch("qualitative")
hcl.swatch("sequential")
hcl.swatch("diverging")
hcl.swatch("divergingx")

## heat maps with sequential HCL palette (purple)
```
image(volcano, col = hcl.colors(11, "purples", rev = TRUE))
filled.contour(volcano, nlevels = 10,
    color.palette = function(n, ...)
    hcl.colors(n, "purples", rev = TRUE, ...))

## list available HCL color palettes
hcl.pals("qualitative")
hcl.pals("sequential")
hcl.pals("diverging")
hcl.pals("divergingx")

---

pdf

**PDF Graphics Device**

### Description

`pdf` starts the graphics device driver for producing PDF graphics.

### Usage

```r
df(file = if(onefile) "Rplots.pdf" else "Rplot%03d.pdf",
    width, height, onefile, family, title, fonts, version,
    paper, encoding, bg, fg, pointsize, pagecentre, colormodel,
    useDingbats, useKerning, fillOddEven, compress)
```

### Arguments

- **file**
  - A character string giving the file path. If it is of the form "|cmd", the output is piped to the command given by cmd. If it is NULL, then no external file is created (effectively, no drawing occurs), but the device may still be queried (e.g., for size of text).
  - For use with `onefile = FALSE` give a C integer format such as "Rplot%03d.pdf" (the default in that case). (See `postscript` for further details.)
  - Tilde expansion (see `path.expand`) is done. An input with a marked encoding is converted to the native encoding or an error is given.

- **width, height**
  - The width and height of the graphics region in inches. The default values are 7.

- **onefile**
  - Logical: if true (the default) allow multiple figures in one file. If false, generate a file with name containing the page number for each page. Defaults to TRUE, and forced to true if file is a pipe.

- **family**
  - The font family to be used, see `postscript`. Defaults to "Helvetica".

- **title**
  - Title string to embed as the ‘/Title’ field in the file. Defaults to "R Graphics Output".

- **fonts**
  - A character vector specifying R graphics font family names for additional fonts which will be included in the PDF file. Defaults to NULL.

- **version**
  - A string describing the PDF version that will be required to view the output. This is a minimum, and will be increased (with a warning) if necessary. Defaults to "1.4", but see ‘Details’.
All arguments except `file` default to values given by `pdf.options()`. The ultimate defaults are quoted in the arguments section.

`pdf()` opens the file `file` and the PDF commands needed to plot any graphics requested are sent to that file.

The `file` argument is interpreted as a C integer format as used by `sprintf`, with integer argument the page number. The default gives files `’Rplot001.pdf’`, `’Rplot999.pdf’`, `’Rplot1000.pdf’`, `’Rplot1001.pdf’`, ... .

The `family` argument can be used to specify a PDF-specific font family as the initial/default font for the device. If additional font families are to be used they should be included in the `fonts` argument.

If a device-independent R graphics font family is specified (e.g., via `par(family = )` in the graphics package), the PDF device makes use of the PostScript font mappings to convert the R graphics font family to a PDF-specific font family description. (See the documentation for `pdfFonts`.)

This device does not embed fonts in the PDF file, so it is only straightforward to use mappings to the font families that can be assumed to be available in any PDF viewer: "Times" (equivalently
"serif"), "Helvetica" (equivalently "sans") and "Courier" (equivalently "mono"). Other families may be specified, but it is the user’s responsibility to ensure that these fonts are available on the system and third-party software (e.g., Ghostscript) may be required to embed fonts so that the PDF can be included in other documents (e.g., LaTeX): see embedFonts. The URW-based families described for postscript can be used with viewers, platform dependently:

**on Unix-alikes** viewers set up to use URW fonts, which is usual with those based on xpdf or Ghostscript.

**on Windows** viewers such as GSView which utilise URW fonts.

Since embedFonts makes use of Ghostscript, it should be able to embed the URW-based families for use with other viewers.

See postscript for details of encodings, as the internal code is shared between the drivers. The native PDF encoding is given in file ’PDFDoc.enc’.

The PDF produced is fairly simple, with each page being represented as a single stream (by default compressed and possibly with references to raster images). The R graphics model does not distinguish graphics objects at the level of the driver interface.

The version argument declares the version of PDF that gets produced. The version must be at least 1.2 when compression is used, 1.4 for semi-transparent output to be understood, and at least 1.3 if CID fonts are to be used: if any of these features are used the version number will be increased (with a warning). (PDF 1.4 was first supported by Acrobat 5 in 2001; it is very unlikely not to be supported in a current viewer.)

Line widths as controlled by par(lwd = ) are in multiples of 1/96 inch. Multiples less than 1 are allowed. pch = "." with cex = 1 corresponds to a square of side 1/72 inch, which is also the ‘pixel’ size assumed for graphics parameters such as "cra".

The paper argument sets the ‘/MediaBox’ entry in the file, which defaults to width by height. If it is set to something other than “special”, a device region of the specified size is (by default) centred on the rectangle given by the paper size: if either width or height is less than 0.1 or too large to give a total margin of 0.5 inch, it is reset to the corresponding paper dimension minus 0.5. Thus if you want the default behaviour of postscript use pdf(paper = "a4r", width = 0, height = 0) to centre the device region on a landscape A4 page with 0.25 inch margins.

When the background colour is fully transparent (as is the initial default value), the PDF produced does not paint the background. Most PDF viewers will use a white canvas so the visual effect is if the background were white. This will not be the case when printing onto coloured paper, though.

**Color models**

The default color model ("srgb") is sRGB. Model "gray" (or "grey") maps sRGB colors to greyscale using perceived luminosity (biased towards green). "cmyk" outputs in CMYK colorspace. The simplest possible conversion from sRGB to CMYK is used (https://en.wikipedia.org/wiki/CMYK_color_model#Mapping_RGB_to_CMYK), and raster images are output in RGB.

Also available for backwards compatibility is model "rgb" which uses uncalibrated RGB and corresponds to the model used with that name in R prior to 2.13.0. Some viewers may render some plots in that colorspace faster than in sRGB, and the plot files will be smaller.

**Conventions**

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

- The default device size is 7 inches square.
• Font sizes are in big points.
• The default font family is Helvetica.
• Line widths are as a multiple of 1/96 inch, with a minimum of 0.01 enforced.
• Circles of any radius are allowed. If `useDingbats = TRUE`, opaque circles of less than 10 big points radius are rendered using char 108 in the Dingbats font: all semi-transparent and larger circles using a Bézier curve for each quadrant.
• Colours are by default specified as sRGB.

At very small line widths, the line type may be forced to solid.

**Printing**

Except on Windows it is possible to print directly from pdf by something like (this is appropriate for a CUPS printing system):

```r
df("\|lp -o landscape", paper = "a4r")
```

This forces `onfile = TRUE`.

**Note**

If you have drawn any typeset glyphs (see `glyphInfo`) then it is highly recommended that you use `embedGlyphs` to embed the relevant fonts.

**Note**

If you see problems with PDF output, do remember that the problem is much more likely to be in your viewer than in R. Try another viewer if possible. Symptoms for which the viewer has been at fault are apparent grids on image plots (turn off graphics anti-aliasing in your viewer if you can) and missing or incorrect glyphs in text (viewers silently doing font substitution).

Unfortunately the default viewers on most Linux and macOS systems have these problems, and no obvious way to turn off graphics anti-aliasing.

Acrobat Reader does not use the fonts specified but rather emulates them from multiple-master fonts. This can be seen in imprecise centering of characters, for example the multiply and divide signs in Helvetica. This can be circumvented by embedding fonts where possible. Most other viewers substitute fonts, e.g. URW fonts for the standard Helvetica and Times fonts, and these too often have different font metrics from the true fonts.

Acrobat Reader can be extended by ‘font packs’, and these will be needed for the full use of encodings other than Latin-1 (although they may be offered for download as needed).

**On some Unix-alike systems:** If `useDingbats = TRUE`, the default plotting character `pch = 1` was displayed in some PDF viewers incorrectly as a "q" character. (These seem to be viewers based on the ‘poppler’ PDF rendering library). This may be due to incorrect or incomplete mapping of font names to those used by the system. Adding the following lines to `~/.fonts.conf` or `/etc/fonts/local.conf` may circumvent this problem, although this has largely been corrected on the affected systems.

```xml
<fontconfig>
  <alias binding="same">
    <family>ZapfDingbats</family>
    <accept><family>Dingbats</family></accept>
  </alias>
</fontconfig>
```
Some further workarounds for problems with symbol fonts on viewers using ‘fontconfig’ are given in the ‘Cairo Fonts’ section of the help for X11.

On Windows: The TeXworks PDF viewer was one of those which has been seen to fail to display Dingbats (used by e.g. pch = 1) correctly. Whereas on other platforms the problems seen were incorrect output, on Windows points were silently omitted: however recent versions seem to manage to display Dingbats.

There was a different font bug in the pdf.js viewer included in Firefox: that mapped Dingbats to the Symbol font and so displayed symbols such pch = 1 as lambda.

See Also

pdfFonts, pdf.options, embedFonts, glyphInfo, Devices, postscript.
ciairo_pdf and (on macOS only) quartz for other devices that can produce PDF.

More details of font families and encodings and especially handling text in a non-Latin-1 encoding and embedding fonts can be found in


Examples

## Test function for encodings

```r
TestChars <- function(encoding = "ISOLatin1", ...) {
  pdf(encoding = encoding, ...)
  par(pty = "s")
  plot(c(-1,16), c(-1,16), type = "n", xlab = "", ylab = "",
       xaxs = "i", yaxs = "i")
  title(paste("Centred chars in encoding", encoding))
  grid(17, 17, lty = 1)
  for(i in c(32:255)) {
    x <- i %% 16
    y <- i %/% 16
    points(x, y, pch = i)
  }
  dev.off()
}
## there will be many warnings.
TestChars("ISOLatin2")
## this does not view properly in older viewers.
TestChars("ISOLatin2", family = "URWHelvetica")
## works well for viewing in gs-based viewers, and often in xpdf.
```

pdf.options

Auxiliary Function to Set/View Defaults for Arguments of pdf

Description

The auxiliary function pdf.options can be used to set or view (if called without arguments) the default values for some of the arguments to pdf.

pdf.options needs to be called before calling pdf, and the default values it sets can be overridden by supplying arguments to pdf.
Usage

```r
df.options(..., reset = FALSE)
```

Arguments

... arguments width, height, onefile, family, title, fonts, paper, encoding, pointsize, bg, fg, pagecentre, useDingbats, colormodel, fillOddEven and compress can be supplied.

reset logical: should the defaults be reset to their ‘factory-fresh’ values?

Details

If both reset = TRUE and ... are supplied the defaults are first reset to the ‘factory-fresh’ values and then the new values are applied.

Value

A named list of all the defaults. If any arguments are supplied the return values are the old values and the result has the visibility flag turned off.

See Also

pdf, ps.options.

Examples

```r
df.options(bg = "pink")
utils::str(df.options())
df.options(reset = TRUE) # back to factory-fresh
```

---

**pictex**

*A PiTeX Graphics Driver*

Description

This function produces simple graphics suitable for inclusion in TeX and LaTeX documents. It dates from the very early days of R and is for historical interest only.

Usage

```r
pictex(file = "Rplots.tex", width = 5, height = 4, debug = FALSE,
bg = "white", fg = "black")
```

Arguments

```r
file the file path where output will appear. Tilde expansion (see `path.expand`) is done. An input with a marked encoding is converted to the native encoding or an error is given.
width The width of the plot in inches.
height the height of the plot in inches.
debug should debugging information be printed.
bg the background color for the plot. Ignored.
fg the foreground color for the plot. Ignored.
```
**Details**

This driver is much more basic than the other graphics drivers included in R. It does not have any font metric information, so the use of `plotmath` is not supported.

Line widths are ignored except when setting the spacing of line textures. `pch = "."` corresponds to a square of side 1pt.

This device does not support colour (nor does the PicTeX package), and all colour settings are ignored.

Note that text is recorded in the file as-is, so annotations involving TeX special characters (such as `&` and `_{`) need to be quoted as they would be when entering TeX.

Multiple plots will be placed as separate environments in the output file.

**Conventions**

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

- The default device size is 5 inches by 4 inches.
- There is no `pointsize` argument: the default size is interpreted as 10 point.
- The only font family is `cmss10`.
- Line widths are only used when setting the spacing on line textures.
- Circle of any radius are allowed.
- Colour is not supported.

**Author(s)**

This driver was provided around 1996–7 by Valerio Aimale of the Department of Internal Medicine, University of Genoa, Italy.

**References**


**See Also**

`postscript`, `pdf`, `Devices`.

The `tikzDevice` in the CRAN package of that name for more modern TeX-based graphics ([https://pgf.sourceforge.net/](https://pgf.sourceforge.net/), although including PDF figures *via* `pdflatex` is most common in (La)TeX documents).

**Examples**

```r
require(graphics)
pictex()
plot(1:11, (-5:5)^2, type = "b", main = "Simple Example Plot")
dev.off()
```
plotmath

Mathematical Annotation in R

Description

If the text argument to one of the text-drawing functions (text, mtext, axis, legend) in R is an expression, the argument is interpreted as a mathematical expression and the output will be formatted according to TeX-like rules. Expressions can also be used for titles, subtitles and x- and y-axis labels (but not for axis labels on persp plots).

In most cases other language objects (names and calls, including formulas) are coerced to expressions and so can also be used.

Details

A mathematical expression must obey the normal rules of syntax for any R expression, but it is interpreted according to very different rules than for normal R expressions.

It is possible to produce many different mathematical symbols, generate sub- or superscripts, produce fractions, etc.

The output from demo(plotmath) includes several tables which show the available features. In these tables, the columns of grey text show sample R expressions, and the columns of black text show the resulting output.

The available features are also described in the tables below:

<table>
<thead>
<tr>
<th>Syntax</th>
<th>Meaning</th>
</tr>
</thead>
<tbody>
<tr>
<td>x + y</td>
<td>x plus y</td>
</tr>
<tr>
<td>x - y</td>
<td>x minus y</td>
</tr>
<tr>
<td>x*y</td>
<td>juxtapose x and y</td>
</tr>
<tr>
<td>x/y</td>
<td>x forwardslash y</td>
</tr>
<tr>
<td>x %+-% y</td>
<td>x plus or minus y</td>
</tr>
<tr>
<td>x %/% y</td>
<td>x divided by y</td>
</tr>
<tr>
<td>x %% y</td>
<td>x times y</td>
</tr>
</tbody>
</table>
x %.% y
x[i]
x^2
paste(x, y, z)
sqrt(x)
sqrt(x, y)
x == y
x != y
x < y
x <= y
x > y
x >= y
!x
x %~~% y
x %=~% y
x %==% y
x %prop% y
plain(x)
bold(x)
bolditalic(x)
symbol(x)
list(x, y, z)
...
cdots
ldots
x %subset% y
x %subseteq% y
x %notsubset% y
x %supset% y
x %supseteq% y
x %in% y
x %notin% y
hat(x)
tilde(x)
dot(x)
ring(x)
bar(xy)
widehat(xy)
widetilde(xy)
x %<->% y
x %->% y
x %<% y
x %up% y
x %down% y
x %<=% y
x %=>% y
x %<=% y
x %dblup% y
x %dbldown% y
alpha – omega

x cdot y
x subscript i
x superscript 2
juxtapose x, y, and z
square root of x
yth root of x
x equals y
x is not equal to y
x is less than y
x is less than or equal to y
x is greater than y
x is greater than or equal to y
not x
x is approximately equal to y
x and y are congruent
x is defined as y
x is proportional to y
x is distributed as y
draw x in normal font
draw x in bold font
draw x in italic font
draw x in bolditalic font
draw x in symbol font
comma-separated list
ellipsis (height varies)
ellipsis (vertically centred)
ellipsis (at baseline)
x is a proper subset of y
x is a subset of y
x is not a subset of y
x is a proper superset of y
x is a superset of y
x is an element of y
x is not an element of y
x with a circumflex
x with a tilde
x with a dot
x with a ring
xy with bar
xy with a wide circumflex
xy with a wide tilde
x double-arrow y
x right-arrow y
x left-arrow y
x up-arrow y
x down-arrow y
x is equivalent to y
x implies y
y implies x
x double-up-arrow y
x double-down-arrow y
Greek symbols
Alpha – Omega  
theta, phi, sigma, omega  
Upsilon
aleph
infinity
partial differential symbol
nabla
32*degree
60*minute
30*second
displaystyle(x)
textstyle(x)
scriptstyle(x)
scriptscriptstyle(x)
underline(x)
\( x + \phantom{0} + y \)
\( x + \over(1, \phantom{0}) \)
frac(x, y)
over(x, y)
\( \text{atop}(x, y) \)
\( \text{sum}(x[i], i==1, n) \)
\( \text{prod}(\text{plain}(P)(X=x), x) \)
\( \text{integral}(f(x)dx, a, b) \)
union(A[i], i==1, n)
intersect(A[i], i==1, n)
\( \lim(f(x), x %->% 0) \)
\( \min(g(x), x > 0) \)
inf(S)
sup(S)
x^y + z
x^(y + z)
group("",list(a, b),"]")
bgroupl("",\text{atop}(x,y),"]")
group(lceil, x, rceili)
group(lfloor, x, langle)
group(rlangeli, list(x, y), rangle)

The supported ‘scalable delimiters’ are | [ { and their right-hand versions. "." is equivalent to "": the corresponding delimiter will be omitted. Delimiter || is supported but has the same effect as |. The special delimiters lceil, lfloor, langle (and their right-hand versions) are not scalable.

Note that paste does not insert spaces when juxtaposing, unlike (by default) the R function of that name.

The symbol font uses Adobe Symbol encoding so, for example, a lower case mu can be obtained either by the special symbol \( \mu \) or by symbol("m"). This provides access to symbols that have no special symbol name, for example, the universal, or forall, symbol is symbol("\forall2"). To see what symbols are available in this way use TestChars(font=5) as given in the examples for points: some are only available on some devices.

Note to TeX users: TeX’s ‘\Upsilon’ is Upsilon1, TeX’s ‘\varepsilon’ is close to epsilon, and
there is no equivalent of TeX’s ‘\epsilon’. TeX’s ‘\varpi’ is close to omega1. vartheta, varphi and varsigma are allowed as synonyms for theta1, phi1 and sigma1.

sigma1 is also known as stigma, its Unicode name.

Control characters (e.g., ‘\n’) are not interpreted in character strings in plotmath, unlike normal plotting.

The fonts used are taken from the current font family, and so can be set by `par(family=)` in base graphics, and `gpar(fontfamily=)` in package `grid`.

Note that bold, italic and bolditalic do not apply to symbols, and hence not to the Greek symbols such as mu which are displayed in the symbol font. They also do not apply to numeric constants.

Other symbols

On many OSes and some graphics devices many other symbols are available as part of the standard text font, and all of the symbols in the Adobe Symbol encoding are in principle available via changing the font face or (see ‘Details’) plotmath: see the examples section of `points` for a function to display them. (‘In principle’ because some of the glyphs are missing from some implementations of the symbol font.) Unfortunately, `postscript` and `pdf` have support for little more than European (not Greek) and CJK characters and the Adobe Symbol encoding (and in a few fonts, also Cyrillic characters).

On Unix-alikes: In a UTF-8 locale any Unicode character can be entered, perhaps as a ‘\uxxxx’ or ‘\Uxxxxxxxx’ escape sequence, but the issue is whether the graphics device is able to display the character. The widest range of characters is likely to be available in the X11 device using cairo: see its help page for how installing additional fonts can help. This can often be used to display Greek letters in bold or italic.

In non-UTF-8 locales there is normally no support for symbols not in the languages for which the current encoding was intended.

On Windows: Any Unicode character can be entered into a text string via a ‘\uxxxx’ escape, or used by number in a call to `points`. The windows family of devices can display such characters if they are available in the font in use. This can often be used to display Greek letters in bold or italic.

A good way to both find out which characters are available in a font and to determine the Unicode number is to use the ‘Character Map’ accessory (usually on the ‘Start’ menu under ‘Accessories->System Tools’). You can also copy-and-paste characters from the ‘Character Map’ window to the Rgui console (but not to Rterm).

References


A list of the symbol codes can be found in decimal, octal and hex at https://www.stat.auckland.ac.nz/~paul/R/CM/AdobeSym.html.

See Also
demo(plotmath), axis, mtext, text, title, substitute quote, bquote
Examples

```
require(graphics)

x <- seq(-4, 4, length.out = 101)
y <- cbind(sin(x), cos(x))
matplot(x, y, type = "l", xaxt = "n",
       main = expression(paste(plain(sin) * phi, " and ",
                            plain(cos) * phi)),
       ylab = expression("sin" * phi, "cos" * phi), # only 1st is taken
xlab = expression("Phase Angle ", phi),
       col.main = "blue")
axis(1, at = c(-pi, -pi/2, 0, pi/2, pi),
     labels = expression(-pi, -pi/2, 0, pi/2, pi))
```

```
## How to combine "math" and numeric variables:
theta <- 1.23; mtext(bquote(hat(theta) == .(theta)), line = .25)
for(i in 2:9)
  text(i, i+1, substitute(list(xi, eta) == group("("),
                     list(x = i, y = i+1)))
## note that both of these use calls rather than expressions.
##
## text(1, 10, "Derivatives:", adj = 0)
text(1, 9.6, expression(" first: \( \frac{df}{dx} \) \(x\) == \( \frac{d}{dx}(f(x)) \), adj = 0)
text(1, 9, expression(" second: \( \frac{d^2f}{dx^2} \) \(x\) == \( \frac{d^2}{dx^2}(f(x)) \), adj = 0)
```

```
## note the "{ .. }") trick to get "chained" equations:
plot(1:10, type="n", main = quote(1 <= {1 < 2}))
text(4, 9, expression(hat(beta) == (X^t * X)^{-1} * X^t * y))
text(4, 8.4, expression(hat(beta) == (X^t * X)^{-1} * X^t * y),
     cex = .8)
text(4, 7, expression(bar(x) == sum(frac(x[i], n), i==1, n)))
text(4, 6.4, expression(bar(x) == sum(frac(x[i], n), i==1, n)),
     cex = .8)
text(8, 5, expression(paste(frac(1, sigma*sqrt(2*pi)), " \ ",
                      plain(e)^{frac(-(x-mu)^2, 2*sigma^2)})),
     cex = 1.2)
```

```
## some other useful symbols
plot.new(); plot.window(c(0,4), c(15,1))
text(1, 1, "universal", adj = 0); text(2.5, 1, "\042")
text(3, 1, expression(symbol("\042")))
text(1, 2, "existential", adj = 0); text(2.5, 2, "\044")
text(3, 2, expression(symbol("\044")))
text(1, 3, "suchthat", adj = 0); text(2.5, 3, "\047")
text(3, 3, expression(symbol("\047")))
text(1, 4, "therefore", adj = 0); text(2.5, 4, "\134")
text(3, 4, expression(symbol("\134")))
text(1, 5, "perpendicular", adj = 0); text(2.5, 5, "\136")
text(3, 5, expression(symbol("\136")))
text(1, 6, "circlemultiply", adj = 0); text(2.5, 6, "\304")
text(3, 6, expression(symbol("\304")))
```
BMP, JPEG, PNG and TIFF graphics devices

Description

Graphics devices for BMP, JPEG, PNG and TIFF format bitmap files.

Usage

```r
bmp(filename = "Rplot%03d.bmp",
     width = 480, height = 480, units = "px", pointsize = 12,
     bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)
```

```r
jpeg(filename = "Rplot%03d.jpeg",
     width = 480, height = 480, units = "px", pointsize = 12,
     quality = 75,
     bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)
```

```r
png(filename = "Rplot%03d.png",
     width = 480, height = 480, units = "px", pointsize = 12,
     bg = "white", res = NA, ...,
     type = c("cairo", "cairo-png", "Xlib", "quartz"), antialias)
```

```r
tiff(filename = "Rplot%03d.tiff",
     width = 480, height = 480, units = "px", pointsize = 12,
     compression = c("none", "rle", "lzw", "jpeg", "zip", "lzw+p", "zip+p"),
     bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)
```

Arguments

- **filename** is the output file path. The page number is substituted if a C integer format is included in the character string, as in the default. (Depending on the platform, the result should be less than PATH_MAX characters long, and may be truncated if not. See `postscript` for further details.) Tilde expansion is performed where supported by the platform. An input with a marked encoding is converted to the native encoding on an error is given.

- **width** is the width of the device.
height

units

can be px (pixels, the default), in (inches), cm or mm.

points

default pointsize of plotted text, interpreted as big points (1/72 inch) at res

ppi.

bg

the initial background colour: can be overridden by setting par(“bg”).

quality

the ‘quality’ of the JPEG image, as a percentage. Smaller values will give more

compression but also more degradation of the image.

compression

the type of compression to be used. Ignored for type = "quartz".

res

The nominal resolution in ppi which will be recorded in the bitmap file, if a

positive integer. Also used for units other than the default, and to convert

points to pixels.

for type = "Xlib" only, additional arguments to the underlying X11 device such

as fonts or family.

For types "cairo" and "quartz", the family argument can be supplied. See

the ‘Cairo fonts’ section in the help for X11.

For type "cairo", the symbolfamily argument can be supplied. See

X11.options.

type

character string, one of "Xlib" or "quartz" (some macOS builds) or "cairo".

The latter will only be available if the system was compiled with support

for cairo – otherwise "Xlib" will be used. The default is set by

getOption("bitmapType") – the ‘out of the box’ default is "quartz" or

"cairo" where available, otherwise "Xlib".

antialias

giving the type of anti-aliasing (if any) to be used for fonts

and lines (but not fills). See X11. The default is set by X11.options. Also for

type = "quartz", where antialiasing is used unless antialias = "none".

Details

Plots in PNG and JPEG format can easily be converted to many other bitmap formats, and both can
be displayed in modern web browsers. The PNG format is lossless and is best for line diagrams and
blocks of colour. The JPEG format is lossy, but may be useful for image plots, for example. BMP
is a standard format on Windows. TIFF is a meta-format: the default format written by tiff is
lossless and stores RGB (and alpha where appropriate) values uncompressed—such files are widely
accepted, which is their main virtue over PNG.

The JPEG format only supports opaque backgrounds.

png supports transparent backgrounds: use bg = "transparent". (Not all PNG viewers render
files with transparency correctly.) When transparency is in use in the type = "Xlib" variant a very
light grey is used as the background and so appears as transparent if used in the plot. This allows
opaque white to be used, as in the example. The type = "cairo", type = "cairo-png" and type

= "quartz" variants allow semi-transparent colours, including on a transparent or semi-transparent
background.

tiff with types "cairo" and "quartz" supports semi-transparent colours, including on a trans-
parent or semi-transparent background. Compression type "zip" is ‘deflate (Adobe-style)’. Com-
pression types "lzw+p" and "zip+p" use horizontal differencing (‘differencing predictor’, section
14 of the TIFF specification) in combination with the compression method, which is effective for
continuous-tone images, especially colour ones.

R can be compiled without support for some or all of the types for each of these devices: this
will be reported if you attempt to use them on a system where they are not supported. For type =
"X11" they may not be usable unless the X11 display is available to the owner of the R process.
type = "cairo" requires cairo 1.2 or later. type = "quartz" uses the quartz device and so is only available where that is (on some macOS builds: see capabilities("aqua")).

By default no resolution is recorded in the file, except for BMP. Viewers will often assume a nominal resolution of 72 ppi when none is recorded. As resolutions in PNG files are recorded in pixels/metre, the reported ppi value will be changed slightly.

For graphics parameters that make use of dimensions in inches (including font sizes in points) the resolution used is res (or 72 ppi if unset).

png will normally use a palette if there are less than 256 colours on the page, and record a 24-bit RGB file otherwise (or a 32-bit ARGB file if type = "cairo" and non-opaque colours are used). However, type = "cairo-png" uses cairographics’ PNG backend which will never use a palette and normally creates a larger 32-bit ARGB file—this may work better for specialist uses with semi-transparent colours.

Quartz-produced PNG and TIFF plots with a transparent background are recorded with a dark grey matte which will show up in some viewers, including Preview on macOS.

Unknown resolutions in BMP files are recorded as 72 ppi.

Value

A plot device is opened: nothing is returned to the R interpreter.

If something goes wrong in writing a TIFF file (for example, an unsupported type of compression), a file is produced, likely invalid.

Warnings

Note that by default the width and height values are in pixels not inches. A warning will be issued if both are less than 20.

If you plot more than one page on one of these devices and do not include something like %d for the sequence number in file, the file will contain the last page plotted.

Differences between OSes

These functions are interfaces to three or more different underlying devices.

• On Windows, devices based on plotting to a hidden screen using Windows’ GDI calls.
• On platforms with support for X11, plotting to a hidden X11 display.
• On macOS when working at the console and when R is compiled with suitable support, using Apple’s Quartz plotting system.
• Where support has been compiled in for cairographics, plotting on cairo surfaces. This may use the native platform support for fonts, or it may use fontconfig to support a wide range of font formats.

Inevitably there will be differences between the options supported and output produced. Perhaps the most important are support for antialiased fonts and semi-transparent colours: the best results are likely to be obtained with the cairo- or Quartz-based devices where available.

The default extensions are ‘.jpg’ and ‘.tif’ on Windows, and ‘.jpeg’ and ‘.tiff’ elsewhere.
Conventions

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

- The default device size is in pixels.
- Font sizes are in big points interpreted at res ppi.
- The default font family is Helvetica.
- Line widths in 1/96 inch (interpreted at res ppi), minimum one pixel for type = "Xlib", 0.01 for type = "cairo".
- For type = "Xlib" circle radii are in pixels with minimum one.
- Colours are interpreted by the viewing application.

For type = "quartz" see the help for quartz.

Note

For type = "Xlib" these devices are based on the X11 device. The colour model used will be that set up by X11.options at the time the first Xlib-based devices was opened (or the first after all such devices have been closed).

Author(s)

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References

The PNG specification, https://www.w3.org/TR/png/.

See Also

Devices, dev.print
capabilities to see if these devices are supported by this build of R, and if type = "cairo" is supported.
bitmap provides an alternative way to generate plots in many bitmap formats that does not depend on accessing the X11 display but does depend on having GhostScript installed.
Ways to write raster images to bitmap formats are available in packages jpeg, png and tiff.

Examples

## these examples will work only if the devices are available
## and cairo or an X11 display or a macOS display is available.

## copy current plot to a (large) PNG file
## Not run: dev.print(png, file = "myplot.png", width = 1024, height = 768)

png(file = "myplot.png", bg = "transparent")
plot(1:10)
rect(1, 5, 3, 7, col = "white")
dev.off()
## will make myplot1.jpeg and myplot2.jpeg
jpeg(file = "myplot%d.jpeg")
example(rect)
dev.off()

### Description

`postscript` starts the graphics device driver for producing PostScript graphics.

### Usage

```r
postscript(file = if(onefile) "Rplots.ps" else "Rplot%03d.ps",
onefile, family, title, fonts, encoding, bg, fg,
width, height, horizontal, pointsize,
paper, pagecentre, print.it, command,
colormodel, useKerning, fillOddEven)
```

### Arguments

- **file**: a character string giving the file path. If it is "", the output is piped to the command given by the argument `command`. If it is of the form "|cmd", the output is piped to the command given by `cmd`.
  - For use with `onelfile = FALSE` give a printf format such as "Rplot%03d.ps" (the default in that case). The string should not otherwise contain a %: if it is really necessary, use % in the string for % in the file name. A single integer format matching the regular expression "%[0-9-]+%[0-9.]*[diouxX]" is allowed.
  - Tilde expansion (see `path.expand`) is done. An input with a marked encoding is converted to the native encoding or an error is given.

- **onelfile**: logical: if true (the default) allow multiple figures in one file. If false, generate a file name containing the page number for each page and use an EPSF header and no DocumentMedia comment. Defaults to `TRUE`.

- **family**: the initial font family to be used, normally as a character string. See the section `Families`. Defaults to "Helvetica".

- **title**: title string to embed as the Title comment in the file. Defaults to "R Graphics Output".

- **fonts**: a character vector specifying additional R graphics font family names for font families whose declarations will be included in the PostScript file and are available for use with the device. See ‘Families’ below. Defaults to NULL.

- **encoding**: the name of an encoding file. Defaults to "default". The latter is interpreted on Unix-alikes as "ISO8859-1.enc" unless the locale is recognized as corresponding to a language using ISO 8859-{2,5,7,13,15} or KOI8-{R,U}.
  - on Windows as "CP1250.enc" (Central European), "CP1251.enc" (Cyrillic), "CP1253.enc" (Greek) or "CP1257.enc" (Baltic) if one of those codepages is in use, otherwise "WinAnsi.enc" (codepage 1252).
The file is looked for in the ‘enc’ directory of package `grDevices` if the path does not contain a path separator. An extension "enc" can be omitted.

bg
the initial background color to be used. If "transparent" (or any other non-opaque colour), no background is painted. Defaults to "transparent".

fg
the initial foreground color to be used. Defaults to "black".

width, height
the width and height of the graphics region in inches. Default to 0.
If paper != "special" and width or height is less than 0.1 or too large to give a total margin of 0.5 inch, the graphics region is reset to the corresponding paper dimension minus 0.5.

horizontal
the orientation of the printed image, a logical. Defaults to true, that is landscape orientation on paper sizes with width less than height.

pointsize
the default point size to be used. Strictly speaking, in bp, that is 1/72 of an inch, but approximately in points. Defaults to 12.

paper
the size of paper in the printer. The choices are "a4", "letter" (or "us"), "legal" and "executive" (and these can be capitalized). Also, "special" can be used, when arguments width and height specify the paper size. A further choice is "default" (the default): If this is selected, the papersize is taken from the option "papersize" if that is set and to "a4" if it is unset or empty.

pagecentre
logical: should the device region be centred on the page? Defaults to true.

print.it
logical: should the file be printed when the device is closed? (This only applies if file is a real file name.) Defaults to false.

command
the command to be used for ‘printing’. Defaults to "default", the value of option "printcmd". The length limit is 2*PATH_MAX, typically 8096 bytes on Unix-alikes and 520 bytes on Windows. Recent Windows systems may be configured to use long paths, raising this limit currently to 10000.

colormodel
a character string describing the color model: currently allowed values as "srgb", "srgb+gray", "rgb", "rgb-nogray", "gray" (or "grey") and "cmyk". Defaults to "srgb". See section ‘Color models’.

useKerning
logical. Should kerning corrections be included in setting text and calculating string widths? Defaults to TRUE.

fillOddEven
logical controlling the polygon fill mode: see `polygon` for details. Default FALSE.

Details
All arguments except file default to values given by `ps.options()`. The ultimate defaults are quoted in the arguments section.

`postscript` opens the file `file` and the PostScript commands needed to plot any graphics requested are written to that file. This file can then be printed on a suitable device to obtain hard copy.

The file argument is interpreted as a C integer format as used by `sprintf`, with integer argument the page number. The default gives files 'Rplot001.ps', ..., 'Rplot999.ps', 'Rplot1000.ps', .... The postscript produced for a single R plot is EPS (Encapsulated PostScript) compatible, and can be included into other documents, e.g., into LaTeX, using \includegraphics{<filename>}. For use in this way you will probably want to use `setEPS()` to set the defaults as horizontal = FALSE, onefile = FALSE, paper = "special". Note that the bounding box is for the device region: if you find the white space around the plot region excessive, reduce the margins of the figure region via `par(mar = )`. 
Most of the PostScript prologue used is taken from the R character vector .ps.prolog. This is marked in the output, and can be changed by changing that vector. (This is only advisable for PostScript experts: the standard version is in namespace:grDevices.)

A PostScript device has a default family, which can be set by the user via family. If other font families are to be used when drawing to the PostScript device, these must be declared when the device is created via fonts; the font family names for this argument are R graphics font family names (see the documentation for postscriptFonts).

Line widths as controlled by par(lwd = ) are in multiples of 1/96 inch: multiples less than 1 are allowed. pch = "." with cex = 1 corresponds to a square of side 1/72 inch, which is also the ‘pixel’ size assumed for graphics parameters such as "cra".

When the background colour is fully transparent (as is the initial default value), the PostScript produced does not paint the background. Almost all PostScript viewers will use a white canvas so the visual effect is if the background were white. This will not be the case when printing onto coloured paper, though.

Families

Font families are collections of fonts covering the five font faces, (conventionally plain, bold, italic, bold-italic and symbol) selected by the graphics parameter par(font = ) or the grid parameter gpar(fontface = ). Font families can be specified either as an initial/default font family for the device via the family argument or after the device is opened by the graphics parameter par(family = ) or the grid parameter gpar(fontfamily = ). Families which will be used in addition to the initial family must be specified in the fonts argument when the device is opened.

Font families are declared via a call to postscriptFonts.

The argument family specifies the initial/default font family to be used. In normal use it is one of "AvantGarde", "Bookman", "Courier", "Helvetica", "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" or "Times", and refers to the standard Adobe PostScript fonts families of those names which are included (or cloned) in all common PostScript devices.

Many PostScript emulators (including those based on ghostscript) use the URW equivalents of these fonts, which are "URWGothic", "URWBookman", "NimbusMon", "NimbusSan", "NimbusSanCond", "CenturySch", "URWPalladio" and "NimbusRom" respectively. If your PostScript device is using URW fonts, you will obtain access to more characters and more appropriate metrics by using these names. To make these easier to remember, "URWHelvetica" == "NimbusSan" and "URWTimes" == "NimbusRom" are also supported.

Another type of family makes use of CID-keyed fonts for East Asian languages – see postscriptFonts.

The Family argument is normally a character string naming a font family, but family objects generated by Type1Font and CIDFont are also accepted. For compatibility with earlier versions of R, the initial family can also be specified as a vector of four or five afm files.

Note that R does not embed the font(s) used in the PostScript output: see embedFonts for a utility to help do so.

Viewers and embedding applications frequently substitute fonts for those specified in the family, and the substitute will often have slightly different font metrics. useKerning = TRUE spaces the letters in the string using kerning corrections for the intended family: this may look uglier than useKerning = FALSE.

Encodings

Encodings describe which glyphs are used to display the character codes (in the range 0–255). Most commonly R uses ISOLatin1 encoding, and the examples for text are in that encoding. However,
the encoding used on machines running R may well be different, and by using the encoding argument the glyphs can be matched to encoding in use. This suffices for European and Cyrillic languages, but not for East Asian languages. For the latter, composite CID fonts are used. These fonts are useful for other languages: for example they may contain Greek glyphs. (The rest of this section applies only when CID fonts are not used.)

None of this will matter if only ASCII characters (codes 32–126) are used as all the encodings (except "TeXtext") agree over that range. Some encodings are supersets of ISO-Latin1, too. However, if accented and special characters do not come out as you expect, you may need to change the encoding. Some other encodings are supplied with R: "WinAnsi.enc" and "MacRoman.enc" correspond to the encodings normally used on Windows and Classic Mac OS (at least by Adobe), and "PDFDoc.enc" is the first 256 characters of the Unicode encoding, the standard for PDF. There are also encodings "ISO-Latin2.enc", "CP1250.enc", "ISO-Latin7.enc" (ISO 8859-13), "CP1257.enc", and "ISO-Latin9.enc" (ISO 8859-15), "Cyrillic.enc" (ISO 8859-5), "KOI8-R.enc", "KOI8-U.enc", "CP1251.enc", "Greek.enc" (ISO 8859-7) and "CP1253.enc". Note that many glyphs in these encodings are not in the fonts corresponding to the standard families. (The Adobe ones for all but Courier, Helvetica and Times cover little more than Latin-1, whereas the URW ones also cover Latin-2, Latin-7, Latin-9 and Cyrillic but no Greek. The Adobe exceptions cover the Latin character sets, but not the Euro.)

If you specify the encoding, it is your responsibility to ensure that the PostScript font contains the glyphs used. One issue here is the Euro symbol which is in the WinAnsi and MacRoman encodings but may well not be in the PostScript fonts. (It is in the URW variants; it is not in the supplied Adobe Font Metric files.)

There is an exception. Character 45 ("-") is always set as minus (its value in Adobe ISO-Latin1) even though it is hyphen in the other encodings. Hyphen is available as character 173 (octal 0255) in all the Latin encodings, Cyrillic and Greek. (This can be entered as "\uad" in a UTF-8 locale.)

There are some discrepancies in accounts of glyphs 39 and 96: the supplied encodings (except CP1250 and CP1251) treat these as 'quoteright' and 'quoteleft' (rather than 'quotesingle'/'acute' and 'grave' respectively), as they are in the Adobe documentation.

TeX fonts

TeX fonts have traditionally made use of fonts such as Computer Modern which are encoded rather differently, in a 7-bit encoding. This encoding can be specified by encoding = "TeXtext.enc", taking care that the ASCII characters < > \ _ { } are not available in those fonts.

There are supplied families "ComputerModern" and "ComputerModernItalic" which use this encoding, and which are only supported for postscript (and not pdf). They are intended to use with the Type 1 versions of the TeX CM fonts. It will normally be possible to include such output in TeX or LaTeX provided it is processed with dvips -Ppdf -j0 or the equivalent on your system. (-j0 turns off font subsetting.) When family = "ComputerModern" is used, the italic/bold-italic fonts used are slanted fonts (cmmi10 and cmbx10). To use text italic fonts instead, set family = "ComputerModernItalic".

These families use the TeX math italic and symbol fonts for a comprehensive but incomplete coverage of the glyphs covered by the Adobe symbol font in other families. This is achieved by special-casing the postscript code generated from the supplied 'CM_symbol_10.afm'.

Color models

The default color model ("srgb") is sRGB.

The alternative "srgb+gray" uses sRGB for colors, but with pure gray colors (including black and white) expressed as greyscales (which results in smaller files and can be advantageous with some
printer drivers). Conversely, its files can be rendered much slower on some viewers, and there can be a noticeable discontinuity in color gradients involving gray or white.

Other possibilities are "gray" (or "grey") which used only greyscales (and converts other colours to a luminance), and "cmyk". The simplest possible conversion from sRGB to CMYK is used (https://en.wikipedia.org/wiki/CMYK_color_model#Mapping_RGB_to_CMYK), and raster images are output in RGB.

Color models provided for backwards compatibility are "rgb" (which is RGB+gray) and "rgb-nogray" which use uncalibrated RGB (as used in R prior to 2.13.0). These result in slightly smaller files which may render faster, but do rely on the viewer being properly calibrated.

Printing

A postscript plot can be printed via postscript in two ways.

1. Setting print.it = TRUE causes the command given in argument command to be called with argument "file" when the device is closed. Note that the plot file is not deleted unless command arranges to delete it.

2. file = "" or file = "|cmd" can be used to print using a pipe. Failure to open the command will probably be reported to the terminal but not to R, in which case close the device by dev.off immediately.

On Windows the default "printcmd" is empty and will give an error if print.it = TRUE is used. Suitable commands to spool a PostScript file to a printer can be found in 'RedMon' suite available from http://pages.cs.wisc.edu/~ghost/index.html. The command will be run in a minimized window. GSView 4.x provides 'gsprint.exe' which may be more convenient (it requires Ghostscript version 6.50 or later).

Conventions

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is Helvetica.
- Line widths are as a multiple of 1/96 inch, with a minimum of 0.01 enforced.
- Circle of any radius are allowed.
- Colours are by default specified as sRGB.

At very small line widths, the line type may be forced to solid.

Raster images are currently limited to opaque colours.

Note

If you see problems with postscript output, do remember that the problem is much more likely to be in your viewer than in R. Try another viewer if possible. Symptoms for which the viewer has been at fault are apparent grids on image plots (turn off graphics anti-aliasing in your viewer if you can) and missing or incorrect glyphs in text (viewers silently doing font substitution).

Unfortunately the default viewers on most Linux and macOS systems have these problems, and no obvious way to turn off graphics anti-aliasing.
Author(s)

Support for Computer Modern fonts is based on a contribution by Brian D’Urso <durso@hussle.harvard.edu>.

References


See Also

`postscriptFonts`, `Devices`, and `check.options` which is called from both `ps.options` and `postscript`.

`cairo_ps` for another device that can produce PostScript.

More details of font families and encodings and especially handling text in a non-Latin-1 encoding and embedding fonts can be found in


Examples

```
require(graphics)

## Not run:
# open the file "foo.ps" for graphics output
postscript("foo.ps")
# produce the desired graph(s)
dev.off() # turn off the postscript device

## On Unix-alikes only:
postscript("|lp -dlw")
# produce the desired graph(s)
dev.off() # plot will appear on printer

## On Windows:
options(printcmd = "redpr -P"\"printhost\lw\"")
postscript(file = tempfile("Rps."), print.it = TRUE)
# produce the desired graph(s)
dev.off() # send plot file to the printer

## alternative using GSView 4.x:
options(printcmd = "/GhostGum/gsview/gsprint -query")

# for URW PostScript devices
postscript("foo.ps", family = "NimbusSan")

## for inclusion in Computer Modern TeX documents, perhaps
postscript("cm_test.eps", width = 4.0, height = 3.0, 
  horizontal = FALSE, onefile = FALSE, paper = "special", 
  family = "ComputerModern", encoding = "TeXtext.enc")

## The resultant postscript file can be used by dvips -Ppfb -j0.

## To test out encodings, you can use
TestChars <- function(encoding = "ISOLatin1", family = "URWHelvetica") {
```
postscriptFonts

postscript(encoding = encoding, family = family)
par(pty = "s")
plot(c(-1,16), c(-1,16), type = "n", xlab = "", ylab = "",
     xaxs = "i", yaxs = "i")
title(paste("Centred chars in encoding", encoding))
grid(17, 17, lty = 1)
for(i in c(32:255)) {
  x <- i %% 16
  y <- i %/% 16
  points(x, y, pch = i)
}
dev.off()
}

## there will be many warnings. We use URW to get a complete enough
## set of font metrics.

TestChars()
TestChars("ISOLatin2")
TestChars("WinAnsi")

## End(Not run)

postscriptFonts

PostScript and PDF Font Families

Description

These functions handle the translation of a R graphics font family name to a PostScript or PDF font description, used by the postscript or pdf graphics devices.

Usage

postscriptFonts(...)
pdffonts(...)  

Arguments

...  

either character strings naming mappings to display, or named arguments specifying mappings to add or change.

Details

If these functions are called with no argument they list all the existing mappings, whereas if they are called with named arguments they add (or change) mappings.

A PostScript or PDF device is created with a default font family (see the documentation for postscript), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for "family" in par and for "fontfamily" in gpar in the grid package).

The font family sent to the device is a simple string name, which must be mapped to a set of PostScript fonts. Separate lists of mappings for postscript and pdf devices are maintained for the current R session and can be added to by the user.
The `postscriptFonts` and `pdfFonts` functions can be used to list existing mappings and to define new mappings. The `Type1Font` and `CIDFont` functions can be used to create new mappings, when the `xxxFonts` function is used to add them to the database. See the examples.

Default mappings are provided for three device-independent family names: "sans" for a sans-serif font (to "Helvetica"), "serif" for a serif font (to "Times") and "mono" for a monospaced font (to "Courier").

Mappings for a number of standard Adobe fonts (and URW equivalents) are also provided: "AvantGarde", "Bookman", "Courier", "Helvetica", "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" and "Times"; "URW Gothic", "URW Bookman", "NimbusMon", "NimbusSan" (synonym "URW Helvetica"), "NimbusSanCond", "Century Sch". "URW Palladio" and "Nimbus Rom" (synonym "URW Times").

There are also mappings for "Computer Modern", "Computer Modern Italic" and "Arial MT" (Monotype Arial).

Finally, there are some default mappings for East Asian locales described in a separate section.

The specification of font metrics and encodings is described in the help for the `postscript` function.

The fonts are not embedded in the resulting PostScript or PDF file, so software including the PostScript or PDF plot file should either embed the font outlines (usually from `.pfb` or `.pfa` files) or use DSC comments to instruct the print spooler or including application to do so (see also `embedFonts`).

A font family has both an R-level name, the argument name used when `postscriptFonts` was called, and an internal name, the `family` component. These two names are the same for all the pre-defined font families.

Once a font family is in use it cannot be changed. ‘In use’ means that it has been specified via a family or fonts argument to an invocation of the same graphics device already in the R session. (For these purposes `xfig` counts the same as `postscript` but only uses some of the predefined mappings.)

Value

A list of one or more font mappings.

**East Asian fonts**

There are some default mappings for East Asian locales: "Japan1", "Japan1HeiMin", "Japan1 Gothic BBB", and "Japan1 Ryumin" for Japanese; "Korea1" and "Korea 1 deb" for Korean; "GB1" (Simplified Chinese) for mainland China and Singapore; "CNS1" (Traditional Chinese) for Hong Kong and Taiwan.

These refer to the following fonts:

- **Japan1 (PS)**: HeiseiKakuGo-W5
  - Linotype Japanese printer font
- **Japan1 (PDF)**: KozMinPro-Regular-Acro
  - from Adobe Reader 7.0 Japanese Font Pack
- **Japan1 HeiMin (PS)**: HeiseiMin-W3
  - Linotype Japanese printer font
- **Japan1 HeiMin (PDF)**: HeiseiMin-W3-Acro
  - from Adobe Reader 7.0 Japanese Font Pack
- **Japan1 Gothic BBB**: Gothic BBB-Medium
  - Japanese-market PostScript printer font
postscriptFonts

<table>
<thead>
<tr>
<th>Font Type</th>
<th>Font Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Japan1Ryumin</td>
<td>Ryumin-Light</td>
<td>Japanese-market PostScript printer font</td>
</tr>
<tr>
<td>Korea1 (PS)</td>
<td>Baekmuk-Batang</td>
<td>TrueType font found on some Linux systems</td>
</tr>
<tr>
<td>Korea1 (PDF)</td>
<td>HYSMyeongJoStd-Medium-Acro</td>
<td>from Adobe Reader 7.0 Korean Font Pack</td>
</tr>
<tr>
<td>Korea1deb (PS)</td>
<td>Batang-Regular</td>
<td>another name for Baekmuk-Batang</td>
</tr>
<tr>
<td>Korea1deb (PDF)</td>
<td>HYGothic-Medium-Acro</td>
<td>from Adobe Reader 4.0 Korean Font Pack</td>
</tr>
<tr>
<td>GB1 (PS)</td>
<td>BousungEG-Light-GB</td>
<td>TrueType font found on some Linux systems</td>
</tr>
<tr>
<td>GB1 (PDF)</td>
<td>STSong-Light-Acro</td>
<td>from Adobe Reader 7.0 Simplified Chinese Font Pack</td>
</tr>
<tr>
<td>CNS1 (PS)</td>
<td>MOESung-Regular</td>
<td>Ken Lunde’s CJKV resources</td>
</tr>
<tr>
<td>CNS1 (PDF)</td>
<td>MSungStd-Light-Acro</td>
<td>from Adobe Reader 7.0 Traditional Chinese Font Pack</td>
</tr>
</tbody>
</table>


These will need to be installed or otherwise made available to the postscript/PDF interpreter such as ghostscript (and not all interpreters can handle TrueType fonts).

You may well find that your postscript/PDF interpreters has been set up to provide aliases for many of these fonts. For example, ghostscript on Windows can optionally be installed to map common East Asian fonts names to Windows TrueType fonts. (You may want to add the `-Acro` versions as well.)

Adding a mapping for a CID-keyed font is for gurus only.

Author(s)

Support for Computer Modern fonts is based on a contribution by Brian D’Urso.

See Also

postscript and pdf; Type1Font and CIDFont for specifying new font mappings.

Examples

```r
caseinsFonts()
## This duplicates "ComputerModernItalic".
CMitalic <- Type1Font("ComputerModern2",
  c("CM_regular_10.afm", "CM_boldx_10.afm",
  "cmti10.afm", "cmbxti10.afm",
  "CM_symbol_10.afm"),
  encoding = "TeXtext.enc")
caseinsFonts(CMitalic = CMitalic)
```
```r
## A CID font for Japanese using a different CMap and
## corresponding cmapEncoding.
Jp_UCS-2 <- CIDFont("TestUCS2",
  c("Adobe-Japan1-UniJIS-UCS2-H.afm",
```
pretty.Date

Pretty Breakpoints for Date-Time Classes

Description
Compute a sequence of about \( n+1 \) equally spaced `nice` values which cover the range of the values in \( x \), possibly of length one, when \( \min.n = 0 \) and there is only one unique \( x \).

Usage

```r
## S3 method for class 'Date'
pretty(x, n = 5, min.n = n %/% 2, sep = " ", ...)  
## S3 method for class 'POSIXt'
pretty(x, n = 5, min.n = n %/% 2, sep = " ", ...)
```

Arguments

- \( x \): an object of class "Date" or "POSIXt" (i.e., "POSIXct" or "POSIXlt").
- \( n \): integer giving the desired number of intervals.
- \( \min.n \): nonnegative integer giving the minimal number of intervals.
- \( \text{sep} \): character string, serving as a separator for certain formats (e.g., between month and year).
- ...: further arguments for compatibility with the generic, ignored.

Value
A vector (of the suitable class) of locations, with attribute "labels" giving corresponding formatted character labels and attribute "format" giving the format specification that was used.

See Also
`pretty` for the default method.

Examples

```r
## time-dependent ==> ignore diffs:
## IGNORE_RDIFF_BEGIN
pretty(Sys.Date())
pretty(Sys.time(), n = 10)  
## IGNORE_RDIFF_END

pretty(as.Date("2000-03-01")) # R 1.0.0 came in a leap year

## time ranges in diverse scales:% also in ../../../../tests/reg-tests-1c.R
require(stats)
```
steps <- setNames(
  c("10 secs", "1 min", "5 mins", "30 mins", "6 hours", "12 hours",
    "1 DSTday", "2 weeks", "1 month", "6 months", "1 year",
    "10 years", "50 years", "1000 years")),
x <- as.POSIXct("2002-02-02 02:02")
lapply(steps,
  function(s) {
    at <- pretty(seq(x, by = s, length.out = 2), n = 5)
    attr(at, "labels")
  })

ps.options
Auxiliary Function to Set/View Defaults for Arguments of postscript

Description
The auxiliary function ps.options can be used to set or view (if called without arguments) the
default values for some of the arguments to postscript.
ps.options needs to be called before calling postscript, and the default values it sets can be
overridden by supplying arguments to postscript.

Usage
ps.options(..., reset = FALSE, override.check = FALSE)
setEPS(...)  
setPS(...)

Arguments

...    arguments onefile, family, title, fonts, encoding, bg, fg, width,  
height, horizontal, pointsize, paper, pagecentre, print.it, command,  
colormodel and fillOddEven can be supplied. onefile, horizontal and  
paper are ignored for setEPS and setPS.
reset    logical: should the defaults be reset to their ‘factory-fresh’ values?
override.check    logical argument passed to check.options. See the Examples.

Details
If both reset = TRUE and ... are supplied the defaults are first reset to the ‘factory-fresh’ values
and then the new values are applied.
For backwards compatibility argument append is accepted but ignored with a warning.
setEPS and setPS are wrappers to set defaults appropriate for figures for inclusion in documents
(the default size is 7 inches square unless width or height is supplied) and for spooling to a
PostScript printer respectively. For historical reasons the latter is the ultimate default.

Value
A named list of all the previous defaults. If ... or reset = TRUE is supplied the result has the
visibility flag turned off.
quartz

macOS Quartz Device

Description

quartz starts a graphics device driver for the macOS system. It supports plotting both to the screen (the default) and to various graphics file formats.

Usage

quartz(title, width, height, pointsize, family, antialias, type, file = NULL, bg, canvas, dpi)
quartz.options(..., reset = FALSE)
quartz.save(file, type = "png", device = dev.cur(), dpi = 100, ...)

Arguments

title title for the Quartz window (applies to on-screen output only), default "Quartz %d". A C-style format for an integer will be substituted by the device number (see the file argument to postscript for further details).

width the width of the plotting area in inches. Default 7.

height the height of the plotting area in inches. Default 7.

pointsize the default pointsize to be used. Default 12.

family this is the family name of the font that will be used by the device. Default "Arial". This will be the base name of a font as shown in Font Book.

antialias whether to use antialiasing. Default TRUE.

type the type of output to use. See ‘Details’ for more information. Default "native".

file an optional target for the graphics device. The default, NULL, selects a default name where one is needed. See ‘Details’ for more information.

bg the initial background colour to use for the device. Default "transparent". An opaque colour such as "white" will normally be required on off-screen types that support transparency such as "png" and "tiff".

See Also

postscript, pdf.options

Examples

ps.options(bg = "pink")
utils::str(ps.options())

### ---- error checking of arguments: ----
ps.options(width = 0:12, onefile = 0, bg = pi)
# override the check for 'width', but not 'bg':
ps.options(width = 0:12, bg = pi, override.check = c(TRUE,FALSE))
utils::str(ps.options())
ps.options(reset = TRUE) # back to factory-fresh
canvas colour to use for an on-screen device. Default "white", and will be forced to be an opaque colour.

dpi resolution of the output. The default (NA_real_) for an on-screen display defaults to the resolution of the main screen, and to 72 dpi otherwise. See ‘Details’.

reset logical: should the defaults be reset to their defaults?

device device number to copy from.

Details

The defaults for all but one of the arguments of quartz are set by quartz.options: the ‘Arguments’ section gives the ‘factory-fresh’ defaults.

The Quartz graphics device supports a variety of output types. On-screen output types are "" or "native" or "Cocoa". Off-screen output types produce output files and utilize the file argument. type = "pdf" gives PDF output. The following bitmap formats may be supported (depending on the OS version): "png", "jpeg", "jpg", "jpeg2000", "tif", "tiff", "gif", "psd" (Adobe Photoshop), "bmp" (Windows bitmap), "sgi" and "pict".

The file argument is used for off-screen drawing. The actual file is only created when the device is closed (e.g., using dev.off()). For the bitmap devices, the page number is substituted if a C integer format is included in the character string, e.g. Rplot%03d.png. (Depending on the platform, the result should be less than PATH_MAX characters long, and may be truncated if not. See postscript for further details.) If a file argument is not supplied, the default is Rplots.pdf or Rplot%03d. Tilde expansion (see path.expand) is done.

If a device-independent R graphics font family is specified (e.g., via par(family =) in the graphics package), the Quartz device makes use of the Quartz font database (see quartzFonts) to convert the R graphics font family to a Quartz-specific font family description. The default conversions are (MonoType TrueType versions of) Helvetica for sans, Times-Roman for serif and Courier for mono.

On-screen devices are launched with a semi-transparent canvas. Once a new plot is created, the canvas is first painted with the canvas colour and then the current background colour (which can be transparent or semi-transparent). Off-screen devices have no canvas colour, and so start with a transparent background where possible (e.g., type = "png" and type = "tiff") – otherwise it appears that a solid white canvas is assumed in the Quartz code. PNG and TIFF files are saved with a dark grey matte which will show up in some viewers, including Preview.

title can be used for on-screen output. It must be a single character string with an optional integer printf-style format that will be substituted by the device number. It is also optionally used (without a format) to give a title to a PDF file.

Calling quartz() sets .Device to "quartz" for on-screen devices and to "quartz_off_screen" otherwise.

The font family chosen needs to cover the characters to be used: characters not in the font are rendered as empty oblongs. For non-Western-European languages something other than the default of "Arial" is likely to be needed—one choice for Chinese is "MingLiU".

quartz.save is a modified version of dev.copy2pdf to copy the plot from the current screen device to a quartz device, by default to a PNG file.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.
The default device size is 7 inches square.
Font sizes are in big points.
The default font family is Arial.
Line widths are a multiple of 1/96 inch with no minimum set by R.
Circle radii are real-valued with no minimum set by R.
Colours are specified as sRGB.

Note
For a long time the default font family was documented as "Helvetica" after it had been changed to "Arial" to work around a deficiency in macOS 10.4. It may be changed back in future.
A fairly common Mac problem is no text appearing on plots due to corrupted or duplicated fonts on your system. You may be able to confirm this by using another font family, e.g. family = "serif". Open the Font Book application (in Applications) and check the fonts that you are using.

See Also
quartzFonts, Devices.
Note for way to access the bitmap types of this device via R’s standard bitmap devices.

Examples
## Not run:
## Only on a Mac,
## put something like this in your .Rprofile to customize the defaults
setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::quartz.options(width = 8, height = 6,
          pointsize = 10))

## End(Not run)

quartzFonts
Quartz Fonts Setup

Description
These functions handle the translation of a device-independent R graphics font family name to a quartz font description.
They are only available on Unix-alikes, i.e. not on Windows, and typically used on the Mac.

Usage
quartzFont(family)
quartzFonts(...)  
Arguments
family a character vector containing the four PostScript font names for plain, bold, italic, and bolditalic versions of a font family.
... either character strings naming mappings to display, or new (named) mappings to define.
Details

A quartz device is created with a default font (see the documentation for quartz), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for gpar in the grid package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to quartz fonts. A list of mappings is maintained and can be modified by the user.

The quartzFonts function can be used to list existing mappings and to define new mappings. The quartzFont function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: "sans" for a sans-serif font, "serif" for a serif font and "mono" for a monospaced font.

See Also

quartz for the default Mac graphics device.

Examples

if(.Platform$OS.type == "unix") { # includes Mac
  utils::str( quartzFonts() ) # a list(serif = .., sans = .., mono = ..)
  quartzFonts("mono") # the list(mono = ..) sublist of quartzFonts()
  *** Not run:
  *** for East Asian locales you can use something like
  quartzFonts(sans = quartzFont(rep("AppleGothic", 4)),
              serif = quartzFont(rep("AppleMyungjp", 4)))
  *** since the default fonts may well not have the glyphs needed
  ***
  *** End(Not run)
}

recordGraphics(expr, list, env)

Arguments

expr object of mode expression or call or an unevaluated expression.
list a list defining the environment in which expr is to be evaluated.
env an environment specifying where R looks for objects not found in list.
recordPlot

Details

The code in `expr` is evaluated in an environment constructed from `list`, with `env` as the parent of that environment.

All three arguments are saved on the graphics engine display list so that on a device resize or copying between devices, the original evaluation environment can be recreated and the code can be re-evaluated to reproduce the graphical output.

Value

The value from evaluating `expr`.

Warning

This function is not intended for general use. Incorrect or improper use of this function could lead to unintended and/or undesirable results.

An example of acceptable use is querying the current state of a graphics device or graphics system setting and then calling a graphics function.

An example of improper use would be calling the `assign` function to performing assignments in the global environment.

See Also

eval

Examples

```r
require(graphics)

plot(1:10)
# This rectangle remains 1inch wide when the device is resized
recordGraphics(
  
  rect(4, 2,
       4 + diff(par("usr")[1:2])/par("pin")[1], 3)
),
list(),
getNamespace("graphics"))
```

recordPlot

Record and Replay Plots

Description

Functions to save the current plot in an R variable, and to replay it.

Usage

```r
recordPlot(load=NULL, attach=NULL)
replayPlot(x, reloadPkgs=FALSE)
```
recordPlot

Arguments

load If not NULL, a character vector of package names, which are saved as part of the recorded plot.

attach If not NULL, a character vector of package names, which are saved as part of the recorded plot.

x A saved plot.

reloadPks A logical indicating whether to reload and/or reattach any packages that were saved as part of the recorded plot.

Details

These functions record and replay the displaylist of the current graphics device. The returned object is of class "recordedplot", and replayPlot acts as a print method for that class.

The returned object is stored as a pairlist, but the usual methods for examining R objects such as deparse and str are liable to mislead.

Value

recordPlot returns an object of class "recordedplot".

replayPlot has no return value.

Warning

The format of recorded plots may change between R versions, so recorded plots should not be used as a permanent storage format for R plots.

As of R 3.3.0, it is possible (again) to replay a plot from another R session using, for example, saveRDS and readRDS. It is even possible to replay a plot from another R version, however, this will produce warnings, may produce errors, or something worse.

Note

Replay of a recorded plot may not produce the correct result (or may just fail) if the display list contains a call to recordGraphics which in turn contains an expression that calls code from a non-base package other than graphics or grid. The most well-known example of this is a plot drawn with the package ggplot2. One solution is to load the relevant package(s) before replaying the recorded plot. The load and attach arguments to recordPlot can be used to automate this - any packages named in load will be reloaded, via loadNamespace, and any packages named in attach will be reattached, via library, as long as reloadPks is TRUE in the call to replayPlot. This is only relevant when attempting to replay in one R session a plot that was recorded in a different R session.

See Also

The displaylist can be turned on and off using dev.control. Initially recording is on for screen devices, and off for print devices.
Description
This function creates colors corresponding to the given intensities (between 0 and max) of the red, green and blue primaries. The colour specification refers to the standard sRGB colorspace (IEC standard 61966).

An alpha transparency value can also be specified (as an opacity, so 0 means fully transparent and max means opaque). If alpha is not specified, an opaque colour is generated.

The names argument may be used to provide names for the colors.

The values returned by these functions can be used with a col= specification in graphics functions or in par.

Usage
rgb(red, green, blue, alpha, names = NULL, maxColorValue = 1)

Arguments
red, blue, green, alpha
numeric vectors with values in [0, M] where M is maxColorValue. When this is 255, the red, blue, green, and alpha values are coerced to integers in 0:255 and the result is computed most efficiently.

names character vector. The names for the resulting vector.

maxColorValue number giving the maximum of the color values range, see above.

Details
The colors may be specified by passing a matrix or data frame as argument red, and leaving blue and green missing. In this case the first three columns of red are taken to be the red, green and blue values.

Semi-transparent colors (0 < alpha < 1) are supported only on some devices: at the time of writing on the pdf, windows, quartz and X11(type = "cairo") devices and associated bitmap devices (jpeg, png, bmp, tiff and bitmap). They are supported by several third-party devices such as those in packages Cairo, cairoDevice and JavaGD. Only some of these devices support semi-transparent backgrounds.

Most other graphics devices plot semi-transparent colors as fully transparent, usually with a warning when first encountered.

NA values are not allowed for any of red, blue, green or alpha.

Value
A character vector with elements of 7 or 9 characters, "#" followed by the red, blue, green and optionally alpha values in hexadecimal (after rescaling to 0 . . . 255). The optional alpha values range from 0 (fully transparent) to 255 (opaque).

R does not use 'premultiplied alpha'.
See Also

col2rgb for translating R colors to RGB vectors; rainbow, hsv, hcl, gray.

Examples

gb(0, 1, 0)

gb((0:15)/15, green = 0, blue = 0, names = paste("red", 0:15, sep = "."))

gb(0, 0:12, 0, maxColorValue = 255) # integer input

ramp <- colorRamp(c("red", "white"))
gb( ramp(seq(0, 1, length.out = 5)), maxColorValue = 255)

rgb2hsv

RGB to HSV Conversion

Description

rgb2hsv transforms colors from RGB space (red/green/blue) into HSV space (hue/saturation/value).

Usage

rgb2hsv(r, g = NULL, b = NULL, maxColorValue = 255)

Arguments

r
vector of ‘red’ values in $[0, M]$, ($M$ = maxColorValue) or 3-row rgb matrix.

g
vector of ‘green’ values, or NULL when r is a matrix.

b
vector of ‘blue’ values, or NULL when r is a matrix.

maxColorValue
number giving the maximum of the RGB color values range. The default 255 corresponds to the typical 0:255 RGB coding as in col2rgb().

details

Value (brightness) gives the amount of light in the color.

Hue describes the dominant wavelength.

Saturation is the amount of Hue mixed into the color.

An HSV colorspace is relative to an RGB colorspace, which in R is sRGB, which has an implicit gamma correction.

Value

A matrix with a column for each color. The three rows of the matrix indicate hue, saturation and value and are named "h", "s", and "v" accordingly.

Author(s)

R interface by Wolfram Fischer <wolfram@fischer-zim.ch>; 
C code mainly by Nicholas Lewin-Koh <nikko@hailmail.net>.
See Also

hsv, col2rgb, rgb.

Examples

```r
## These (saturated, bright ones) only differ by hue
(rc <- col2rgb(c("red", "yellow", "green", "cyan", "blue", "magenta")))
(hc <- rgb2hsv(rc))
6 * hc["h",] # the hues are equispaced
```

```r
(rgb3 <- floor(256 * matrix(stats::runif(3*12), 3, 12)))
(hsv3 <- rgb2hsv(rgb3))

## Consistency:
stopifnot(rgb3 == col2rgb(hsv(h = hsv3[1,], s = hsv3[2,], v = hsv3[3,]),
                          all.equal(hsv3, rgb2hsv(rgb3/255, maxColorValue = 1))))

## A (simplified) pure R version -- originally by Wolfram Fischer --
## showing the exact algorithm:
rgb2hsvR <- function(rgb, gamma = 1, maxColorValue = 255) {
  if(!is.numeric(rgb)) stop("rgb matrix must be numeric")
  d <- dim(rgb)
  if(d[1] != 3) stop("rgb matrix must have 3 rows")
  n <- d[2]
  if(n == 0) return(cbind(c(h = 1, s = 1, v = 1))[,0])
  rgb <- rgb/maxColorValue
  if(gamma != 1) rgb <- rgb ^ (1/gamma)

  ## get the max and min
  v <- apply(rgb, 2, max)
  s <- apply(rgb, 2, min)
  D <- v - s # range

  ## set hue to zero for undefined values (gray has no hue)
  h <- numeric(n)
  notgray <- (s != v)

  ## blue hue
  idx <- (v == rgb[3,] & notgray)
  if (any(idx))
    h[idx] <- 2/3 + 1/6 * (rgb[1,idx] - rgb[2,idx]) / D[idx]

  ## green hue
  idx <- (v == rgb[2,] & notgray)
  if (any(idx))
    h[idx] <- 1/3 + 1/6 * (rgb[3,idx] - rgb[1,idx]) / D[idx]

  ## red hue
  idx <- (v == rgb[1,] & notgray)
  if (any(idx))

  ## correct for negative red
  idx <- (h < 0)
  h[idx] <- 1-h[idx]

  ## set the saturation
```
s[! notgray] <- 0;
s[notgray] <- 1 - s[notgray] / v[notgray]

rbind( h = h, s = s, v = v )
}

## confirm the equivalence:
all.equal(rgb2hsv (rgb3),
   rgb2hsvR(rgb3), tolerance = 1e-14) # TRUE

---

**savePlot**

**Save Cairo X11 Plot to File**

**Description**

Save the current page of a cairo X11() device to a file.

**Usage**

```r
savePlot(filename = paste0("Rplot.", type),
   type = c("png", "jpeg", "tiff", "bmp"),
   device = dev.cur())
```

**Arguments**

- `filename`: filename to save to.
- `type`: file type.
- `device`: the device to save from.

**Details**

Only cairo-based X11 devices are supported.

This works by copying the image surface to a file. For PNG will always be a 24-bit per pixel PNG 'DirectClass' file, for JPEG the quality is 75% and for TIFF there is no compression.

For devices with buffering this copies the buffer's image surface, so works even if `dev.hold` has been called.

The plot is saved after rendering onto the canvas (default opaque white), so for the default bg = "transparent" the effective background colour is the canvas colour.

**Value**

Invisible NULL.

**Note**

There is a similar function of the same name but more types for windows devices on Windows: that has an additional argument `restoreConsole` which is only supported on Windows.

**See Also**

`recordPlot()` which is device independent. Further, `X11`, `dev.copy`, `dev.print`
trans3d

3D to 2D Transformation for Perspective Plots

Description

Projection of 3-dimensional to 2-dimensional points using a 4x4 viewing transformation matrix. Mainly for adding to perspective plots such as `persp`.

Usage

```r
trans3d(x, y, z, pmat, continuous = FALSE, verbose = TRUE)
```

Arguments

- `x`, `y`, `z` numeric vectors of equal length, specifying points in 3D space.
- `pmat` a $4 \times 4$ viewing transformation matrix, suitable for projecting the 3D coordinates $(x, y, z)$ into the 2D plane using homogeneous 4D coordinates $(x, y, z, t)$; such matrices are returned by `persp()`.
- `continuous` logical flag specifying if the transformation should check if the transformed points are continuous in the sense that they do not jump over $a/0$ discontinuity. As these assume $(x,y,z)$ to describe a continuous curve, the default must be false. In case of projecting such a curve however, setting `continuous=TRUE` may be advisable.
- `verbose` only for `continuous=TRUE`, indicates if a warning should be issued when points are cut off.

Value

a list with two components

- `x`, `y` the projected 2d coordinates of the 3d input $(x,y,z)$.

See Also

`persp`

Examples

```r
## See help(persp) (after attaching the 'graphics' package)
##
## Example for 'continuous = TRUE' (vs default):
##
## require(graphics)
x <- -10:10/10 # [-1, 1]
y <- -16:16/16 # [-1, 1] ==> z = fxy := outer(x,y) is also in [-1,1]
p <- persp(x, y, fxy <- outer(x,y), phi = 20, theta = 15, r = 3, ltheta = -75,
           shade = 0.8, col = "green3", ticktype = "detailed")
## 5 axis-parallel auxiliary lines in x-y and y-z planes :
lines(trans3d(-.5 , y=-1:1, z=min(fxy), pmat=p), lty=2)
lines(trans3d( 0 , y=-1:1, z=min(fxy), pmat=p), lty=2)
lines(trans3d(-1:1, y = -.7, z=min(fxy), pmat=p), lty=2)
```
lines(trans3d(-1, y= -0.7, z=c(-1,1), pmat=p), lty=2)
lines(trans3d(-1, y=1:1, z= -0.5, pmat=p), lty=2)
## 2 pillars to carry the horizontals below:
lines(trans3d( -0.5, y= -0.7, z=c(-1,-0.5), pmat=p), lwd=1.5, col="gray10")
lines(trans3d( 0 , y= -0.7, z=c(-1,-0.5), pmat=p), lwd=1.5, col="gray10")
## now some "horizontal rays" (going from center to very left or very right):
doHor <- function(x1, x2, z, CNT=FALSE, ...)
  lines(trans3d(x=seq(x1, x2, by=0.5), y= -0.7, z = z, pmat = p, continuous = CNT),
  lwd = 3, type="b", xpd=NA, ...)
doHor(-10, 0, z = -0.5, col = 2) # x in [-10, 0] -- to the very left : fine
doHor(-0.5, 2, z = -0.52, col = 4) # x in [-0.5, 2] only {to the right} --> all fine
## but now, x in [-0.5, 20] -- "too far" ==> "wrap around" problem (without 'continuous=TRUE'):
doHor(-0.5, 20, z = -0.58, col = "steelblue", lty=2)
## but it is fixed with continuous = CNT = TRUE:
doHor(-0.5, 20, z = -0.55, CNT=TRUE, col = "skyblue")

Type1Font

Type 1 and CID Fonts

Description

These functions are used to define the translation of a R graphics font family name to a Type 1 or CID font descriptions, used by both the postscript and pdf graphics devices.

Usage

Type1Font(family, metrics, encoding = "default")

CIDFont(family, cmap, cmapEncoding, pdfresource = "")

Arguments

family a character string giving the name to be used internally for a Type 1 or CID-keyed font family. This needs to uniquely identify each family, so if you modify a family which is in use (see postscriptFonts) you need to change the family name.

metrics a character vector of four or five strings giving paths to the afm (Adobe Font Metric) files for the font.

cmap the name of a CMap file for a CID-keyed font.

encoding for Type1Font, the name of an encoding file. Defaults to "default", which maps on Unix-alikes to "ISOLatin1.enc" and on Windows to "WinAnsi.enc". Otherwise, a file name in the ‘enc’ directory of the grDevices package, which is used if the path does not contain a path separator. An extension ".enc" can be omitted.

cmapEncoding The name of a character encoding to be used with the named CMap file: strings will be translated to this encoding when written to the file.

pdfresource A chunk of PDF code; only required for using a CID-keyed font on pdf; users should not be expected to provide this.
Details

For Type1Fonts, if four `.afm` files are supplied the fifth is taken to be "Symbol.afm". Relative paths are taken relative to the directory `R_HOME/library/grDevices/afm`. The fifth (symbol) font must be in AdobeSym encoding. However, the glyphs in the first four fonts are referenced by name and any encoding given within the `.afm` files is not used.

The `.afm` files may be compressed with (or without) final extension `.gz`: the files which ship with R are installed as compressed files with this extension.

Glyphs in CID-keyed fonts are accessed by ID (number) and not by name. The CMap file maps encoded strings (usually in a MBCS) to IDs, so cmap and cmapEncoding specifications must match. There are no real bold or italic versions of CID fonts (bold/italic were very rarely used in traditional East Asian topography), and for the pdf device all four font faces will be identical. However, for the postscript device, bold and italic (and bold italic) are emulated.

CID-keyed fonts are intended only for use for the glyphs of East Asian languages, which are all monospaced and are all treated as filling the same bounding box. (Thus plotmath will work with such characters, but the spacing will be less carefully controlled than with Western glyphs.) The CID-keyed fonts do contain other characters, including a Latin alphabet: non-East-Asian glyphs are regarded as monospaced with half the width of East Asian glyphs. This is often the case, but sometimes Latin glyphs designed for proportional spacing are used (and may look odd). We strongly recommend that CID-keyed fonts are only used for East Asian glyphs.

Value

A list of class "Type1Font" or "CIDFont".

See Also

postscript, pdf, postscriptFonts, and pdfFonts.

Examples

```r
## This duplicates "ComputerModernItalic".
CMitalic <- Type1Font("ComputerModern2",
c("CM_regular_10.afm", "CM_boldx_10.afm",
"cmti10.afm", "cmbxti10.afm",
"CM_symbol_10.afm"),
encoding = "TeXtext.enc")

## Not run:
## This could be used by
postscript(family = CMitalic)
## or
postscriptFonts(CMitalic = CMitalic)  # once in a session
postscript(family = "CMitalic", encoding = "TeXtext.enc")

## End(Not run)
```
Description

Available only on Windows. A graphics device is opened. For windows, win.graph, x11 and X11 this is a window on the current Windows display: the multiple names are for compatibility with other systems. win.metafile prints to a file and win.print to the Windows print system.

Usage

```r
windows(width, height, pointsize, record, rescale, xpinch, ypinch,
bg, canvas, gamma, xpos, ypos, buffered, title,
restoreConsole, clickToConfirm, fillOddEven,
family, antialias)
```

```r
win.graph(width, height, pointsize)
```

```r
win.metafile(filename = "", width = 7, height = 7, pointsize = 12,
family, restoreConsole = TRUE,
oxpinch = NA_real_, ypinch = NA_real_)
```

```r
win.print(width = 7, height = 7, pointsize = 12, printer = "",
family, antialias, restoreConsole = TRUE)
```

Arguments

- **width, height**  
  the (nominal) width and height of the canvas of the plotting window in inches. Default 7.
- **pointsize**  
  the default pointsize of plotted text, interpreted as big points (1/72 inch). Values are rounded to the nearest integer: values less than or equal to zero are reset to 12, the default.
- **record**  
  logical: sets the initial state of the flag for recording plots. Default FALSE.
- **rescale**  
  character, one of c("R", "fit", "fixed"). Controls the action for resizing of the device. Default "R". See the 'Resizing options' section.
- **xpinch, ypinch**  
  double. Pixels per inch, horizontally and vertically. Default NA_real_, which means to take the value from Windows.
- **bg**  
  color. The initial background color. Default "transparent".
- **canvas**  
  color. The color of the canvas which is visible when the background color is transparent. Should be a solid color (and any alpha value will be ignored). Default "white".
- **gamma**  
  gamma correction fudge factor. Colours in R are sRGB; if your monitor does not conform to sRGB, you might be able to improve things by tweaking this parameter to apply additional gamma correction to the RGB channels. By default 1 (no additional gamma correction).
- **xpos, ypos**  
  integer. Position of the top left of the window, in pixels. Negative values are taken from the opposite edge of the monitor. Missing values (the default) mean take the default from the ‘Rconsole’ file, which in turn defaults to xpos = -25, ypos = 0: this puts the right edge of the window 25 pixels from the right edge of the monitor.
buffered  logical. Should the screen output be double-buffered? Default TRUE.

title  character string, up to 100 bytes. With the default "", a suitable title is created internally. A C-style format for an integer will be substituted by the device number.

filename  the name of the output file: it will be an enhanced Windows metafile, usually given extension '.emf' or '.wmf'. Up to 511 characters are allowed. The page number is substituted if an integer format is included in the character string (see postscript for further details) and tilde-expansion (see path.expand) is performed. (The result must be less than 600 characters long.) The default, "", means the clipboard.

printer  The name of a printer as known to Windows. The default causes a dialog box to come up for the user to choose a printer.

restoreConsole  logical: see the 'Details' below. Defaults to FALSE for screen devices.

clickToConfirm  logical: if true confirmation of a new frame will be by clicking on the device rather than answering a problem in the console. Default TRUE.

fillOddEven  logical controlling the polygon fill mode: see polygon for details. Default TRUE.

family  A length-one character vector specifying the default font family. See section 'Fonts'.

antialias  A length-one character vector, requesting control over font antialiasing. This is partially matched to "default", "none", "cleartype" or "gray". See the 'Fonts' section.

Details

All these devices are implemented as variants of the same device.

All arguments of windows have defaults set by windows.options: the defaults given in the arguments section are the defaults for the defaults. These defaults also apply to the internal values of gamma, xpinch, ypinch, buffered, restoreConsole and antialias for win.graph, x11 and X11.

The size of a window is computed from information provided about the display: it depends on the system being configured accurately. By default a screen device asks Windows for the number of pixels per inch. This can be overridden (it is often wrong) by specifying xpinch and ypinch, most conveniently via windows.options. For example, a 13.3 inch 1280x800 screen (a typical laptop display) was reported as 96 dpi even though it is physically about 114 dpi. These arguments may also be useful to match the scale of output to the size of a metafile (which otherwise depends on the system being configured accurately).

The different colours need to be distinguished carefully. Areas outside the device region are coloured in the Windows application background colour. The device region is coloured in the canvas colour. This is over-painted by the background colour of a plot when a new page is called for, but that background colour can be transparent (and is by default). One difference between setting the canvas colour and the background colour is that when a plot is saved the background colour is copied but the canvas colour is not. The argument bg sets the initial value of par("bg") in base graphics and gpar("fill") in grid graphics

Recorded plot histories are of class "SavedPlots". They have a print method, and a subset method. As the individual plots are of class "recordedplot" they can be replayed by printing them: see recordPlot. The active plot history is stored in variable .SavedPlots in the workspace.

When a screen device is double-buffered (the default) the screen is updated 100ms after last plotting call or every 500ms during continuous plotting. These times can be altered by setting options("windowsTimeout") to a vector of two integers before opening the device.
Line widths as controlled by `par(lwd =)` are in multiples of 1/96inch. Multiples less than 1 are allowed, down to one pixel width.

For `win.metafile` only one plot is allowed per file, and Windows seems to disallow reusing the file. So the only way to allow multiple plots is to use a parametrized filename as in the example. If the filename is omitted (or specified as ""), the output is copied to the clipboard when the device is closed.

The `restoreConsole` argument is a temporary fix for a problem in the current implementation of several Windows graphics devices, and is likely to be removed in an upcoming release. If set to `FALSE`, the console will not receive the focus after the new device is opened.

There is support for semi-transparent colours of lines, fills and text on the screen devices. These work for saving (from the 'File' menu) to PDF, PNG, BMP, JPEG and TIFF, but will be ignored if saving to Metafile and PostScript. Limitations in the underlying Windows API mean that a semi-transparent object must be contained strictly within the device region (allowing for line widths and joins).

**Value**

A plot device is opened: nothing is returned to the R interpreter.

**Resizing options**

If a screen device is re-sized, the default behaviour ("R") is to redraw the plot(s) as if the new size had been specified originally. Using "fit" will rescale the existing plot(s) to fit the new device region, preserving the aspect ratio. Using "fixed" will leave the plot size unchanged, adding scrollbars if part of the plot is obscured.

A graphics window will never be created at more than 85% of the screen width or height, but can be resized to a larger size. For the first two rescale options the width and height are rescaled proportionally if necessary, and if `rescale = "fit"` the plot(s) are rescaled accordingly. If `rescale = "fixed"` the initially displayed portion is selected within these constraints, separately for width and height. In MDI mode, the limit is 85% of the MDI client region.

Using `strwidth` or `strheight` after a window has been rescaled (when using "fit") gives dimensions in the original units, but only approximately as they are derived from the metrics of the rescaled fonts (which are in integer sizes)

The displayed region may be bigger than the 'paper' size, and area(s) outside the 'paper' are coloured in the Windows application background colour. Graphics parameters such as "din" refer to the scaled plot if rescaling is in effect.

**Fonts**

The fonts used for text drawn in a Windows device may be controlled in two ways. The file `R_HOME\etc\Rdevga` can be used to specify mappings for `par(font =)` (or the grid equivalent). Alternatively, a font family can be specified by a non-empty family argument (or by e.g. `par(family =)` in the graphics package) and this will be used for fonts 1:4 via the Windows font database (see `windowsFonts`).

How the fonts look depends on the antialiasing settings, both through the `antialias` argument and the machine settings. These are hints to Windows GDI that may not be able to be followed, but `antialias = "none"` should ensure that no antialiasing is used. For a screen device the default depends on the machine settings: it will be "cleartype" if that has been enabled. Note that the greyscale antialiasing that is used only for small fonts (below about 9 pixels, around 7 points on a typical display).
When accessing a system through Remote Desktop, both the Remote Desktop settings and the user’s local account settings are relevant to whether antialiasing is used.

Some fonts are intended only to be used with ClearType antialiasing, for example the Meiryo Japanese font.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

• The default device size is 7 inches square, although this is often incorrectly implemented by Windows: see ‘Details’.
• Font sizes are in big points.
• The default font family is Arial.
• Line widths are as a multiple of 1/96 inch, with a minimum of one pixel.
• The minimum radius of a circle is 1 pixel.
• \texttt{pch = "."} with \texttt{cex = 1} corresponds to a rectangle of sides the larger of one pixel and 0.01 inch.
• Colours are interpreted via the unprofiled colour mapping of the graphics card – this is assumed to conform to sRGB.

Note

\texttt{x11()}, \texttt{X11()} and \texttt{win.graph()} are simple wrappers calling \texttt{windows()}, and mainly exist for compatibility reasons.

Further, \texttt{x11()} and \texttt{X11()} have their own help page for Unix-alikes (where they also have more arguments).

See Also

\texttt{windowsFonts, savePlot, bringToTop, Devices, postscript, x11} for Unix-alikes.

Examples

\begin{verbatim}
## Not run: ## A series of plots written to a sequence of metafiles
if(.Platform$OS.type == "windows")
  win.metafile("Rplot%02d.wmf", pointsize = 10)

## End(Not run)
\end{verbatim}

windows.options

\textit{Auxiliary Function to Set/View Defaults for Arguments of windows()}

Description

The auxiliary function \texttt{windows.options} can be used to set or view (if called without arguments) the default values for the arguments of \texttt{windows}.

\texttt{windows.options} needs to be called before calling \texttt{windows}, and the default values it sets can be overridden by supplying arguments to \texttt{windows}. 
windowsFonts

Usage

windows.options(..., reset = FALSE)

Arguments

... arguments width, height, pointsize, record, rescale, xpinch, ypinch, bg, canvas, gamma, xpos, ypos, buffered, restoreConsole, clickToConfirm, title, fillOddEven and antialias can be supplied.
reset logical: should the defaults be reset to their ‘factory-fresh’ values?

Details

If both reset = TRUE and ... are supplied the defaults are first reset to the ‘factory-fresh’ values and then the new values are applied.

Option antialias applies to screen devices (windows, win.graph, X11 and x11). There is a separate option, bitmap.aa.win, for bitmap devices with type = "windows".

Value

A named list of all the defaults. If any arguments are supplied the returned values are the old values and the result has the visibility flag turned off.

See Also

windows, ps.options.

Examples

## Not run:
## put something like this in your .Rprofile to customize the defaults
setHook(packageEvent("grDevices", "onLoad"),
function(...)
  grDevices::windows.options(width = 8, height = 6,
                           xpos = 0, pointsize = 10,
                           bitmap.aa.win = "cleartype")

## End(Not run)

windowsFonts

Windows Fonts

Description

These functions handle the translation of a device-independent R graphics font family name to a windows font description and are available only on Windows.

Usage

windowsFont(family)

windowsFonts(...)
Arguments

family a character vector containing the font family name ("TT" as the first two characters indicates a TrueType font).

... either character strings naming mappings to display, or new (named) mappings to define.

Details

A windows device is created with a default font (see the documentation for windows), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for "family" in par and for "fontfamily" in gpar in the grid package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to windows fonts. A list of mappings is maintained and can be modified by the user.

The windowsFonts function can be used to list existing mappings and to define new mappings. The windowsFont function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: "sans" for a sans-serif font, "serif" for a serif font and "mono" for a monospaced font.

These mappings will only be used if the current font face is 1 (plain), 2 (bold), 3 (italic), or 4 (bolditalic).

See Also

windows

Examples

if(.Platform$OS.type == "windows") withAutoprint({
  windowsFonts()
  windowsFonts("mono")
})
## Not run: ## set up for Japanese: needs the fonts installed
windows() # make sure we have the right device type (available on Windows only)
Sys.setlocale("LC_ALL", "ja")
windowsFonts(JP1 = windowsFont("MS Mincho"),
            JP2 = windowsFont("MS Gothic"),
            JP3 = windowsFont("Arial Unicode MS"))
plot(1:10)
text(5, 2, "\u{4E10}\u{4E00}\u{4E01}", family = "JP1")
text(7, 2, "\u{4E10}\u{4E00}\u{4E01}", family = "JP1", font = 2)
text(5, 1.5, "\u{4E10}\u{4E00}\u{4E01}", family = "JP1", family = "JP3")
## End(Not run)
x11

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Description
on Windows, the X11() and x11() functions are simple wrappers to windows() for historical
compatibility convenience: Calling x11() or X11() would work in most cases to open an
interactive graphics device.
In R versions before 3.6.0, the Windows version had a shorter list of formal arguments. Consequently, calls to X11(*) with arguments should name them for back compatibility.
Almost all information below does not apply on Windows.
on Unix-alikes X11 starts a graphics device driver for the X Window System (version 11). This
can only be done on machines/accounts that have access to an X server.
x11 is recognized as a synonym for X11.
The R function is a wrapper for two devices, one based on Xlib (https://en.wikipedia.
org/wiki/Xlib) and one using cairographics (https://www.cairographics.org).
Usage
X11(display = "", width, height, pointsize, gamma, bg, canvas,
fonts, family, xpos, ypos, title, type, antialias, symbolfamily)
X11.options(..., reset = FALSE)
Arguments
display

the display on which the graphics window will appear. The default is to use
the value in the user’s environment variable DISPLAY. This is ignored (with a
warning) if an X11 device is already open on another display.

width, height

the width and height of the plotting window, in inches. If NA, taken from the
resources and if not specified there defaults to 7 inches. See also ‘Resources’.

pointsize

the default pointsize to be used. Defaults to 12.

gamma

gamma correction fudge factor. Colours in R are sRGB; if your monitor does
not conform to sRGB, you might be able to improve things by tweaking this parameter to apply additional gamma correction to the RGB channels. By default
1 (no additional gamma correction).

bg

colour, the initial background colour. Default "transparent".

canvas

colour. The colour of the canvas, which is visible only when the background
colour is transparent. Should be an opaque colour (and any alpha value will be
ignored). Default "white".

fonts

for type = "Xlib" only: X11 font description strings into which weight, slant
and size will be substituted. There are two, the first for fonts 1 to 4 and the
second for font 5, the symbol font. See section ‘Fonts’.

family

The default family: a length-one character string. This is primarily intended for
cairo-based devices, but for type = "Xlib", the X11Fonts() database is used to
map family names to fonts (and this argument takes precedence over that one).

xpos, ypos

integer: initial position of the top left corner of the window, in pixels. Negative
values are from the opposite corner, e.g. xpos = -100 says the top right corner
should be 100 pixels from the right edge of the screen. If NA (the default),
successive devices are cascaded in 20 pixel steps from the top left. See also
‘Resources’.


title character string, up to 100 bytes. With the default, ",", a suitable title is created internally. A C-style format for an integer will be substituted by the device number (see the file argument to postscript for further details). How non-ASCII titles are handled is implementation-dependent.

type character string, one of "Xlib", "cairo", "nbcairo" or "dbcairo". Only the first will be available if the system was compiled without support for cairographics. The default is "cairo" where R was built using pangocairo (often not the case on macOS), otherwise "Xlib".

antialias for cairo types, the type of anti-aliasing (if any) to be used. One of c("default", "none", "gray", "subpixel").

symbolfamily for cairo-based devices only: a length-one character string that specifies the font family to be used as the "symbol" font (e.g., for plotmath output). The default value is "default", which means that R will choose a default "symbol" font based on the graphics device capabilities.

reset logical: should the defaults be reset to their defaults?

... Any of the arguments to X11, plus colortype and maxcubesize (see section 'Colour Rendering').

Details

The defaults for all of the arguments of X11 are set by X11.options: the 'Arguments' section gives the 'factory-fresh' defaults.

The initial size and position are only hints, and may not be acted on by the window manager. Also, some systems (especially laptops) are set up to appear to have a screen of a different size to the physical screen.

Option type selects between two separate devices: R can be built with support for neither, type = "Xlib" or both. Where both are available, types "cairo", "nbcairo" and "dbcairo" offer

- antialiasing of text and lines.
- translucent colours.
- scalable text, including to sizes like 4.5 pt.
- full support for UTF-8, so on systems with suitable fonts you can plot in many languages on a single figure (and this will work even in non-UTF-8 locales). The output should be locale-independent.

There are three variants of the cairo-based device. type = "nbcairo" has no buffering. type = "cairo" has some buffering, and supports dev.hold and dev.flush. type = "dbcairo" buffers output and updates the screen about every 100ms (by default). The refresh interval can be set (in units of seconds) by e.g. options(X11updates = 0.25): the value is consulted when a device is opened. Updates are only looked for every 50ms (at most), and during heavy graphics computations only every 500ms.

Which version will be fastest depends on the X11 connection and the type of plotting. You will probably want to use a buffered type unless backing store is in use on the X server (which for example it always is on the x86_64 macOS XQuartz server), as otherwise repainting when the window is exposed will be slow. On slow connections type = "dbcairo" will probably give the best performance.

Because of known problems with font selection on macOS without Pango (for example, most CRAN distributions), type = "cairo" is not the default there. These problems have included mixing up bold and italic (since worked around), selecting incorrect glyphs and ugly or missing symbol glyphs.
All devices which use an X11 server (including the type = "Xlib" versions of bitmap devices such as png) share internal structures, which means that they must use the same display and visual. If you want to change display, first close all such devices.

The cursor shown indicates the state of the device. If quiescent the cursor is an arrow: when the locator is in use it is a crosshair cursor, and when plotting computations are in progress (and this can be detected) it is a watch cursor. (The exact cursors displayed will depend on the window manager in use.)

**X11 Fonts**

This section applies only to type = "Xlib".

An initial/default font family for the device can be specified via the fonts argument, but if a device-independent R graphics font family is specified (e.g., via par(family =) in the graphics package), the X11 device makes use of the X11 font database (see X11Fonts) to convert the R graphics font family to an X11-specific font family description. If family is supplied as an argument, the X11 font database is used to convert that, but otherwise the argument fonts (with default given by X11.options) is used.

X11 chooses fonts by matching to a pattern, and it is quite possible that it will choose a font in the wrong encoding or which does not contain glyphs for your language (particularly common in iso10646-1 fonts).

The fonts argument is a two-element character vector, and the first element will be crucial in successfully using non-Western-European fonts. Settings that have proved useful include 
"*-mincho-%s-%s-***d-*******" for CJK languages and 
"*-cronyx-helvetica-%s-%s-***d-*******" for Russian.

For UTF-8 locales, the XLC_LOCALE databases provide mappings between character encodings, and you may need to add an entry for your locale (e.g., Fedora Core 3 lacked one for ru_RU.utf8).

**Cairo Fonts**

The cairographics-based devices work directly with font family names such as "Helvetica" which can be selected initially by the family argument and subsequently by par or gpar. There are mappings for the three device-independent font families, "sans" for a sans-serif font (to "Helvetica"), "serif" for a serif font (to "Times") and "mono" for a monospaced font (to "Courier").

The font selection is handled by Pango (usually via fontconfig) or fontconfig (on macOS and perhaps elsewhere). The results depend on the fonts installed on the system running R – setting the environment variable FCDEBUG to 1 normally allows some tracing of the selection process.

This works best when high-quality scalable fonts are installed, usually in Type 1 or TrueType formats: see the ‘R Installation and Administration’ manual for advice on how to obtain and install such fonts. At present the best rendering (including using kerning) will be achieved with TrueType fonts: see https://www.freedesktop.org/software/fontconfig/fontconfig-user.html for ways to set up your system to prefer them. The default family ("Helvetica") is likely not to use kerning: alternatives which should if you have them installed are "Arial", "DejaVu Sans" and "Liberation Sans" (and perhaps "FreeSans"). For those who prefer fonts with serifs, try "Times New Roman", "DejaVu Serif" and "Liberation Serif". To match LaTeX text, use something like "CM Roman".

Fedora systems from version 31 on do not like the default "symbol" font family for rendering symbols (e.g., plotmath). For those systems, users should specify a different font via symbolfamily. The default can also be changed via X11.options.

Problems with incorrect rendering of symbols (e.g., of quote(pi) and expression(10^degree)) have been seen on Linux systems which have the Wine symbol font installed – fontconfig then
prefers this and misinterprets its encoding. Adding the following lines to ‘~/.fonts.conf’ or ‘/etc/fonts/local.conf’ may circumvent this problem by preferring the URW Type 1 symbol font.

```xml
<fontconfig>
<match target="pattern">
  <test name="family"><string>Symbol</string></test>
  <edit name="family" mode="prepend" binding="same">
    <string>Standard Symbols L</string>
  </edit>
</match>
</fontconfig>
```

A test for this is to run at the command line `fc-match Symbol`. If that shows `symbol.ttf` that may be the Wine symbol font – use `locate symbol.ttf` to see if it is found from a directory with ‘wine’ in the name.

**Resources**

The standard X11 resource `geometry` can be used to specify the window position and/or size, but will be overridden by values specified as arguments or non-NA defaults set in `X11.options`. The class looked for is `R_x11`. Note that the resource specifies the width and height in pixels and not in inches. See for example ‘man X’ (or https://www.x.org/releases/current/). An example line in ‘~/.Xresources’ might be

```
R_x11*geometry: 900x900-0+0
```

which specifies a 900 x 900 pixel window at the top right of the screen.

**Colour Rendering**

X11 supports several ‘visual’ types, and nowadays almost all systems support ‘truecolor’ which X11 will use by default. This uses a direct specification of any RGB colour up to the depth supported (usually 8 bits per colour). Other visuals make use of a palette to support fewer colours, only grays or even only black/white. The palette is shared between all X11 clients, so it can be necessary to limit the number of colours used by `R`.

The default for type = "Xlib" is to use the best possible colour model for the visual of the X11 server: these days this will almost always be ‘truecolor’. This can be overridden by the `colortype` argument of `X11.options`. **Note:** All `X11` and type = "Xlib" `bmp`, `jpeg`, `png` and `tiff` devices share a `colortype` which is set when the first device to be opened. To change the `colortype` you need to close all open such devices, and then use `X11.options(colortype =)`. The `colortype` types are tried in the order "true", "pseudo", "gray" and "mono" (black or white only). The values "pseudo" and "pseudo.cube" provide two colour strategies for a pseudocolor visual. The first strategy provides on-demand colour allocation which produces exact colours until the colour resources of the display are exhausted (when plotting will fail). The second allocates (if possible) a standard colour cube, and requested colours are approximated by the closest value in the cube.

With `colortype` equal to "pseudo.cube" or "gray" successively smaller palettes are tried until one is completely allocated. If allocation of the smallest attempt fails the device will revert to "mono". For "gray" the search starts at 256 grays for a display with depth greater than 8, otherwise with half the available colours. For "pseudo.cube" the maximum cube size is set by `X11.options(maxcolors=)` and defaults to 256. With that setting the largest cube tried is 4 levels each for RGB, using 64 colours in the palette.
The cairographics-based devices most likely only work (or work correctly) with ‘TrueColor’ visuals, although in principle this depends on the cairo installation: a warning is given if any other visual is encountered.


Anti-aliasing

Anti-aliasing is only supported for cairographics-based devices, and applies to both graphics and fonts. It is generally preferable for lines and text, but can lead to undesirable effects for fills, e.g. for image plots, and so is never used for fills.

antialias = "default" is in principle platform-dependent, but seems most often equivalent to antialias = "gray".

Conventions

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

• The default device size is 7 inches square.
• Font sizes are in big points.
• The default font family is Helvetica.
• Line widths in 1/96 inch, minimum one pixel for type = "Xlib", 0.01 otherwise.
• For type = "Xlib" circle radii are in pixels with minimum one.
• Colours are interpreted by the X11 server, which is assumed to conform to sRGB.

Warning

Support for all the Unix devices is optional, so in packages X11() should be used conditionally after checking capabilities("X11").

See Also

Devices, X11Fonts, savePlot.

Examples

## Not run:
if(.Platform$OS.type == "unix") { # Only on unix-alikes, possibly Mac,
## put something like this is your .Rprofile to customize the defaults
setHook(packageEvent("grDevices", "onLoad"),
  function(...) grDevices::X11.options(width = 8, height = 6, xpos = 0,
  pointsize = 10))
}
## End(Not run)
Description

These functions handle the translation of a device-independent \texttt{R} graphics font family name to an X11 font description on Unix-alike platforms.

Usage

\begin{verbatim}
X11Font(font)
X11Fonts(...)  
\end{verbatim}

Arguments

- \texttt{font} \hspace{1cm} a character string containing an X11 font description.
- \texttt{...} \hspace{1cm} either character strings naming mappings to display, or new (named) mappings to define.

Details

These functions apply only to an X11 device with type = "Xlib" – X11(type = "cairo") uses a different mechanism to select fonts.

Such a device is created with a default font (see the documentation for \texttt{X11}), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for "family" in \texttt{par} and for "fontfamily" in \texttt{gpar} in the \texttt{grid} package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to X11 fonts. A list of mappings is maintained and can be modified by the user.

The \texttt{X11Fonts} function can be used to list existing mappings and to define new mappings. The \texttt{X11Font} function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: "sans" for a sans-serif font, "serif" for a serif font and "mono" for a monospaced font. Further mappings are provided for "Helvetica" (the device default), "Times", "CyrHelvetica", "CyrTimes" (versions of these fonts with Cyrillic support, at least on Linux), "Arial" (on some platforms including macOS) and "Mincho" (a CJK font).

Note

Available only when \texttt{capabilities()["X11"]} is true.

See Also

\texttt{X11}
xfig

Examples

```r
## IGNORE_RDIFF_BEGIN
if(capabilities()["X11"]) withAutoprint(
  X11Fonts()
  X11Fonts("mono")

utopia <- X11Font("-*utopia-*-*-*-*-*-*-*-*-*-*-*-*-*-*")
X11Fonts(utopia = utopia)
)
## IGNORE_RDIFF_END
```

xfig

XFig Graphics Device

Description

`xfig` starts the graphics device driver for producing XFig (version 3.2) graphics. The auxiliary function `ps.options` can be used to set and view (if called without arguments) default values for the arguments to `xfig` and `postscript`.

Usage

```r
xfig(file = if(onefile) "Rplots.fig" else "Rplot%03d.fig",
     onefile = FALSE, encoding = "none",
     paper = "default", horizontal = TRUE,
     width = 0, height = 0, family = "Helvetica",
     pointsize = 12, bg = "transparent", fg = "black",
     pagecentre = TRUE, defaultfont = FALSE, textspecial = FALSE)
```

Arguments

- `file` a character string giving the file path. For use with `onefile = FALSE` give a C integer format such as "Rplot%03d.fig" (the default in that case). (See `postscript` for further details.)
- `onefile` logical: if true allow multiple figures in one file. If false, assume only one page per file and generate a file number containing the page number.
- `encoding` The encoding in which to write text strings. The default is not to re-encode. This can be any encoding recognized by `iconv` in a Western UTF-8 locale you probably want to select an 8-bit encoding such as `latin1`, and in an East Asian locale an EUC encoding. If re-encoding fails, the text strings will be written in the current encoding with a warning.
- `paper` the size of paper region. The choices are "A4", "Letter" and "Legal" (and these can be lowercase). A further choice is "default", which is the default. If this is selected, the papersize is taken from the option "papersize" if that is set to a non-empty value, otherwise "A4".
- `horizontal` the orientation of the printed image, a logical. Defaults to true, that is landscape orientation.
- `width, height` the width and height of the graphics region in inches. The default is to use the entire page less a 0.5 inch overall margin in each direction. (See `postscript` for further details.)
family  the font family to be used. This must be one of "AvantGarde", "Bookman", "Courier", "Helvetica" (the default), "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" or "Times". Any other value is replaced by "Helvetica", with a warning.

pointsize  the default point size to be used.

bg  the initial background color to be used.

fg  the initial foreground color to be used.

pagecentre  logical: should the device region be centred on the page?

defaultfont  logical: should the device use xfig's default font?

textspecial  logical: should the device set the textspecial flag for all text elements. This is useful when generating pstex from xfig figures.

Details

Although xfig can produce multiple plots in one file, the XFig format does not say how to separate or view them. So onefile = FALSE is the default.

The file argument is interpreted as a C integer format as used by sprintf, with integer argument the page number. The default gives files ‘Rplot001.fig’, ‘Rplot999.fig’, ‘Rplot1000.fig’, ...

Line widths as controlled by par(lwd =) are in multiples of 5/6*1/72 inch. Multiples less than 1 are allowed. pch = " . " with cex = 1 corresponds to a square of side 1/72 inch.

Windows users can make use of WinFIG (http://www.schmidt-web-berlin.de/WinFIG.htm, shareware), or XFig under Cygwin.

Conventions

This section describes the implementation of the conventions for graphics devices set out in the ‘R Internals’ manual.

• The default device size is the paper size with a 0.25 inch border on all sides.
• Font sizes are in big points.
• The default font family is Helvetica.
• Line widths are integers, multiples of 5/432 inch.
• Circle radii are multiples of 1/1200 inch.
• Colours are interpreted by the viewing/printing application.

Note

Only some line textures (0 <= lty < 4) are used. Eventually this may be partially remedied, but the XFig file format does not allow as general line textures as the R model. Unimplemented line textures are displayed as dash-double-dotted.

There is a limit of 512 colours (plus white and black) per file.

Author(s)

Brian Ripley. Support for defaultFont and textSpecial contributed by Sebastian Fischmeister.

See Also

Devices, postscript, ps.options.
Description

`xy.coords` is used by many functions to obtain x and y coordinates for plotting. The use of this common mechanism across all relevant R functions produces a measure of consistency.

Usage

```r
xy.coords(x, y = NULL, xlab = NULL, ylab = NULL, log = NULL,
           recycle = FALSE, setLab = TRUE)
```

Arguments

- `x, y` the x and y coordinates of a set of points. Alternatively, a single argument `x` can be provided.
- `xlab, ylab` names for the x and y variables to be extracted.
- `log` character, "x", "y" or both, as for `plot`. Sets negative values to `NA` and gives a warning of class "log_le_0".
- `recycle` logical; if `TRUE`, recycle (rep) the shorter of `x` or `y` if their lengths differ.
- `setLab` logical indicating if the resulting `xlab` and `ylab` should be constructed from the "kind" of `(x, y)"; otherwise, the arguments `xlab` and `ylab` are used.

Details

An attempt is made to interpret the arguments `x` and `y` in a way suitable for bivariate plotting (or other bivariate procedures).

If `y` is `NULL` and `x` is a

- **formula**: of the form `yvar ~ xvar`. `xvar` and `yvar` are used as x and y variables.
- **list**: containing components `x` and `y`, these are used to define plotting coordinates.
- **time series**: the x values are taken to be `time(x)` and the y values to be the time series.

**matrix or data.frame with two or more columns**: the first is assumed to contain the x values and the second the y values. Note that is also true if `x` has columns named "x" and "y"; these names will be irrelevant here.

In any other case, the x argument is coerced to a vector and returned as `y` component where the resulting `x` is just the index vector `1:n`. In this case, the resulting `xlab` component is set to "Index" (if `setLab` is true as by default).

If `x` (after transformation as above) inherits from class "POSIXt" it is coerced to class "POSIXct".

Value

A list with the components

- `x` numeric (i.e., "double") vector of abscissa values.
- `y` numeric vector of the same length as `x`.
- `xlab` character(1) or `NULL`, the 'label' of `x`.
- `ylab` character(1) or `NULL`, the 'label' of `y`. 
See Also

`plot.default`, `lines`, `points` and `lowess` are examples of functions which use this mechanism.

Examples

```r
ff <- stats::fft(1:9)
exy.coords(ff)
exy.coords(ff, xlab = "fft") # labels "Re(fft)", "Im(fft)"

with(cars, exy.coords(dist ~ speed, NULL)$xlab ) # = "speed"

exy.coords(1:3, 1:2, recycle = TRUE) # otherwise error "lengths differ"
exy.coords(-2:10, log = "y")
##> xlab: "Index" \ warning: 3 y values <= 0 omitted ..
opt <- options(warn = 2)# => warnings would be errors, we suppress the one "we know":
suppressWarnings(exy.coords(-2:10, log = "y"), classes="log_le_0") -> xy
options(opt) # revert
stopifnot(is.list(xy), identical (1:13 +0, xy$x),
identical(c(rep(NA, 3), 1:10 +0), xy$y))
```

xyTable

*Multiplicities of (x,y) Points, e.g., for a Sunflower Plot*

Description

Given (x,y) points, determine their multiplicity – checking for equality only up to some (crude kind of) noise. Note that this is special kind of 2D binning.

Usage

```r
xyTable(x, y = NULL, digits)
```

Arguments

- `x, y` numeric vectors of the same length; alternatively other (x, y) argument combinations as allowed by `exy.coords(x, y)`.
- `digits` integer specifying the significant digits to be used for determining equality of coordinates. These are compared after rounding them via `signif(*, digits)`.

Value

A list with three components of same length,
- `x` x coordinates, rounded and sorted.
- `y` y coordinates, rounded (and sorted within x).
- `number` multiplicities (positive integers); i.e., `number[i]` is the multiplicity of `(x[i], y[i])`.

See Also

`sunflowerplot` which typically uses `xyTable(); signif`.
xyz.coords

Examples

```r
xyTable(iris[, 3:4], digits = 6)

## Discretized uncorrelated Gaussian:
require(stats)
xy <- data.frame(x = round(sort(rnorm(100))), y = rnorm(100))
xyTable(xy, digits = 1)
```

xyz.coords

Extracting Plotting Structures

Description

Utility for obtaining consistent x, y and z coordinates and labels for three dimensional (3D) plots.

Usage

```r
xyz.coords(x, y = NULL, z = NULL,
    xlab = NULL, ylab = NULL, zlab = NULL,
    log = NULL, recycle = FALSE, setLab = TRUE)
```

Arguments

- `x`, `y`, `z` the x, y and z coordinates of a set of points. Both y and z can be left at NULL. In this case, an attempt is made to interpret x in a way suitable for plotting. If the argument is a formula `zvar ~ xvar + yvar`, `xvar`, `yvar` and `zvar` are used as x, y and z variables; if the argument is a list containing components x, y and z, these are assumed to define plotting coordinates; if the argument is a matrix or `data.frame` with three or more columns, the first is assumed to contain the x values, the 2nd the y ones, and the 3rd the z ones – independently of any column names that x may have. Alternatively two arguments x and y can be provided (leaving z = NULL). One may be real, the other complex; in any other case, the arguments are coerced to vectors and the values plotted against their indices.

- `xlab`, `ylab`, `zlab` names for the x, y and z variables to be extracted.

- `log` character, "x", "y", "z" or combinations. Sets negative values to NA and gives a warning of class "log_le_0".

- `recycle` logical; if TRUE, recycle (rep) the shorter ones of x, y or z if their lengths differ.

- `setLab` logical indicating if the resulting `xlab` and `ylab` should be constructed from the "kind" of (x,y); otherwise, the arguments `xlab` and `ylab` are used.

Value

A list with the components

- `x` numeric (i.e., double) vector of abscissa values.

- `y` numeric vector of the same length as `x`.

- `z` numeric vector of the same length as `x`. 

xyz.coords

  `xlab` character(1) or NULL, the axis label of `x`.
  `ylab` character(1) or NULL, the axis label of `y`.
  `zlab` character(1) or NULL, the axis label of `z`.

Author(s)
Uwe Ligges and Martin Maechler

See Also
`xy.coords` for 2D.

Examples

xyz.coords(data.frame(10*1:9, -4), `y` = NULL, `z` = NULL)
xyz.coords(1:5, stats::fft(1:5), `z` = NULL, `xlab` = "X", `ylab` = "Y")
y <- 2 * (x2 <- 10 + (x1 <- 1:10))
xyz.coords(y ~ x1 + x2, `y` = NULL, `z` = NULL)
xyz.coords(data.frame(x = -1:9, y = 2:12, z = 3:13), `y` = NULL, `z` = NULL,
            `log` = "xy")
##> Warning message: 2 x values <= 0 omitted ...
## Suppress this specific warning:
suppressWarnings(xyz.coords(x = -1:9, `y` = 2:12, z = 3:13, `log` = "xy"),
                 classes = "log_le_0")
Chapter 5

The graphics package

---

**Description**

R functions for base graphics

**Details**

This package contains functions for ‘base’ graphics. Base graphics are traditional S-like graphics, as opposed to the more recent grid graphics.

For a complete list of functions with individual help pages, use `library(help = "graphics")`.

**Author(s)**

R Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

**References**


---

**abline**

*Add Straight Lines to a Plot*

**Description**

This function adds one or more straight lines through the current plot.

**Usage**

```r
abline(a = NULL, b = NULL, h = NULL, v = NULL, reg = NULL, 
       coef = NULL, untf = FALSE, ...)
```
Arguments

a, b
the intercept and slope, single values.

untf
logical asking whether to untransform. See ‘Details’.

h
the y-value(s) for horizontal line(s).

v
the x-value(s) for vertical line(s).

coef
a vector of length two giving the intercept and slope.

reg
an object with a coef method. See ‘Details’.

... graphical parameters such as col, lty and lwd (possibly as vectors: see ‘Details’) and xpd and the line characteristics lend, ljoin and lmitre.

Details

Typical usages are

abline(a, b, ...)
abline(h =, ...)
abline(v =, ...)
abline(coef =, ...)
abline(reg =, ...)

The first form specifies the line in intercept/slope form (alternatively a can be specified on its own and is taken to contain the slope and intercept in vector form).

The h= and v= forms draw horizontal and vertical lines at the specified coordinates.

The coef form specifies the line by a vector containing the slope and intercept.

reg is a regression object with a coef method. If this returns a vector of length 1 then the value is taken to be the slope of a line through the origin, otherwise, the first 2 values are taken to be the intercept and slope.

If untf is true, and one or both axes are log-transformed, then a curve is drawn corresponding to a line in original coordinates, otherwise a line is drawn in the transformed coordinate system. The h and v parameters always refer to original coordinates.

The graphical parameters col, lty and lwd can be specified; see par for details. For the h= and v= usages they can be vectors of length greater than one, recycled as necessary.

Specifying an xpd argument for clipping overrides the global par("xpd") setting used otherwise.

References


See Also

lines and segments for connected and arbitrary lines given by their endpoints. par.
arrows

Examples

## Setup up coordinate system (with x == y aspect ratio):
plot(c(-2,3), c(-1,5), type = "n", xlab = "x", ylab = "y", asp = 1)
## the x- and y-axis, and an integer grid
abline(h = 0, v = 0, col = "gray60")
text(1,0, "abline( h = 0 )", col = "gray60", adj = c(0, -.1))
abline(h = -1:5, v = -2:3, col = "lightgray", lty = 3)
abline(a = 1, b = 2, col = 2)
text(1,3, "abline( 1, 2 )", col = 2, adj = c(-.1, -.1))

## Simple Regression Lines:
require(stats)
sale5 <- c(6, 4, 9, 7, 6, 12, 8, 10, 9, 13)
plot(sale5)
abline(lsfit(1:10, sale5))
abline(lsfit(1:10, sale5, intercept = FALSE), col = 4) # less fitting

z <- lm(dist ~ speed, data = cars)
plot(cars)
abline(z) # equivalent to abline(reg = z) or
abline(coef = coef(z))

## trivial intercept model
abline(mC <- lm(dist ~ 1, data = cars)) ## the same as
abline(a = coef(mC), b = 0, col = "blue")

Add Arrows to a Plot

Description

Draw arrows between pairs of points.

Usage

arrows(x0, y0, x1 = x0, y1 = y0, length = 0.25, angle = 30,
       code = 2, col = par("fg"), lty = par("lty"),
       lwd = par("lwd"), ...)

Arguments

x0, y0 coordinates of points from which to draw.

x1, y1 coordinates of points to which to draw. At least one must the supplied

length length of the edges of the arrow head (in inches).

angle angle from the shaft of the arrow to the edge of the arrow head.

code integer code, determining kind of arrows to be drawn.

col, lty, lwd graphical parameters, possible vectors. NA values in col cause the arrow to be

omitted.

... graphical parameters such as xpd and the line characteristics lend, ljoin and

lmitre: see par.
**assocplot**

**Description**

Produce a Cohen-Friendly association plot indicating deviations from independence of rows and columns in a 2-dimensional contingency table.

**Usage**

```r
assocplot(x, col = c("black", "red"), space = 0.3,
          main = NULL, xlab = NULL, ylab = NULL)
```
assocplot

Arguments

x a two-dimensional contingency table in matrix form.
col a character vector of length two giving the colors used for drawing positive and negative Pearson residuals, respectively.
space the amount of space (as a fraction of the average rectangle width and height) left between each rectangle.
main overall title for the plot.
xlab a label for the x axis. Defaults to the name (if any) of the row dimension in x.
ylab a label for the y axis. Defaults to the name (if any) of the column dimension in x.

Details

For a two-way contingency table, the signed contribution to Pearson’s $\chi^2$ for cell $i,j$ is $d_{ij} = (f_{ij} - e_{ij})/\sqrt{e_{ij}}$, where $f_{ij}$ and $e_{ij}$ are the observed and expected counts corresponding to the cell. In the Cohen-Friendly association plot, each cell is represented by a rectangle that has (signed) height proportional to $d_{ij}$ and width proportional to $\sqrt{e_{ij}}$, so that the area of the box is proportional to the difference in observed and expected frequencies. The rectangles in each row are positioned relative to a baseline indicating independence ($d_{ij} = 0$). If the observed frequency of a cell is greater than the expected one, the box rises above the baseline and is shaded in the color specified by the first element of col, which defaults to black; otherwise, the box falls below the baseline and is shaded in the color specified by the second element of col, which defaults to red.

A more flexible and extensible implementation of association plots written in the grid graphics system is provided in the function assoc in the contributed package vcd (Meyer, Zeileis and Hornik, 2006).

References


See Also

mosaicplot, chisq.test.

Examples

### Aggregate over sex:
x <- marginSums(HairEyeColor, c(1, 2))
x assocplot(x, main = "Relation between hair and eye color")
Axis

Generic Function to Add an Axis to a Plot

Description

Generic function to add a suitable axis to the current plot.

Usage

Axis(x = NULL, at = NULL, ..., side, labels = NULL)

Arguments

x an object which indicates the range over which an axis should be drawn
at the points at which tick-marks are to be drawn.
side an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
labels this can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks, or a character or expression vector of labels to be placed at the tickpoints. If this is specified as a character or expression vector, at should be supplied and they should be the same length.
... arguments to be passed to methods and perhaps then to axis.

Details

This is a generic function. It works in a slightly non-standard way: if x is supplied and non-NULL it dispatches on x, otherwise if at is supplied and non-NULL it dispatches on at, and the default action is to call axis, omitting argument x.

The idea is that for plots for which either or both of the axes are numerical but with a special interpretation, the standard plotting functions (including boxplot, contour, coplot, filled.contour, pairs, plot.default, rug and stripchart) will set up user coordinates and Axis will be called to label them appropriately.

There are "Date" and "POSIXt" methods which can pass an argument format on to the appropriate axis method (see axis.POSIXct).

Value

The numeric locations on the axis scale at which tick marks were drawn when the plot was first drawn (see ‘Details’).

This function is usually invoked for its side effect, which is to add an axis to an already existing plot.

See Also

axis (which is eventually called from all Axis() methods) in package graphics.
**axis**

Add an Axis to a Plot

### Description

Adds an axis to the current plot, allowing the specification of the side, position, labels, and other options.

### Usage

```r
axis(side, at = NULL, labels = TRUE, tick = TRUE, line = NA,
pos = NA, outer = FALSE, font = NA, lty = "solid",
lwd = 1, lwd.ticks = lwd, col = NULL, col.ticks = NULL,
hadj = NA, padj = NA, gap.axis = NA, ...)
```

### Arguments

- **side**: an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
- **at**: the points at which tick-marks are to be drawn. Non-finite (infinite, `NaN` or `NA`) values are omitted. By default (when `NULL`) tickmark locations are computed, see 'Details' below.
- **labels**: this can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks, or a character or expression vector of labels to be placed at the tickpoints. (Other objects are coerced by `as.graphicsAnnot`.) If this is not logical, `at` should also be supplied and of the same length. If `labels` is of length zero after coercion, it has the same effect as supplying `TRUE`.
- **tick**: a logical value specifying whether tickmarks and an axis line should be drawn.
- **line**: the number of lines into the margin at which the axis line will be drawn, if not `NA`.
- **pos**: the coordinate at which the axis line is to be drawn: if not `NA` this overrides the value of `line`.
- **outer**: a logical value indicating whether the axis should be drawn in the outer plot margin, rather than the standard plot margin.
- **font**: font for text. Defaults to `par("font")`.
- **lty**: line type for both the axis line and the tick marks.
- **lwd, lwd.ticks**: line widths for the axis line and the tick marks. Zero or negative values will suppress the line or ticks.
- **col, col.ticks**: colors for the axis line and the tick marks respectively. `col = NULL` means to use `par("fg")`, possibly specified inline, and `col.ticks = NULL` means to use whatever color `col` resolved to.
- **hadj**: adjustment (see `par("adj")`) for all labels parallel (‘horizontal’) to the reading direction. If this is not a finite value, the default is used (centring for strings parallel to the axis, justification of the end nearest the axis otherwise).
- **padj**: adjustment for each tick label perpendicular to the reading direction. For labels parallel to the axes, `padj = 0` means left or bottom alignment, and `padj = 1` means right or top alignment (relative to the line). This can be a vector given a value for each string, and will be recycled as necessary.
If `padj` is not a finite value (the default), the value of `par("las")` determines the adjustment. For strings plotted perpendicular to the axis the default is to centre the string.

**gap.axis**

an optional (typically non-negative) numeric factor to be multiplied with the size of an ‘m’ to determine the minimal gap between labels that are drawn, see ‘Details’. The default, `NA`, corresponds to 1 for tick labels drawn parallel to the axis and 0.25 otherwise, i.e., the default is equivalent to

```r
perpendicular <- function(side, las) {
  is.x <- (side %% 2 == 1) # is horizontal x-axis
  (is.x && (las %in% 2:3)) ||
  (!is.x && (las %in% 1:2))
}

gap.axis <- if(perpendicular(side, las)) 0.25 else 1
```

gap.axis may typically be relevant when `at = ..` tick-mark positions are specified explicitly.

... other graphical parameters may also be passed as arguments to this function, particularly, `cex.axis`, `col.axis` and `font.axis` for axis annotation, i.e. tick labels, `mgp` and `xaxp` or `yaxp` for positioning, `tck` or `tcl` for tick mark length and direction, `las` for vertical/horizontal label orientation, or `fg` instead of `col`, and `xpd` for clipping. See `par` on these.

Parameters `xaxt` (sides 1 and 3) and `yaxt` (sides 2 and 4) control if the axis is plotted at all.

Note that `lab` will partial match to argument `labels` unless the latter is also supplied. (Since the default axes have already been set up by `plot.window`, `lab` will not be acted on by `axis`.)

**Details**

The axis line is drawn from the lowest to the highest value of `at`, but will be clipped at the plot region. By default, only ticks which are drawn from points within the plot region (up to a tolerance for rounding error) are plotted, but the ticks and their labels may well extend outside the plot region. Use `xpd = TRUE` or `xpd = NA` to allow axes to extend further.

When `at = NULL`, pretty tick mark locations are computed internally (the same way `axTicks(side)` would) from `par("xaxp")` or `"yaxp"` and `par("xlog")` (or "ylog"). Note that these locations may change if an on-screen plot is resized (for example, if the plot argument `asp` (see `plot.window`) is set.)

If `labels` is not specified, the numeric values supplied or calculated for `at` are converted to character strings as if they were a numeric vector printed by `print.default(digits = 7)`.

The code tries hard not to draw overlapping tick labels, and so will omit labels where they would abut or overlap previously drawn labels. This can result in, for example, every other tick being labelled. The ticks are drawn left to right or bottom to top, and space at least the size of an ‘m’, multiplied by `gap.axis`, is left between labels. In previous R versions, this applied only for labels written parallel to the axis direction, hence not for e.g., `las = 2`. Using `gap.axis = -1` restores that (buggy) previous behaviour (in the perpendicular case).

If either `line` or `pos` is set, they (rather than `par("mgp")`[3]) determine the position of the axis line and tick marks, and the tick labels are placed `par("mgp")`[2] further lines into (or towards for `pos`) the margin.

Several of the graphics parameters affect the way axes are drawn. The vertical (for sides 1 and 3) positions of the axis and the tick labels are controlled by `mgp[2:3]` and `mex`, the size and direction of
the ticks is controlled by tck and tcl and the appearance of the tick labels by cex.axis, col.axis and font.axis with orientation controlled by las (but not srt, unlike S which uses srt if at is supplied and las if it is not). Note that adj is not supported and labels are always centered. See \texttt{par} for details.

**Value**

The numeric locations on the axis scale at which tick marks were drawn when the plot was first drawn (see ‘Details’).

This function is usually invoked for its side effect, which is to add an axis to an already existing plot.

**References**


**See Also**

\texttt{Axis} for a generic interface.

\texttt{axTicks} returns the axis tick locations corresponding to at = \texttt{NULL}; \texttt{pretty} is more flexible for computing pretty tick coordinates and does not depend on (nor adapt to) the coordinate system in use.

Several graphics parameters affecting the appearance are documented in \texttt{par}.

**Examples**

```r
require(stats) # for rnorm
plot(1:4, rnorm(4), axes = FALSE)
axis(1, 1:4, LETTERS[1:4])
axis(2)
box() #-- to make it look "as usual"

plot(1:7, rnorm(7), main = "axis() examples",
     type = "s", xaxt = "n", frame.plot = FALSE, col = "red")
axis(1, 1:7, LETTERS[1:7], col.axis = "blue")
# unusual options:
axis(4, col = "violet", col.axis = "dark violet", lwd = 2)
axis(3, col = "gold", lty = 2, lwd = 0.5)

# one way to have a custom x axis
plot(1:10, xaxt = "n")
axis(1, xaxp = c(2, 9, 7))

## Changing default gap between labels:
plot(0:100, type="n", axes=FALSE, ann=FALSE)
title(quote("axis(1, ..., gap.axis = f)," ~ f > 0))
axis(2, at = 5*(0:20), las = 1, gap.axis = 1/4)
gaps <- c(4, 2, 1, 1/2, 1/4, 0.1, 0)
chG <- paste0(ifelse(gaps == 1, "default: ", ""),
     "gap.axis="", formatC(gaps))
jj <- seq_along(gaps)
linG <- -2.5*(jj-1)
for(j in jj) {
  isD <- gaps[j] == 1 # is default
```
axis.POSIXct

Date and Date-time Plotting Functions

Description

Functions to plot objects of classes "POSIXlt", "POSIXct" and "Date" representing calendar dates and times.

Usage

axis.POSIXct(side, x, at, format, labels = TRUE, ...)
axis.Date(side, x, at, format, labels = TRUE, ...)

Arguments

x, at  A date-time or date object, or other types of objects that can be converted appropriately.
side  See axis.
format  See strftime. If missing, a good guess for an appropriate format is made by looking at the argument at and its granularity.
labels  Either a logical value specifying whether annotations are to be made at the tickmarks, or a vector of character strings to be placed at the tickpoints.
...  Further arguments to be passed from or to other methods, typically graphical parameters.

Details

axis.POSIXct and axis.Date work quite hard (from R-4.3.0 by using pretty for DateTime-Classes) to choose suitable time units (years, months, days, hours, minutes, or seconds) and a sensible output format, but this can be overridden by supplying a format specification.

If at is supplied it specifies the locations of the ticks and labels whereas if x is specified a suitable grid of labels is chosen. Printing of tick labels can be suppressed by using labels = FALSE.

The date-times for a "POSIXct" input are interpreted in the time zone give by the "tzone" attribute if there is one, otherwise the current time zone.

The way the date-times are rendered (especially month names) is controlled by the locale setting of category "LC_TIME" (see Sys.setlocale).

Value

The locations on the axis scale at which tick marks were drawn.
axis.POSIXct

See Also

DateTimeClasses, Dates for details of the classes.

Examples

```
with(beaver1, {
  opar <- par(mfrow = c(2,1))
  time <- strptime(paste(1990, day, time %/% 100, time %% 100),
                  "%Y %j %H %M")
  plot(time, temp, type = "l")  # axis at 5-hour intervals.
  # now label every hour on the time axis
  r <- as.POSIXct(round(range(time), "hours"))
  axis.POSIXct(1, at = seq(r[1], r[2], by = "hour"), format = "%H")
  par(opar)  # reset changed par settings
})
```

```
plot(.leap.seconds, seq_along(.leap.seconds), type = "n", yaxt = "n",
     xlab = "leap seconds", ylab = "", bty = "n")
rug(.leap.seconds)
## or as dates
lps <- as.Date(.leap.seconds)
plot(lps, seq_along(.leap.seconds),
     type = "n", yaxt = "n", xlab = "leap seconds", ylab = "",
     bty = "n")
rug(lps)
```

```
## 100 random dates in a 10-week period
random.dates <- as.Date("2001/1/1") + 70*sort(stats::runif(100))
plot(random.dates, 1:100)
# or for a better axis labelling
plot(random.dates, 1:100, xaxt = "n")
axis.Date(1, at = seq(as.Date("2001/1/1"), max(random.dates)+6, "weeks"))
axis.Date(1, at = seq(as.Date("2001/1/1"), max(random.dates)+6, "days"),
           labels = FALSE, tcl = -0.2)
```

```
## axis.Date() with various data types:
```
```
x <- seq(as.Date("2022-01-20"), as.Date("2023-03-21"), by = "days")
plot(data.frame(x, y = 1), xaxt = "n")
legend("topleft", title = "input",
       legend = c("character", "Date", "POSIXct", "POSIXlt", "numeric"),
       fill = c("violet", "red", "orange", "coral1", "darkgreen"))
axis.Date(1)
```
```
```
```
```
```
```
```
```
```
```
```
Compute Axis Tickmark Locations

Description

Compute pretty tickmark locations, the same way as R does internally. This is only non-trivial when log coordinates are active. By default, gives the at values which axis(side) would use.

Usage

```r
axTicks(side, axp = NULL, usr = NULL, log = NULL, nintLog = NULL)
```

Arguments

- **side**: integer in 1:4, as for `axis`.
- **axp**: numeric vector of length three, defaulting to `par("xaxp")` or `par("yaxp")` depending on the side argument (par("xaxp") if side is 1 or 3, par("yaxp") if side is 2 or 4).
- **usr**: numeric vector of length two giving user coordinate limits, defaulting to the relevant portion of `par("usr")` (par("usr")[1:2] or par("usr")[3:4] for side in (1,3) or (2,4) respectively).
- **log**: logical indicating if log coordinates are active; defaults to `par("xlog")` or `par("ylog")` depending on side.
- **nintLog**: (only used when log is true): approximate (lower bound for the) number of tick intervals; defaults to `par("lab")[j]` where `j` is 1 or 2 depending on side. Set this to Inf if you want the same behavior as in earlier R versions (than 2.14.x).
The `axp`, `usr`, and `log` arguments must be consistent as their default values (the `par(....)` results) are. If you specify all three (as non-NULL), the graphics environment is not used at all. Note that the meaning of `axp` differs significantly when `log` is TRUE; see the documentation on `par(xaxp = .).

`axTicks()` may be seen as an R implementation of the C function `CreateAtVector()` in ‘..../src/main/plot.c’ which is called by `axis(side, *)` when no argument at is specified or directly by `axisTicks()` (in package `grDevices`).

The delicate case, `log = TRUE`, now makes use of `axisTicks` unless `nintLog = Inf` which exists for back compatibility.

Value

numeric vector of coordinate values at which axis tickmarks can be drawn. By default, when only the first argument is specified, these values should be identical to those that `axis(side)` would use or has used. Note that the values are decreasing when `usr` is (“reverse axis” case).

See Also

`axis`, `par`, `pretty` uses the same algorithm (but independently of the graphics environment) and has more options. However it is not available for `log = TRUE`.

`axisTicks()` (package `grDevices`).

Examples

```
plot(1:7, 10*21:27)
axTicks(1)
axTicks(2)
stopifnot(identical(axTicks(1), axTicks(3)),
          identical(axTicks(2), axTicks(4)))

## Show how axTicks() and axis() correspond :
op <- par(mfrow = c(3, 1))
for(x in 9999 * c(1, 2, 8)) {
  plot(x, 9, log = "x")
  cat(formatC(par("xaxp"), width = 5), ";", T <- axTicks(1), 
       "n")
  rug(T, col = adjustcolor("red", 0.5), lwd = 4)
}
par(op)

x <- 9.9*10^-3:10
plot(x, 1:14, log = "x")
axTicks(1) # now length 7
axTicks(1, nintLog = Inf) # rather too many

## An example using axTicks() without reference to an existing plot
## (copying R’s internal procedures for setting axis ranges etc.),
## You do need to supply _all_ of axp, usr, log, nintLog
## standard logarithmic y axis labels
ylims <- c(0.2, 88)
get_axp <- function(x) 10^ceiling(x[1]), floor(x[2]))
## mimic par("yaxs") == "i"
usr.i <- log10(ylims)
(aT.i <- axTicks(side = 2, usr = usr.i,
```
axp = c(get_axp(usr.i), n = 3, log = TRUE, nintLog = 5))
## mimic (default) par("yaxs") == "r"
usr.r <- extendrange(r = log10(ylims), f = 0.04)
(aT.r <- axTicks(side = 2, usr = usr.r,
    axp = c(get_axp(usr.r), 3), log = TRUE, nintLog = 5))
## Prove that we got it right :
plot(0:1, ylims, log = "y", yaxs = "i")
stopifnot(all.equal(aT.i, axTicks(side = 2)))
plot(0:1, ylims, log = "y", yaxs = "r")
stopifnot(all.equal(aT.r, axTicks(side = 2)))

barplot

Bar Plots

Description

Creates a bar plot with vertical or horizontal bars.

Usage

barplot(height, ...) 
## Default S3 method: 
barplot(height, width = 1, space = NULL,
    names.arg = NULL, legend.text = NULL, beside = FALSE,
    horiz = FALSE, density = NULL, angle = 45,
    col = NULL, border = par("fg"),
    main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
    xlim = NULL, ylim = NULL, xpd = TRUE, log = "",
    axes = TRUE, axisnames = TRUE,
    cex.axis = par("cex.axis"), cex.names = par("cex.axis"),
    inside = TRUE, plot = TRUE, axis.lty = 0, offset = 0,
    add = FALSE, ann = !add & & par("ann"), args.legend = NULL, ...)
## S3 method for class 'formula'
barplot(formula, data, subset, na.action,
    horiz = FALSE, xlab = NULL, ylab = NULL, ...)

Arguments

height either a vector or matrix of values describing the bars which make up the plot.
If height is a vector, the plot consists of a sequence of rectangular bars with heights given by the values in the vector. If height is a matrix and beside is FALSE then each bar of the plot corresponds to a column of height, with the values in the column giving the heights of stacked sub-bars making up the bar. If height is a matrix and beside is TRUE, then the values in each column are juxtaposed rather than stacked.

width optional vector of bar widths. Re-cycled to length the number of bars drawn. Specifying a single value will have no visible effect unless xlim is specified.
space

the amount of space (as a fraction of the average bar width) left before each bar. May be given as a single number or one number per bar. If height is a matrix and beside is TRUE, space may be specified by two numbers, where the first is the space between bars in the same group, and the second the space between the groups. If not given explicitly, it defaults to c(0,1) if height is a matrix and beside is TRUE, and to 0.2 otherwise.

names.arg

a vector of names to be plotted below each bar or group of bars. If this argument is omitted, then the names are taken from the names attribute of height if this is a vector, or the column names if it is a matrix.

legend.text

a vector of text used to construct a legend for the plot, or a logical indicating whether a legend should be included. This is only useful when height is a matrix. In that case given legend labels should correspond to the rows of height; if legend.text is true, the row names of height will be used as labels if they are non-null.

beside

a logical value. If FALSE, the columns of height are portrayed as stacked bars, and if TRUE the columns are portrayed as juxtaposed bars.

horiz

a logical value. If FALSE, the bars are drawn vertically with the first bar to the left. If TRUE, the bars are drawn horizontally with the first at the bottom.

density

a vector giving the density of shading lines, in lines per inch, for the bars or bar components. The default value of NULL means that no shading lines are drawn. Non-positive values of density also inhibit the drawing of shading lines.

angle

the slope of shading lines, given as an angle in degrees (counter-clockwise), for the bars or bar components.

col

a vector of colors for the bars or bar components. By default, "grey" is used if height is a vector, and a gamma-corrected grey palette if height is a matrix; see grey.colors.

border

the color to be used for the border of the bars. Use border = NA to omit borders. If there are shading lines, border = TRUE means use the same colour for the border as for the shading lines.

main,sub

main title and subtitle for the plot.

xlab

a label for the x axis.

ylab

a label for the y axis.

xlim

limits for the x axis.

ylim

limits for the y axis.

xpd

logical. Should bars be allowed to go outside region?

log

string specifying if axis scales should be logarithmic; see plot.default.

axes

logical. If TRUE, a vertical (or horizontal, if horiz is true) axis is drawn.

axisnames

logical. If TRUE, and if there are names.arg (see above), the other axis is drawn (with lty = 0) and labeled.

cex.axis

expansion factor for numeric axis labels (see par(’cex’)).

cex.names

expansion factor for axis names (bar labels).

inside

logical. If TRUE, the lines which divide adjacent (non-stacked!) bars will be drawn. Only applies when space = 0 (which partly is when beside = TRUE).

plot

logical. If FALSE, nothing is plotted.

axis.lty

the graphics parameter lty (see par(’lty’)) applied to the axis and tick marks of the categorical (default horizontal) axis. Note that by default the axis is suppressed.
offset a vector indicating how much the bars should be shifted relative to the x axis.
add logical specifying if bars should be added to an already existing plot; defaults to FALSE.
ann logical specifying if the default annotation (main, sub, xlab, ylab) should appear on the plot, see title.
args.legend list of additional arguments to pass to legend(); names of the list are used as argument names. Only used if legend.text is supplied.
formula a formula where the y variables are numeric data to plot against the categorical x variables. The formula can have one of three forms:

\[ y \sim x \]
\[ y \sim x1 + x2 \]
\[ \text{cbind}(y1, y2) \sim x \]

(see the examples).
data a data frame (or list) from which the variables in formula should be taken.
subset an optional vector specifying a subset of observations to be used.
na.action a function which indicates what should happen when the data contain NA values. The default is to ignore missing values in the given variables.
... arguments to be passed to/from other methods. For the default method these can include further arguments (such as axes, asp and main) and graphical parameters (see par) which are passed to plot.window(), title() and axis.

Value

A numeric vector (or matrix, when beside = TRUE), say mp, giving the coordinates of all the bar midpoints drawn, useful for adding to the graph.

If beside is true, use colMeans(mp) for the midpoints of each group of bars, see example.

Author(s)

R Core, with a contribution by Arni Magnusson.

References


See Also

plot(..., type = "h"), dotchart, hist for bars of a continuous variable. mosaicplot(), more sophisticated to visualize several categorical variables.

Examples

# Formula method
barplot(GNP ~ Year, data = longley)
barplot(cbind(Employed, Unemployed) ~ Year, data = longley)

## 3rd form of formula - 2 categories :
op <- par(mfrow = 2:1, mgp = c(3,1,0)/2, mar = .1+c(3,3:1))
summary(d.Titanic <- as.data.frame(Titanic))
barplot(Freq ~ Class + Survived, data = d.Titanic,
    subset = Age == "Adult" & Sex == "Male",
    main = "barplot(Freq ~ Class + Survived, *)", ylab = "# {passengers}", legend.text = TRUE)

# Corresponding table :
(xt <- xtabs(Freq ~ Survived + Class + Sex, d.Titanic, subset = Age=="Adult"))
# Alternatively, a mosaic plot :
mosaicplot(xt[,","Male"], main = "mosaicplot(Freq ~ Class + Survived, *)", color=TRUE)

par(op)

# Default method
require(grDevices) # for colours
tN <- table(Ni <- stats::rpois(100, lambda = 5))
r <- barplot(tN, col = rainbow(20))

#- type = "h" plotting *is* `barplot
lines(r, tN, type = "h", col = "red", lwd = 2)

barplot(tN, space = 1.5, axisnames = FALSE,
    sub = "barplot(..., space= 1.5, axisnames = FALSE")

barplot(VADeaths, plot = FALSE)
barplot(VADeaths, plot = FALSE, beside = TRUE)

mp <- barplot(VADeaths) # default
tot <- colMeans(VADeaths)
text(mp, tot + 3, format(tot), xpd = TRUE, col = "blue")
barplot(VADeaths, beside = TRUE,
    col = c("lightblue", "mistyrose", "lightcyan",
        "lavender", "cornsilk"),
    legend.text = rownames(VADeaths), ylim = c(0, 100))
title(main = "Death Rates in Virginia", font.main = 4)

hh <- t(VADeaths)
mybarcol <- "gray20"
mp <- barplot(hh, beside = TRUE,
    col = c("lightblue", "mistyrose",
        "lightcyan", "lavender"),
    legend.text = colnames(VADeaths), ylim = c(0,100),
    main = "Death Rates in Virginia", font.main = 4,
    sub = "Faked upper 2*sigma error bars", col.sub = mybarcol,
    cex.names = 1.5)
segments(mp, hh, mp, hh + 2*sqrt(100*hh/100), col = mybarcol, lwd = 1.5)
stopifnot(dim(mp) == dim(hh)) # corresponding matrices
mtext(side = 1, at = colMeans(mp), line = -2,
    text = paste("Mean", formatC(colMeans(hh))), col = "red")

# Bar shading example
barplot(VADeaths, angle = 15+10*1:5, density = 20, col = "black",
    legend.text = rownames(VADeaths))
title(main = list("Death Rates in Virginia", font = 4))

# Border color
barplot(VADeaths, border = "dark blue")
# Log scales (not much sense here)
barplot(tN, col = heat.colors(12), log = "y")
barplot(tN, col = gray.colors(20), log = "xy")

# Legend location
barplot(height = cbind(x = c(465, 91) / 465 * 100,
          y = c(840, 200) / 840 * 100,
          z = c(37, 17) / 37 * 100),
        beside = FALSE,
        width = c(465, 840, 37),
        col = c(1, 2),
        legend.text = c("A", "B"),
        args.legend = list(x = "topleft"))

box

\textit{Draw a Box around a Plot}

\textbf{Description}

This function draws a box around the current plot in the given color and linetype. The \texttt{bty} parameter determines the type of box drawn. See \texttt{par} for details.

\textbf{Usage}

\texttt{box(\texttt{which} = "plot", \texttt{lt} = "solid", \ldots )}

\textbf{Arguments}

- \texttt{which} character, one of \texttt{"plot", "figure", "inner" and "outer"}.
- \texttt{lt} line type of the box.
- \ldots further graphical parameters, such as \texttt{bty}, \texttt{col}, or \texttt{lwd}, see \texttt{par}. Note that \texttt{xpd} is not accepted as clipping is always to the device region.

\textbf{Details}

The choice of colour is complicated. If \texttt{col} was supplied and is not \texttt{NA}, it is used. Otherwise, if \texttt{fg} was supplied and is not \texttt{NA}, it is used. The final default is \texttt{par("col")}.

\textbf{References}


\textbf{See Also}

\texttt{rect} for drawing of arbitrary rectangles.

\textbf{Examples}

\begin{verbatim}
plot(1:7, abs(stats::rnorm(7)), type = "h", axes = FALSE)
axis(1, at = 1:7, labels = letters[1:7])
box(lty = "1373", col = "red")
\end{verbatim}
Description

Produce box-and-whisker plot(s) of the given (grouped) values.

Usage

boxplot(x, ...)

## S3 method for class 'formula'
boxplot(formula, data = NULL, ..., subset, na.action = NULL,
xlab = mklab(y_var = horizontal),
 ylab = mklab(y_var = !horizontal),
 add = FALSE, ann = !add, horizontal = FALSE,
drop = FALSE, sep = ",", lex.order = FALSE)

## Default S3 method:
boxplot(x, ..., range = 1.5, width = NULL, varwidth = FALSE,
notch = FALSE, outline = TRUE, names, plot = TRUE,
border = par("fg"), col = "lightgray", log = "",
pars = list(boxwex = 0.8, staplewex = 0.5, outwex = 0.5),
ann = !add, horizontal = FALSE, add = FALSE, at = NULL)

Arguments

formula a formula, such as y ~ grp, where y is a numeric vector of data values to be split into groups according to the grouping variable grp (usually a factor). Note that ~ g1 + g2 is equivalent to g1:g2.
data a data.frame (or list) from which the variables in formula should be taken.
subset an optional vector specifying a subset of observations to be used for plotting.
na.action a function which indicates what should happen when the data contain NAs. The default is to ignore missing values in either the response or the group.
xlab, ylab x- and y-axis annotation, since R 3.6.0 with a non-empty default. Can be suppressed by ann=FALSE.
ann logical indicating if axes should be annotated (by xlab and ylab).
drop, sep, lex.order passed to split.default, see there.
x for specifying data from which the boxplots are to be produced. Either a numeric vector, or a single list containing such vectors. Additional unnamed arguments specify further data as separate vectors (each corresponding to a component boxplot). NAs are allowed in the data.
...

For the formula method, named arguments to be passed to the default method. For the default method, unnamed arguments are additional data vectors (unless x is a list when they are ignored), and named arguments are arguments and graphical parameters to be passed to bxp in addition to the ones given by argument pars (and override those in pars). Note that bxp may or may not make use of graphical parameters it is passed: see its documentation.
the plot whiskers extend out from the box. If range is positive, the whiskers extend to the most extreme data point which is no more than range times the interquartile range from the box. A value of zero causes the whiskers to extend to the data extremes.

width
a vector giving the relative widths of the boxes making up the plot.

varwidth
if varwidth is TRUE, the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.

notch
if notch is TRUE, a notch is drawn in each side of the boxes. If the notches of two plots do not overlap this is 'strong evidence' that the two medians differ (Chambers et al, 1983, p. 62). See boxplot.stats for the calculations used.

outline
if outline is not true, the outliers are not drawn (as points whereas S+ uses lines).

names
group labels which will be printed under each boxplot. Can be a character vector or an expression (see plotmath).

boxwex
a scale factor to be applied to all boxes. When there are only a few groups, the appearance of the plot can be improved by making the boxes narrower.

staplewex
staple line width expansion, proportional to box width.

outwex
outlier line width expansion, proportional to box width.

plot
if TRUE (the default) then a boxplot is produced. If not, the summaries which the boxplots are based on are returned.

border
an optional vector of colors for the outlines of the boxplots. The values in border are recycled if the length of border is less than the number of plots.

col
if col is non-null it is assumed to contain colors to be used to colour the bodies of the box plots. By default they are in the background colour.

log
character indicating if x or y or both coordinates should be plotted in log scale.

pars
a list of (potentially many) more graphical parameters, e.g., boxwex or outpch; these are passed to bxp (if plot is true); for details, see there.

horizontal
logical indicating if the boxplots should be horizontal; default FALSE means vertical boxes.

add
logical, if true add boxplot to current plot.

at
numeric vector giving the locations where the boxplots should be drawn, particularly when add = TRUE; defaults to 1:n where n is the number of boxes.

Details
The generic function boxplot currently has a default method (boxplot.default) and a formula interface (boxplot.formula).

If multiple groups are supplied either as multiple arguments or via a formula, parallel boxplots will be plotted, in the order of the arguments or the order of the levels of the factor (see factor).

Missing values are ignored when forming boxplots.

Value
List with the following components:

stats
a matrix, each column contains the extreme of the lower whisker, the lower hinge, the median, the upper hinge and the extreme of the upper whisker for one group/plot. If all the inputs have the same class attribute, so will this component.
n  a vector with the number of (non-NA) observations in each group.
conf  a matrix where each column contains the lower and upper extremes of the notch.
out  the values of any data points which lie beyond the extremes of the whiskers.
group  a vector of the same length as out whose elements indicate to which group the outlier belongs.
names  a vector of names for the groups.

References

See also
boxplot.stats which does the computation, bxp for the plotting and more examples; and stripchart for an alternative (with small data sets).

Examples
```r
## boxplot on a formula:
boxplot(count ~ spray, data = InsectSprays, col = "lightgray")
# *add* notches (somewhat funny here <-> warning "notches .. outside hinges"):
boxplot(count ~ spray, data = InsectSprays,
       notch = TRUE, add = TRUE, col = "blue")

boxplot(decrease ~ treatment, data = OrchardSprays, col = "bisque",
        log = "y")
## horizontal=TRUE, switching y <-> x :
boxplot(decrease ~ treatment, data = OrchardSprays, col = "bisque",
        log = "x", horizontal=TRUE)

rb <- boxplot(decrease ~ treatment, data = OrchardSprays, col = "bisque")
title("Comparing boxplot()s and non-robust mean +/- SD")
mn.t <- tapply(OrchardSprays$decrease, OrchardSprays$treatment, mean)
sd.t <- tapply(OrchardSprays$decrease, OrchardSprays$treatment, sd)
xi <- 0.3 + seq(rb$n)
points(xi, mn.t, col = "orange", pch = 18)
arrows(xi, mn.t - sd.t, xi, mn.t + sd.t,
       code = 3, col = "pink", angle = 75, length = .1)

## boxplot on a matrix:
mat <- cbind(Uni05 = (1:100)/21, Norm = rnorm(100),
             `5T` = rt(100, df = 5), Gam2 = rgamma(100, shape = 2))
boxplot(mat) # directly, calling boxplot.matrix()

## boxplot on a data frame:
df. <- as.data.frame(mat)
par(las = 1) # all axis labels horizontal
boxplot(df., main = "boxplot(\text{*}, horizontal = TRUE)", horizontal = TRUE)
```
## Using 'at =' and adding boxplots -- example idea by Roger Bivand:

```r
boxplot(len ~ dose, data = ToothGrowth,
        boxwex = 0.25, at = 1:3 - 0.2,
        subset = supp == "VC", col = "yellow",
        main = "Guinea Pigs’ Tooth Growth",
        xlab = "Vitamin C dose mg",
        ylab = "tooth length",
        xlim = c(0.5, 3.5), ylim = c(0, 35), yaxs = "i")
```

```r
boxplot(len ~ dose, data = ToothGrowth, add = TRUE,
        boxwex = 0.25, at = 1:3 + 0.2,
        subset = supp == "OJ", col = "orange")
```

```r
legend(2, 9, c("Ascorbic acid", "Orange juice"),
       fill = c("yellow", "orange"))
```

```r
## With less effort (slightly different) using factor *interaction*:

```r
boxplot(len ~ dose:supp, data = ToothGrowth,
        boxwex = 0.5, col = c("orange", "yellow"),
        main = "Guinea Pigs’ Tooth Growth",
        xlab = "Vitamin C dose mg", ylab = "tooth length",
        sep = ":", lex.order = TRUE, ylim = c(0, 35), yaxs = "i")
```

```r
## more examples in help(bxp)
```

---

**boxplot.matrix**

*Draw a Boxplot for each Column (Row) of a Matrix*

**Description**

Interpreting the columns (or rows) of a matrix as different groups, draw a boxplot for each.

**Usage**

```r
## S3 method for class 'matrix'

boxplot(x, use.cols = TRUE, ...)
```

**Arguments**

- **x** a numeric matrix.
- **use.cols** logical indicating if columns (by default) or rows (use.cols = FALSE) should be plotted.
- **...** Further arguments to boxplot.

**Value**

A list as for boxplot.

**Author(s)**

Martin Maechler, 1995, for S+, then R package sfsmisc.

**See Also**

- boxplot.default which already works nowadays with data.frames; boxplot.formula, plot.factor which work with (the more general concept) of a grouping factor.
Examples

```r
## Very similar to the example in ?boxplot
mat <- cbind(Uni05 = (1:100)/21, Norm = rnorm(100),
             T5 = rt(100, df = 5), Gam2 = rgamma(100, shape = 2))
boxplot(mat, main = "boxplot.matrix(...., main = ...)",
        notch = TRUE, col = 1:4)
```

Description

`bxp` draws box plots based on the given summaries in `z`. It is usually called from within `boxplot`, but can be invoked directly.

Usage

```r
bxp(z, notch = FALSE, width = NULL, varwidth = FALSE,
    outline = TRUE, notch.frac = 0.5, log = "",
    border = par("fg"), pars = NULL, frame.plot = axes,
    horizontal = FALSE, ann = TRUE,
    add = FALSE, at = NULL, show.names = NULL,
    
    ...)```

Arguments

- `z`: a list containing data summaries to be used in constructing the plots. These are usually the result of a call to `boxplot`, but can be generated in any fashion.
- `notch`: if `notch` is `TRUE`, a notch is drawn in each side of the boxes. If the notches of two plots do not overlap then the medians are significantly different at the 5 percent level.
- `width`: a vector giving the relative widths of the boxes making up the plot.
- `varwidth`: if `varwidth` is `TRUE`, the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.
- `outline`: if `outline` is not `true`, the outliers are not drawn.
- `notch.frac`: numeric in (0,1). When `notch = TRUE`, the fraction of the box width that the notches should use.
- `border`: character or numeric (vector), the color of the box borders. Is recycled for multiple boxes. Is used as default for the `boxcol`, `medcol`, `whiskcol`, `staplecol`, and `outcol` options (see below).
- `log`: character, indicating if any axis should be drawn in logarithmic scale, as in `plot.default`.
- `frame.plot`: logical, indicating if a ‘frame’ (box) should be drawn; defaults to `TRUE`, unless `axes = FALSE` is specified.
- `horizontal`: logical indicating if the boxplots should be horizontal; default `FALSE` means vertical boxes.
- `ann`: a logical value indicating whether the default annotation (title and x and y axis labels) should appear on the plot.
add logical, if true add boxplot to current plot.

at numeric vector giving the locations where the boxplots should be drawn, particularly when add = TRUE; defaults to 1:n where n is the number of boxes.

show.names Set to TRUE or FALSE to override the defaults on whether an x-axis label is printed for each group.

pars,... graphical parameters (etc) can be passed as arguments to this function, either as a list (pars) or normally(...), see the following. (Those in ... take precedence over those in pars.)

Currently, yaxs and ylim are used 'along the boxplot', i.e., vertically, when horizontal is false, and xlim horizontally. xaxt, yaxt, las, cex.axis, gap.axis, and col.axis are passed to axis, and main, cex.main, col.main, sub, cex.sub, col.sub, xlab, ylab, cex.lab, and col.lab are passed to title.

In addition, axes is accepted (see plot.window), with default TRUE.

The following arguments (or pars components) allow further customization of the boxplot graphics. Their defaults are typically determined from the non-prefixed version (e.g., boxlty from lty), either from the specified argument or pars component or the corresponding par one.

boxwex: a scale factor to be applied to all boxes. When there are only a few groups, the appearance of the plot can be improved by making the boxes narrower. The default depends on at and typically is 0.8.

staplewex, outwex: staple and outlier line width expansion, proportional to box width; both default to 0.5.

boxlty, boxlwd, boxcol, boxfill: box outline type, width, color, and fill color
(which currently defaults to col and will in future default to par("bg")).

medlty, medlwd, medpch, medcex, medcol, medbg: median line type, line width, point character, point size expansion, color, and background color.

The default medpch = NA suppresses the point, and medlty = "blank" does so for the line. Note that medlwd defaults to 3× the default lwd.

whisklty, whisklwd, whiskcol: whisker line type (default: "dashed"), width, and color.

staplelty, staplelwd, staplecol: staple (= end of whisker) line type, width, and color.

outlty, outlwd, outpch, outcex, outcol, outbg: outlier line type, line width, point character, point size expansion, color, and background color. The default outlty = "blank" suppresses the lines and outpch = NA suppresses points.

Value
An invisible vector, actually identical to the at argument, with the coordinates ("x" if horizontal is false, "y" otherwise) of box centers, useful for adding to the plot.

Note
When add = FALSE, xlim now defaults to xlim = range(at, *) + c(-0.5, 0.5). It will usually be a good idea to specify xlim if the "x" axis has a log scale or width is far from uniform.

Author(s)
The R Core development team and Arni Magnusson (then at U Washington) who has provided most changes for the box*, med*, whisk*, staple*, and out* arguments.
Examples

```r
require(stats)
set.seed(753)
(bx.p <- boxplot(split(rt(100, 4), gl(5, 20))))

op <- par(mfrow = c(2, 2))
bxp(bx.p, xaxt = "n")
bxp(bx.p, notch = TRUE, axes = FALSE, pch = 4, boxfill = 1:5)

do.ci <- TRUE, boxfill = "lightblue", frame.plot = FALSE,

outline = FALSE, main = "bxp(*, frame.plot= FALSE, outline= FALSE)"

bxp(bx.p, notch = TRUE, boxfill = "lightblue", border = 2:6,

ylim = c(-4, 4), pch = 22, bg = "green", log = "x",
main = "... log = 'x', ylim = *")

par(op)

d <<- par(mfrow = c(1, 2))

## single group -- no label
boxplot (weight ~ group, data = PlantGrowth, subset = group == "ctrl")

## with label
bx <- boxplot(weight ~ group, data = PlantGrowth,

subset = group == "ctrl", plot = FALSE)
bxp(bx, show.names=TRUE)

par(op)

## passing gap.axis=* to axis(), PR#18109:
boxplot(matrix(100*rnorm(1e3), 50, 20),

cex.axis = 1.5, gap.axis = -1)# showing *all* labels

z <- split(rnorm(1000), rpois(1000, 2.2))
boxplot(z, whisklty = 3, main = "boxplot(z, whisklty = 3)"

## Colour support similar to plot.default:
op <- par(mfrow = 1:2, bg = "light gray", fg = "midnight blue")
boxplot(z, col.axis = "skyblue3", main = "boxplot(*, col.axis=..,main=..)"

plot(z[[1]], col.axis = "skyblue3", main = "plot(*, col.axis=..,main=..)"

mtext("par(bg="light gray", fg="midnight blue")", outer = TRUE, line = -1.2)

par(op)

## Mimic S-Plus:
splus <- list(boxwex = 0.4, staplewex = 1, outwex = 1, boxfill = "grey40",

medlwd = 3, medcol = "white", whisklty = 3, outlyt = 1, outpch = NA)
boxplot(z, pars = splus)

## Recycled and "sweeping" parameters
op <- par(mfrow = c(1,2))
boxplot(z, border = 1:5, lty = 3, medlty = 1, medlwd = 2.5)
boxplot(z, boxfill = 1:3, pch = 1:5, lwd = 1.5, medcol = "white")
par(op)

## too many possibilities
boxplot(z, boxfill = "light gray", outpch = 21:25, outlyt = 2,

bg = "pink", lwd = 2,

References

cdplot

Description
Computes and plots conditional densities describing how the conditional distribution of a categorical variable \( y \) changes over a numerical variable \( x \).

Usage

```r
cdplot(x, ...)  
  ## Default S3 method:
  cdplot(x, y,  
    plot = TRUE, tol.ylab = 0.05, ylevels = NULL,  
    bw = "nrd0", n = 512, from = NULL, to = NULL,  
    col = NULL, border = 1, main = "", xlab = NULL, ylab = NULL,  
    yaxlabels = NULL, xlim = NULL, ylim = c(0, 1), weights = NULL, ...)  
  ## S3 method for class 'formula'
  cdplot(formula, data = list(),  
    plot = TRUE, tol.ylab = 0.05, ylevels = NULL,  
    bw = "nrd0", n = 512, from = NULL, to = NULL,  
    col = NULL, border = 1, main = "", xlab = NULL, ylab = NULL,  
    yaxlabels = NULL, xlim = NULL, ylim = c(0, 1), ...,
    subset = NULL, weights = NULL)
```

Arguments

- **x** an object, the default method expects a single numerical variable (or an object coercible to this).
- **y** a "factor" interpreted to be the dependent variable
- **formula** a "formula" of type \( y \sim x \) with a single dependent "factor" and a single numerical explanatory variable.
- **data** an optional data frame.
- **plot** logical. Should the computed conditional densities be plotted?
- **tol.ylab** convenience tolerance parameter for y-axis annotation. If the distance between two labels drops under this threshold, they are plotted equidistantly.
- **ylevels** a character or numeric vector specifying in which order the levels of the dependent variable should be plotted.
- **bw, n, from, to, ...** arguments passed to `density`
- **col** a vector of fill colors of the same length as `levels(y)`. The default is to call `gray.colors`.
- **border** border color of shaded polygons.
- **main, xlab, ylab** character strings for annotation
The function `cdplot` computes the conditional densities of \( x \) given the levels of \( y \). The densities are derived cumulatively over the levels of \( y \).

This visualization technique is similar to spinograms (see `spineplot`) and plots \( P(y|x) \) against \( x \). The conditional probabilities are not derived by discretization (as in the spinogram), but using a smoothing approach via `density`.

Note, that the estimates of the conditional densities are more reliable for high-density regions of \( x \). Conversely, the are less reliable in regions with only few \( x \) observations.

**Value**

The conditional density functions (cumulative over the levels of \( y \)) are returned invisibly.

**Author(s)**

Achim Zeileis <Achim.Zeileis@R-project.org>

**References**


**See Also**

`spineplot`, `density`

**Examples**

```r
## NASA space shuttle o-ring failures
fail <- factor(c(2, 2, 2, 1, 1, 1, 1, 1, 2, 1, 2, 1, 2, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1, 1, 1),
               levels = 1:2, labels = c("no", "yes"))
temperature <- c(53, 57, 58, 63, 66, 67, 67, 67, 68, 69, 70, 70, 70, 70, 72, 73, 75, 75, 76, 76, 78, 79, 81)

## CD plot
cdplot(fail ~ temperature)
cdplot(fail ~ temperature, bw = 2)
cdplot(fail ~ temperature, bw = "SJ")

## compare with spinogram
(spineplot(fail ~ temperature, breaks = 3))

## highlighting for failures
cdplot(fail ~ temperature, ylevels = 2:1)

## scatter plot with conditional density
```
cdens <- cdplot(fail ~ temperature, plot = FALSE)
plot(I(as.numeric(fail) - 1) ~ jitter(temperature, factor = 2),
     xlab = "Temperature", ylab = "Conditional failure probability")
lines(53:81, 1 - cdens[[1]](53:81), col = 2)

--

clip

**Set Clipping Region**

**Description**

Set clipping region in user coordinates

**Usage**

clip(x1, x2, y1, y2)

**Arguments**

x1, x2, y1, y2  user coordinates of clipping rectangle

**Details**

How the clipping rectangle is set depends on the setting of `par("xpd")`: this function changes the current setting until the next high-level plotting command resets it.

Clipping of lines, rectangles and polygons is done in the graphics engine, but clipping of text is if possible done in the device, so the effect of clipping text is device-dependent (and may result in text not wholly within the clipping region being omitted entirely).

Exactly when the clipping region will be reset can be hard to predict. `plot.new` always resets it. Functions such as `lines` and `text` only reset it if `par("xpd")` has been changed. However, functions such as `box`, `mtext`, `title` and `plot.dendrogram` can manipulate the `xpd` setting.

**See Also**

`par`

**Examples**

x <- rnorm(1000)
hist(x, xlim = c(-4,4))
usr <- par("usr")
clip(usr[1], -2, usr[3], usr[4])
hist(x, col = 'red', add = TRUE)
clip(2, usr[2], usr[3], usr[4])
hist(x, col = 'blue', add = TRUE)
do.call("clip", as.list(usr))  # reset to plot region
## contour

**Display Contours**

Create a contour plot, or add contour lines to an existing plot.

```r
countour(x, ...)```

### Default S3 method:

```r
contour(x = seq(0, 1, length.out = nrow(z)),
         y = seq(0, 1, length.out = ncol(z)),
         z,
         nlevels = 10, levels = pretty(zlim, nlevels),
         labels = NULL,
         xlim = range(x, finite = TRUE),
         ylim = range(y, finite = TRUE),
         zlim = range(z, finite = TRUE),
         labcex = 0.6, drawlabels = TRUE, method = "flattest",
         vfont, axes = TRUE, frame.plot = axes,
         col = par("fg"), lty = par("lty") lwd = par("lwd"),
         add = FALSE, ...)```

### Arguments

- `x, y` locations of grid lines at which the values in `z` are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If `x` is a list, its components `x$x` and `x$y` are used for `x` and `y`, respectively. If the list has component `z` this is used for `z`.
- `z` a matrix containing the values to be plotted (NA's are allowed). Note that `x` can be used instead of `z` for convenience.
- `nlevels` number of contour levels desired if `levels` is not supplied.
- `levels` numeric vector of levels at which to draw contour lines.
- `labels` a vector giving the labels for the contour lines. If NULL then the levels are used as labels, otherwise this is coerced by `as.character`.
- `labcex` cex for contour labelling. This is an absolute size, not a multiple of par("cex").
- `drawlabels` logical. Contours are labelled if TRUE.
- `method` character string specifying where the labels will be located. Possible values are "simple", "edge" and "flattest" (the default). See the 'Details' section.
- `vfont` if NULL, the current font family and face are used for the contour labels. If a character vector of length 2 then Hershey vector fonts are used for the contour labels. The first element of the vector selects a typeface and the second element selects a fontindex (see `text` for more information). The default is NULL on graphics devices with high-quality rotation of text and `c("sans serif", "plain")` otherwise.
- `xlim, ylim, zlim` x-, y- and z-limits for the plot.
axes, frame.plot
  logical indicating whether axes or a box should be drawn, see plot.default.
col
  colour(s) for the lines drawn.
lty
  line type(s) for the lines drawn.
lwd
  line width(s) for the lines drawn.
add
  logical. If TRUE, add to a current plot.
...
  additional arguments to plot.window, title, Axis and box, typically graphical parameters such as cex.axis.

Details
contour is a generic function with only a default method in base \( \mathbb{R} \).
The methods for positioning the labels on contours are "simple" (draw at the edge of the plot, overlaying the contour line), "edge" (draw at the edge of the plot, embedded in the contour line, with no labels overlapping) and "flattest" (draw on the flattest section of the contour, embedded in the contour line, with no labels overlapping). The second and third may not draw a label on every contour line.
For information about vector fonts, see the help for text and Hershey.
Notice that contour interprets the \( z \) matrix as a table of \( f(x[i], y[j]) \) values, so that the \( x \) axis corresponds to row number and the \( y \) axis to column number, with column 1 at the bottom, i.e. a 90 degree counter-clockwise rotation of the conventional textual layout.
Vector (of length > 1) \( \text{col} \), \( \text{lty} \), and \( \text{lwd} \) are applied along levels and recycled, see the Examples.
Alternatively, use \text{contourplot} from the \text{lattice} package where the \text{formula} notation allows to use vectors \( x \), \( y \), and \( z \) of the same length.
There is limited control over the axes and frame as arguments \( \text{col} \), \( \text{lwd} \) and \( \text{lty} \) refer to the contour lines (rather than being general graphical parameters). For more control, add contours to a plot, or add axes and frame to a contour plot.

References

See Also
options("max.contour.segments") for the maximal complexity of a single contour line.
\text{contourlines}, \text{filled.contour} for color-filled contours, \text{contourplot} (and \text{levelplot}) from package \text{lattice}. Further, \text{image} and the graphics demo which can be invoked as \text{demo(graphics)}.

Examples
require(grDevices) # for colours
x <- -6:16
op <- par(mfrow = c(2, 2))
contour(outer(x, x), method = "edge", vfont = c("sans serif", "plain"))
z <- outer(x, sqrt(abs(x)), FUN = `/`
image(x, x, z)
contour(x, x, z, col = "pink", add = TRUE, method = "edge",
vfont = c("sans serif", "plain"))
contour(x, x, z, ylim = c(1, 6), method = "simple", labcex = 1,
xlab = quote(x[1]), ylab = quote(x[2]))
convertXY

Convert between Graphics Coordinate Systems

Description

Convert between graphics coordinate systems.
Usage

grconvertX(x, from = "user", to = "user")
grconvertY(y, from = "user", to = "user")

Arguments

x, y numeric vector of coordinates.
from, to character strings giving the coordinate systems to convert between.

Details

The coordinate systems are

"user" user coordinates.
"inches" inches.
"device" the device coordinate system.
"ndc" normalized device coordinates.
"nfc" normalized figure coordinates.
"npc" normalized plot coordinates.
"nic" normalized inner region coordinates. (The ‘inner region’ is that inside the outer margins.)
"lines" lines of margin (based on \texttt{mex}).
"chars" lines of text (based on \texttt{cex}).

(These names can be partially matched.) For the ‘normalized’ coordinate systems the lower left has value 0 and the top right value 1.

Device coordinates are those in which the device works: they are usually in pixels where that makes sense and in big points (1/72 inch) otherwise (e.g., \texttt{pdf} and \texttt{postscript}).

Value

A numeric vector of the same length as the input.

Examples

op <- par(omd=c(0.1, 0.9, 0.1, 0.9), mfrow = c(1, 2))
plot(1:4)
for(tp in c("in", "dev", "ndc", "nfc", "npc", "nic", "lines", "chars"))
  print(grconvertX(c(1.0, 4.0), "user", tp))
par(op)
Description

This function produces two variants of the conditioning plots discussed in the reference below.

Usage

\[
\text{coplot}(\text{formula, data, given.values, panel = points, rows, columns, show.given = TRUE, col = \text{par("fg")}, pch = \text{par("pch")}, bar.bg = c(\text{num = gray(0.8), fac = gray(0.95)}, xlab = c(x.name, \text{paste("Given ": a.name)}), ylab = c(y.name, \text{paste("Given ": b.name)}), subscripts = FALSE, axlabels = \text{function(f) abbreviate(levels(f))}, number = 6, overlap = 0.5, xlim, ylim, ...))}
\]

Arguments

- **formula**: a formula describing the form of conditioning plot. A formula of the form \( y \sim x \mid a \) indicates that plots of \( y \) versus \( x \) should be produced conditional on the variable \( a \). A formula of the form \( y \sim x \mid a \times b \) indicates that plots of \( y \) versus \( x \) should be produced conditional on the two variables \( a \) and \( b \).
- **data**: a data frame containing values for any variables in the formula. By default the environment where \text{coplot} was called from is used.
- **given.values**: a value or list of two values which determine how the conditioning on \( a \) and \( b \) is to take place.
  - When there is no \( b \) (i.e., conditioning only on \( a \)), usually this is a matrix with two columns each row of which gives an interval, to be conditioned on, but is can also be a single vector of numbers or a set of factor levels (if the variable being conditioned on is a factor). In this case (no \( b \)), the result of \text{co.intervals} can be used directly as \text{given.values} argument.
- **panel**: a function\((x, y, \text{col}, \text{pch}, ...)\) which gives the action to be carried out in each panel of the display. The default is \text{points}.
- **rows**: the panels of the plot are laid out in a rows by columns array. rows gives the number of rows in the array.
- **columns**: the number of columns in the panel layout array.
- **show.given**: logical (possibly of length 2 for 2 conditioning variables): should conditioning plots be shown for the corresponding conditioning variables (default \text{TRUE}).
- **col**: a vector of colors to be used to plot the points. If too short, the values are recycled.
- **pch**: a vector of plotting symbols or characters. If too short, the values are recycled.
bar.bg a named vector with components "num" and "fac" giving the background colors for the (shingle) bars, for numeric and factor conditioning variables respectively.

xlab character; labels to use for the x axis and the first conditioning variable. If only one label is given, it is used for the x axis and the default label is used for the conditioning variable.

ylab character; labels to use for the y axis and any second conditioning variable.

subscripts logical: if true the panel function is given an additional (third) argument subscripts giving the subscripts of the data passed to that panel.

axlabels function for creating axis (tick) labels when x or y are factors.

number integer; the number of conditioning intervals, for a and b, possibly of length 2. It is only used if the corresponding conditioning variable is not a factor.

overlap numeric < 1; the fraction of overlap of the conditioning variables, possibly of length 2 for x and y direction. When overlap < 0, there will be gaps between the data slices.

xlim the range for the x axis.

ylim the range for the y axis.

... additional arguments to the panel function.

x a numeric vector.

Details

In the case of a single conditioning variable a, when both rows and columns are unspecified, a 'close to square' layout is chosen with columns >= rows.

In the case of multiple rows, the order of the panel plots is from the bottom and from the left (corresponding to increasing a, typically).

A panel function should not attempt to start a new plot, but just plot within a given coordinate system: thus plot and boxplot are not panel functions.

The rendering of arguments xlab and ylab is not controlled by par arguments cex.lab and font.lab even though they are plotted by mtext rather than title.

Value

co.intervals(. , number , . ) returns a (number × 2) matrix, say ci, where ci[k,] is the range of x values for the k-th interval.

References


See Also

pairs, panel.smooth, points.
Examples

```r
## Tonga Trench Earthquakes
coplot(lat ~ long | depth, data = quakes)
given.depth <- co.intervals(quakes$depth, number = 4, overlap = .1)
coplot(lat ~ long | depth, data = quakes, given.values = given.depth, rows = 1)

## Conditioning on 2 variables:
ll.dm <- lat ~ long | depth * mag
coplot(ll.dm, data = quakes)
coplot(ll.dm, data = quakes, number = c(4, 7), show.given = c(TRUE, FALSE))
coplot(ll.dm, data = quakes, number = c(3, 7),
       overlap = c(-.5, .1)) # negative overlap DROPS values

## given two factors
Index <- seq_len(nrow(warpbreaks)) # to get nicer default labels
coplot(breaks ~ Index | wool * tension, data = warpbreaks,
       show.given = 0:1)
coplot(breaks ~ Index | wool * tension, data = warpbreaks,
       col = "red", bg = "pink", pch = 21,
       bar.bg = c(fac = "light blue"))

## Example with empty panels:
with(data.frame(state.x77), {
coplot(Life.Exp ~ Income | Illiteracy * state.region, number = 3,
       panel = function(x, y, ...) panel.smooth(x, y, span = .8, ...))
## y ~ factor -- not really sensible, but 'show off':
coplot(Life.Exp ~ state.region | Income * state.division,
       panel = panel.smooth)
})
```

Description

Draws a curve corresponding to a function over the interval [from, to]. `curve` can plot also an expression in the variable xname, default ‘x’.

Usage

```r
curve(expr, from = NULL, to = NULL, n = 101, add = FALSE,
type = "l", xname = "x", xlab = xname, ylab = NULL,
log = NULL, xlim = NULL, ...)
```

Arguments

- `expr` The name of a function, or a call or an expression written as a function of x which will evaluate to an object of the same length as x.
- `x` a ‘vectorizing’ numeric R function.
- `y` alias for from for compatibility with plot
curve

from, to

the range over which the function will be plotted.

n

integer; the number of x values at which to evaluate.

add

logical; if TRUE add to an already existing plot; if NA start a new plot taking the defaults for the limits and log-scaling of the x-axis from the previous plot. Taken as FALSE (with a warning if a different value is supplied) if no graphics device is open.

xlim

NULL or a numeric vector of length 2; if non-NULL it provides the defaults for c(from, to) and, unless add = TRUE, selects the x-limits of the plot – see plot.window.

type

plot type: see plot.default.

xname

character string giving the name to be used for the x axis.

xlab, ylab, log, ...

labels and graphical parameters can also be specified as arguments. See ‘Details’ for the interpretation of the default for log.

For the "function" method of plot, ... can include any of the other arguments of curve, except expr.

Details

The function or expression expr (for curve) or function x (for plot) is evaluated at n points equally spaced over the range [from, to]. The points determined in this way are then plotted.

If either from or to is NULL, it defaults to the corresponding element of xlim if that is not NULL.

What happens when neither from/to nor xlim specifies both x-limits is a complex story. For plot(<function>) and for curve(add = FALSE) the defaults are (0, 1). For curve(add = NA) and curve(add = TRUE) the defaults are taken from the x-limits used for the previous plot. (This differs from versions of R prior to 2.14.0.)

The value of log is used both to specify the plot axes (unless add = TRUE) and how 'equally spaced' is interpreted: if the x component indicates log-scaling, the points at which the expression or function is plotted are equally spaced on log scale.

The default value of log is taken from the current plot when add = TRUE, whereas if add = NA the x component is taken from the existing plot (if any) and the y component defaults to linear. For add = FALSE the default is ""

This used to be a quick hack which now seems to serve a useful purpose, but can give bad results for functions which are not smooth.

For expensive-to-compute expressions, you should use smarter tools.

The way curve handles expr has caused confusion. It first looks to see if expr is a name (also known as a symbol), in which case it is taken to be the name of a function, and expr is replaced by a call to expr with a single argument with name given by xname. Otherwise it checks that expr is either a call or an expression, and that it contains a reference to the variable given by xname (using all.vars): anything else is an error. Then expr is evaluated in an environment which supplies a vector of name given by xname of length n, and should evaluate to an object of length n. Note that this means that curve(x, ...) is taken as a request to plot a function named x (and it is used as such in the function method for plot).

The plot method can be called directly as plot.function.

Value

A list with components x and y of the points that were drawn is returned invisibly.
Warning

For historical reasons, add is allowed as an argument to the "function" method of plot, but its behaviour may surprise you. It is recommended to use add only with curve.

See Also

splinefun for spline interpolation, lines.

Examples

plot(qnorm) # default range c(0, 1) is appropriate here,
   # but end values are +/-Inf and so are omitted.
plot(qlogis, main = "The Inverse Logit : qlogis()")
abline(h = 0, v = 0:2/2, lty = 3, col = "gray")

curve(sin, -2*pi, 2*pi, xname = "t")
curve(tan, xname = "t", add = NA,
   main = "curve(tan) --> same x-scale as previous plot")

op <- par(mfrow = c(2, 2))
curve(x^3 - 3*x, -2, 2)
curve(x^2 - 2, add = TRUE, col = "violet")

## simple and advanced versions, quite similar:
plot(cos, -pi, 3*pi)
curve(cos, xlim = c(-pi, 3*pi), n = 1001, col = "blue", add = TRUE)

chippy <- function(x) sin(cos(x)*exp(-x/2))
curve(chippy, -8, 7, n = 2001)
plot(chippy, -8, -5)

for(ll in c("", "x", "y", "xy"))
  curve(log(1+x), 1, 100, log = ll, sub = paste0("log = ", ll, " "))
par(op)

dotchart

Cleveland's Dot Plots

Description

Draw a Cleveland dot plot.

Usage

dotchart(x, labels = NULL, groups = NULL, gdata = NULL, offset = 1/8,
   ann = par("ann"), xaxt = par("xaxt"), frame.plot = TRUE, log = "",
   cex = par("cex"), pt.cex = cex,
   pch = 21, gpch = 21, bg = par("bg"),
   color = par("fg"), gcolor = par("fg"), lcolor = "gray",
   xlim = range(x[is.finite(x)]),
   main = NULL, xlab = NULL, ylab = NULL, ...)
Arguments

- **x**: either a vector or matrix of numeric values (NAs are allowed). If x is a matrix the overall plot consists of juxtaposed dotplots for each row. Inputs which satisfy `is.numeric(x)` but not `is.vector(x) || is.matrix(x)` are coerced by `as.numeric`, with a warning.

- **labels**: a vector of labels for each point. For vectors the default is to use `names(x)` and for matrices the row labels `dimnames(x)[[1]]`.

- **groups**: an optional factor indicating how the elements of x are grouped. If x is a matrix, groups will default to the columns of x.

- **gdata**: data values for the groups. This is typically a summary such as the median or mean of each group.

- **offset**: offset in inches of ylab and labels.

- **ann**: a logical value indicating whether the default annotation (title and x and y axis labels) should appear on the plot.

- **xaxt**: a string indicating the x-axis style; use "n" to suppress and see also `par("xaxt")`.

- **frame.plot**: a logical indicating whether a box should be drawn around the plot.

- **log**: a character string indicating if one or the other axis should be logarithmic, see `plot.default`.

- **cex**: the character size to be used. Setting cex to a value smaller than one can be a useful way of avoiding label overlap. Unlike many other graphics functions, this sets the actual size, not a multiple of `par("cex")`.

- **pt.cex**: the `cex` to be applied to plotting symbols. This behaves like `cex` in `plot()`.

- **pch**: the plotting character or symbol to be used.

- **gpch**: the plotting character or symbol to be used for group values.

- **bg**: the background color of plotting characters or symbols to be used; use `par(bg=*)` to set the background color of the whole plot.

- **color**: the color(s) to be used for points and labels.

- **gcolor**: the single color to be used for group labels and values.

- **lcolor**: the color(s) to be used for the horizontal lines.

- **xlim**: horizontal range for the plot, see `plot.window`, for example.

- **main**: overall title for the plot, see `title`.

- **xlab, ylab**: axis annotations as in `title`.

- **...**: graphical parameters can also be specified as arguments.

Value

This function is invoked for its side effect, which is to produce two variants of dotplots as described in Cleveland (1985).

Dot plots are a reasonable substitute for bar plots.

References


Examples

dotchart(VADeaths, main = "Death Rates in Virginia - 1940")

op <- par(xaxs = "i") # 0 -- 100%
dotchart(t(VADeaths), xlim = c(0,100), bg = "skyblue", main = "Death Rates in Virginia - 1940", xlab = "rate [ % ]", ylab = "Grouping: Age x Urbanity . Gender")
par(op)

filled.contour Level (Contour) Plots

Description

This function produces a contour plot with the areas between the contours filled in solid color (Cleveland calls this a level plot). A key showing how the colors map to z values is shown to the right of the plot.

Usage

filled.contour(x = seq(0, 1, length.out = nrow(z)),
       y = seq(0, 1, length.out = ncol(z)),
       z,
       xlim = range(x, finite = TRUE),
       ylim = range(y, finite = TRUE),
       zlim = range(z, finite = TRUE),
       levels = pretty(zlim, nlevels), nlevels = 20,
       color.palette = function(n) hcl.colors(n, "YlOrRd", rev = TRUE),
       col = color.palette(length(levels) - 1),
       plot.title, plot.axes, key.title, key.axes,
       asp = NA, xaxs = "i", yaxs = "i", las = 1,
       axes = TRUE, frame.plot = axes, ...)

 Arguments

x, y locations of grid lines at which the values in z are measured. These must be in ascending order. (The rest of this description does not apply to .filled.contour.) By default, equally spaced values from 0 to 1 are used.

If x is a list, its components x$x and x$y are used for x and y, respectively. If the list has component z this is used for z.

z a numeric matrix containing the values to be plotted. Note that x can be used instead of z for convenience.

xlim x limits for the plot.

ylim y limits for the plot.

zlim z limits for the plot.

levels a set of levels which are used to partition the range of z. Must be strictly increasing (and finite). Areas with z values between consecutive levels are painted with the same color.
nlevels  if `levels` is not specified, the range of `z`, values is divided into approximately this many levels.
color.palette a color palette function to be used to assign colors in the plot.
col an explicit set of colors to be used in the plot. This argument overrides any palette function specification. There should be one less color than `levels`
plot.title statements which add titles to the main plot.
plot.axes statements which draw axes (and a box) on the main plot. This overrides the default axes.
key.title statements which add titles for the plot key.
key.axes statements which draw axes on the plot key. This overrides the default axis.
asp the y/x aspect ratio, see `plot.window`.
xaxs the x axis style. The default is to use internal labeling.
yaxs the y axis style. The default is to use internal labeling.
las the style of labeling to be used. The default is to use horizontal labeling.
axes, frame.plot logicals indicating if axes and a box should be drawn, as in `plot.default`.
... additional graphical parameters, currently only passed to `title()`.

Details

The values to be plotted can contain NAs. Rectangles with two or more corner values are NA are omitted entirely: where there is a single NA value the triangle opposite the NA is omitted.
Values to be plotted can be infinite: the effect is similar to that described for NA values.
`.filled.contour` is a ‘bare bones’ interface to add just the contour plot to an already-set-up plot region. It is is intended for programmatic use, and the programmer is responsible for checking the conditions on the arguments.

Note

`filled.contour` uses the `layout` function and so is restricted to a full page display.
The output produced by `filled.contour` is actually a combination of two plots; one is the filled contour and one is the legend. Two separate coordinate systems are set up for these two plots, but they are only used internally – once the function has returned these coordinate systems are lost. If you want to annotate the main contour plot, for example to add points, you can specify graphics commands in the `plot.axes` argument. See the examples.

Author(s)

Ross Ihaka and R Core Team

References


See Also

`contour`, `image`, `hcl.colors`, `gray.colors`, `palette`; `contourplot` and `levelplot` from package `lattice`. 
Examples

```r
require("grDevices") # for colours
filled.contour(volcano, asp = 1) # simple

x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
filled.contour(x, y, volcano,
    color.palette = function(n) hcl.colors(n, "terrain"),
    plot.title = title(main = "The Topography of Maunga Whau",
        xlab = "Meters North", ylab = "Meters West"),
    plot.axes = { axis(1, seq(100, 800, by = 100))
        axis(2, seq(100, 600, by = 100)) },
    key.title = title(main = "Height
(meters)"),
    key.axes = axis(4, seq(90, 190, by = 10))) # maybe also asp = 1
mtext(paste("filled.contour(.) from", R.version.string),
    side = 1, line = 4, adj = 1, cex = .66)

# Annotating a filled contour plot
a <- expand.grid(1:20, 1:20)
b <- matrix(a[,1] + a[,2], 20)
filled.contour(x = 1:20, y = 1:20, z = b,
    plot.axes = { axis(1); axis(2); points(10, 10) })

## Persian Rug Art:
x <- y <- seq(-4*pi, 4*pi, length.out = 27)
r <- sqrt(outer(x^2, y^2, `+`))
filled.contour(cos(r^2)*exp(-r/(2*pi)), axes = FALSE)

## rather, the key *should* be labeled:
filled.contour(cos(r^2)*exp(-r/(2*pi)), frame.plot = FALSE,
    plot.axes = {})```

Description

Creates a fourfold display of a 2 by 2 by \( k \) contingency table on the current graphics device, allowing for the visual inspection of the association between two dichotomous variables in one or several populations (strata).

Usage

```r
fourfoldplot(x, color = c("#99CCFF", "#6699CC"),
    conf.level = 0.95,
    std = c("margins", "ind.max", "all.max"),
    margin = c(1, 2), space = 0.2, main = NULL,
    mfrow = NULL, mfc = NULL)
```

Arguments

- `x`: a 2 by 2 by \( k \) contingency table in array form, or as a 2 by 2 matrix if \( k \) is 1.
- `color`: a vector of length 2 specifying the colors to use for the smaller and larger diagonals of each 2 by 2 table.
conf.level: confidence level used for the confidence rings on the odds ratios. Must be a single nonnegative number less than 1; if set to 0, confidence rings are suppressed.

std: a character string specifying how to standardize the table. Must match one of "margins", "ind.max", or "all.max", and can be abbreviated to the initial letter. If set to "margins", each 2 by 2 table is standardized to equate the margins specified by margin while preserving the odds ratio. If "ind.max" or "all.max", the tables are either individually or simultaneously standardized to a maximal cell frequency of 1.

margin: a numeric vector with the margins to equate. Must be one of 1, 2, or c(1, 2) (the default), which corresponds to standardizing the row, column, or both margins in each 2 by 2 table. Only used if std equals "margins".

space: the amount of space (as a fraction of the maximal radius of the quarter circles) used for the row and column labels.

main: character string for the fourfold title.

mfrow: a numeric vector of the form c(nr, nc), indicating that the displays for the 2 by 2 tables should be arranged in an nr by nc layout, filled by rows.

mfcol: a numeric vector of the form c(nr, nc), indicating that the displays for the 2 by 2 tables should be arranged in an nr by nc layout, filled by columns.

Details

The fourfold display is designed for the display of 2 by 2 by k tables. Following suitable standardization, the cell frequencies $f_{ij}$ of each 2 by 2 table are shown as a quarter circle whose radius is proportional to $\sqrt{f_{ij}}$ so that its area is proportional to the cell frequency. An association (odds ratio different from 1) between the binary row and column variables is indicated by the tendency of diagonally opposite cells in one direction to differ in size from those in the other direction; color is used to show this direction. Confidence rings for the odds ratio allow a visual test of the null of no association; the rings for adjacent quadrants overlap if and only if the observed counts are consistent with the null hypothesis.

Typically, the number k corresponds to the number of levels of a stratifying variable, and it is of interest to see whether the association is homogeneous across strata. The fourfold display visualizes the pattern of association. Note that the confidence rings for the individual odds ratios are not adjusted for multiple testing.

References


See Also

mosaicplot

Examples

```r
## Use the Berkeley admission data as in Friendly (1995).
x <- aperm(UCBAdmissions, c(2, 1, 3))
dimnames(x)[[2]] <- c("Yes", "No")
names(dimnames(x)) <- c("Sex", "Admit?", "Department")
stats::ftable(x)
```
## Fourfold display of data aggregated over departments, with frequencies standardized to equate the margins for admission and sex.
## Figure 1 in Friendly (1994).
fourfoldplot(marginSums(x, c(1, 2)))

## Fourfold display of x, with frequencies in each table standardized to equate the margins for admission and sex.
## Figure 2 in Friendly (1994).
fourfoldplot(x)

## Fourfold display of x, with frequencies in each table standardized to equate the margins for admission, but not for sex.
## Figure 3 in Friendly (1994).
fourfoldplot(x, margin = 2)

---

**Description**

This function (frame is an alias for plot.new) causes the completion of plotting in the current plot (if there is one) and an advance to a new graphics frame. This is used in all high-level plotting functions and also useful for skipping plots when a multi-figure region is in use.

**Usage**

```r
plot.new()
frame()
```

**Details**

The new page is painted with the background colour (par("bg")), which is often transparent. For devices with a canvas colour (the on-screen devices X11, windows and quartz), the window is first painted with the canvas colour and then the background colour.

There are two hooks called “before.plot.new” and “plot.new” (see setHook) called immediately before and after advancing the frame. The latter is used in the testing code to annotate the new page. The hook function(s) are called with no argument. (If the value is a character string, get is called on it from within the graphics namespace.)

**References**


**See Also**

plot.window, plot.default.
grid

Add Grid to a Plot

Description

ggrid adds an nx by ny rectangular grid to an existing plot.

Usage

ggrid(nx = NULL, ny = nx, col = "lightgray", lty = "dotted",
lwd = par("lwd"), equilogs = TRUE)

Arguments

nx, ny number of cells of the grid in x and y direction. When NULL, as per default, the
ggrid aligns with the tick marks on the corresponding default axis (i.e., tickmarks
as computed by axTicks). When NA, no grid lines are drawn in the corresponding
direction.

col character or (integer) numeric; color of the grid lines.
lty character or (integer) numeric; line type of the grid lines.
lwd non-negative numeric giving line width of the grid lines.
equilogs logical, only used when log coordinates and alignment with the axis tick marks
are active. Setting equilogs = FALSE in that case gives non equidistant tick
aligned grid lines.

Note

If more fine tuning is required, use abline(h = ., v = .) directly.

References


See Also

plot, abline, lines, points.

Examples

plot(1:3)
ggrid(NA, 5, lwd = 2) # grid only in y-direction

## maybe change the desired number of tick marks: par(lab = c(mx, my, 7))
op <- par(mfcol = 1:2)
with(iris,
    {
        plot(Sepal.Length, Sepal.Width, col = as.integer(Species),
             xlim = c(4, 8), ylim = c(2, 4.5), panel.first = grid(),
             main = "with(iris, plot(...., panel.first = grid(), ..) )")
        plot(Sepal.Length, Sepal.Width, col = as.integer(Species),
             panel.first = grid(3, lty = 1, lwd = 2),
             main = ".... panel.first = grid(3, lty = 1, lwd = 2), ..")
    }
The generic function `hist` computes a histogram of the given data values. If `plot = TRUE`, the resulting object of class "histogram" is plotted by `plot.histogram`, before it is returned.

### Default S3 method:

```
hist(x, breaks = "Sturges",
     freq = NULL, probability = !freq,
     include.lowest = TRUE, right = TRUE, fuzz = 1e-7,
     density = NULL, angle = 45, col = "lightgray", border = NULL,
     main = paste("Histogram of", xname),
     xlim = range(breaks), ylim = NULL,
     xlab = xname, ylab,
     axes = TRUE, plot = TRUE, labels = FALSE,
     nclass = NULL, warn.unused = TRUE, ...)
```

#### Arguments

- **x**: a vector of values for which the histogram is desired.
- **breaks**: one of:
  - a vector giving the breakpoints between histogram cells,
  - a function to compute the vector of breakpoints,
  - a single number giving the number of cells for the histogram,
  - a character string naming an algorithm to compute the number of cells (see ‘Details’),
  - a function to compute the number of cells.

In the last three cases the number is a suggestion only; as the breakpoints will be set to `pretty` values, the number is limited to `1e6` (with a warning if it was larger). If `breaks` is a function, the `x` vector is supplied to it as the only argument (and the number of breaks is only limited by the amount of available memory).

- **freq**: logical; if `TRUE`, the histogram graphic is a representation of frequencies, the counts component of the result; if `FALSE`, probability densities, component density, are plotted (so that the histogram has a total area of one). Defaults to `TRUE` if and only if `breaks` are equidistant (and probability is not specified).
- **probability**: an *alias* for `!freq`, for S compatibility.
include.lowest  logical; if TRUE, an x[i] equal to the breaks value will be included in the first (or last, for right = FALSE) bar. This will be ignored (with a warning) unless breaks is a vector.

right      logical; if TRUE, the histogram cells are right-closed (left open) intervals.

fuzz      non-negative number, for the case when the data is “pretty” and some observations x[.] are close but not exactly on a break. For counting fuzzy breaks proportional to fuzz are used. The default is occasionally suboptimal.

density the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn. Non-positive values of density also inhibit the drawing of shading lines.

angle the slope of shading lines, given as an angle in degrees (counter-clockwise).

col      a colour to be used to fill the bars.

border the color of the border around the bars. The default is to use the standard foreground color.

main, xlab, ylab main title and axis labels: these arguments to title() get “smart” defaults here, e.g., the default ylab is "Frequency" iff freq is true.

xlim, ylim the range of x and y values with sensible defaults. Note that xlim is not used to define the histogram (breaks), but only for plotting (when plot = TRUE).

axes logical. If TRUE (default), axes are draw if the plot is drawn.

plot logical. If TRUE (default), a histogram is plotted, otherwise a list of breaks and counts is returned. In the latter case, a warning is used if (typically graphical) arguments are specified that only apply to the plot = TRUE case.

labels logical or character string. Additionally draw labels on top of bars, if not FALSE; see plot.histogram.

nclass numeric (integer). For S(-PLUS) compatibility only, nclass is equivalent to breaks for a scalar or character argument.

warn.unused logical. If plot = FALSE and warn.unused = TRUE, a warning will be issued when graphical parameters are passed to hist.default().

... further arguments and graphical parameters passed to plot.histogram and thence to title and axis (if plot = TRUE).

Details

The definition of histogram differs by source (with country-specific biases). R’s default with equi-spaced breaks (also the default) is to plot the counts in the cells defined by breaks. Thus the height of a rectangle is proportional to the number of points falling into the cell, as is the area provided the breaks are equally-spaced.

The default with non-equi-spaced breaks is to give a plot of area one, in which the area of the rectangles is the fraction of the data points falling in the cells.

If right = TRUE (default), the histogram cells are intervals of the form (a, b], i.e., they include their right-hand endpoint, but not their left one, with the exception of the first cell when include.lowest is TRUE.

For right = FALSE, the intervals are of the form [a, b), and include.lowest means ‘include highest’.

A numerical tolerance of $10^{-7}$ times the median bin size (for more than four bins, otherwise the median is substituted) is applied when counting entries on the edges of bins. This is not included in the reported breaks nor in the calculation of density.
The default for breaks is "Sturges": see `nclass.Sturges`. Other names for which algorithms are supplied are "Scott" and "FD" / "Freedman-Diaconis" (with corresponding functions `nclass.scott` and `nclass.FD`). Case is ignored and partial matching is used. Alternatively, a function can be supplied which will compute the intended number of breaks or the actual breakpoints as a function of x.

Value

an object of class "histogram" which is a list with components:

breaks the \( n + 1 \) cell boundaries (= breaks if that was a vector). These are the nominal breaks, not with the boundary fuzz.

counts \( n \) integers; for each cell, the number of \( x[] \) inside.

density values \( \hat{f}(x_i) \), as estimated density values. If all(diff(breaks) == 1), they are the relative frequencies counts/\( n \) and in general satisfy \( \sum_i \hat{f}(x_i)(b_{i+1} - b_i) = 1 \), where \( b_i = \text{breaks}[i] \).

mids the \( n \) cell midpoints.

xname a character string with the actual \( x \) argument name.

equidist logical, indicating if the distances between breaks are all the same.

References


See Also

`nclass.Sturges`, `stem`, `density`, `truehist` in package `MASS`.

Typical plots with vertical bars are not histograms. Consider `barplot` or `plot(*, type = "h")` for such bar plots.

Examples

```r
op <- par(mfrow = c(2, 2))
hist(islands)
utils::str(hist(islands, col = "gray", labels = TRUE))

hist(sqrt(islands), breaks = 12, col = "lightblue", border = "pink")
#-- For non-equidistant breaks, counts should NOT be graphed unscaled:
r <- hist(sqrt(islands), breaks = c(4*0:5, 10*3:5, 70, 100, 140),
          col = "blue1")
text(r$mids, r$density, r$counts, adj = c(.5, -.5), col = "blue3")
sapply(r[2:3], sum) # == 1
lines(r, lty = 3, border = "purple") # -> lines.histogram(*)
par(op)

require(utils) # for str
str(hist(islands, breaks = 12, plot = FALSE)) #-> 10 (= 12) breaks
str(hist(islands, breaks = c(12,20,36,80,200,1000,17000), plot = FALSE))

hist(islands, breaks = c(12,20,36,80,200,1000,17000), freq = TRUE,
```
## Extreme outliers; the "FD" rule would take very large number of 'breaks':
XXL <- c(1:9, c(-1,1)*1e300)
hh <- hist(XXL, "FD") # did not work in R <= 3.4.1; now gives warning
## pretty() determines how many counts are used (platform dependently!):
length(hh$breaks) ## typically 1 million -- though 1e6 was "a suggestion only"

## R >= 4.2.0: no ".5" labels on y-axis:
hist(c(2,3,3,5,5,6,6,6,7))

hist.POSIXt

Histogram of a Date or Date-Time Object

Description

Methods for hist applied to date (class "Date") or date-time (class "POSIXt") objects.

Usage

### S3 method for class 'POSIXt'

```r
hist(x, breaks, ..., 
  xlab = deparse1(substitute(x)), 
  plot = TRUE, freq = FALSE, 
  start.on.monday = TRUE, format, right = TRUE)
```

### S3 method for class 'Date'

```r
hist(x, breaks, ..., 
  xlab = deparse1(substitute(x)), 
  plot = TRUE, freq = FALSE, 
  start.on.monday = TRUE, format, right = TRUE)
```

Arguments

- `x`: an object inheriting from class "POSIXt" or "Date".
breaks

a vector of cut points or number giving the number of intervals which \( x \) is to be cut into or an interval specification, one of "days", "weeks", "months", "quarters" or "years", plus "secs", "mins", "hours" for date-time objects.

... graphical parameters, or arguments to \texttt{hist.default} such as \texttt{include.lowest}, density and labels.

xlab

a character string giving the label for the x axis, if plotted.

plot

logical. If \texttt{TRUE} (default), a histogram is plotted, otherwise a list of breaks and counts is returned.

freq

logical; if \texttt{TRUE}, the histogram graphic is a representation of frequencies, i.e., the counts component of the result; if \texttt{FALSE}, relative frequencies (probabilities) are plotted.

start.on.monday

logical. If \texttt{breaks = "weeks"}, should the week start on Mondays or Sundays?

format

for the x-axis labels. See \texttt{strptime}.

right

logical; if \texttt{TRUE}, the histogram cells are right-closed (left open) intervals.

Details

Note that unlike the default method, \texttt{breaks} is a required argument.

Using \texttt{breaks = "quarters"} will create intervals of 3 calendar months, with the intervals beginning on January 1, April 1, July 1 or October 1, based upon \texttt{min(x)} as appropriate.

With the default \texttt{right = TRUE}, breaks will be set on the last day of the previous period when \texttt{breaks} is "months", "quarters" or "years". Use \texttt{right = FALSE} to set them to the first day of the interval shown in each bar.

Value

An object of class "histogram": see \texttt{hist}.

See Also

\texttt{seq.POSIXt, axis.POSIXct, hist}

Examples

\begin{verbatim}
hist(.leap.seconds, "years", freq = TRUE)
brks <- seq(ISODate(1970, 1, 1), ISODate(2030, 1, 1), "5 years")
hist(.leap.seconds, brks)
rug(.leap.seconds, lwd=2)
## show that 'include.lowest' 'works'
stopifnot(identical(c(2L, rep(1L,11)),
    hist(brks, brks, plot=FALSE, include.lowest=TRUE )$counts))
tools::assertError(verbose=TRUE, ###-> 'breaks' do not span range of 'x'
    hist(brks, brks, plot=FALSE, include.lowest=FALSE))
## The default fuzz in hist.default() "kills" this, with a "wrong" message:
try ( hist(brks[-13] + 1, brks, include.lowest = FALSE) )
## and decreasing 'fuzz' solves the issue:
hb <- hist(brks[-13] + 1, brks, include.lowest = FALSE, fuzz = 1e-10)
stopifnot(hb$counts == 1)

## 100 random dates in a 10-week period
random.dates <- as.Date("2001/1/1") + 70*stats::runif(100)
hist(random.dates, "weeks", format = "%d %b")
\end{verbatim}
identify is a generic function, and only the default method is described here.

identify is only supported on screen devices such as X11, windows and quartz. On other devices the call will do nothing.

Clicking near (as defined by tolerance) a point adds it to the list of identified points. Points can be identified only once, and if the point has already been identified or the click is not near any of the points a message is printed immediately on the \texttt{R} console.
If `plot` is `TRUE`, the point is labelled with the corresponding element of `labels`. If `atpen` is false (the default) the labels are placed below, to the left, above or to the right of the identified point, depending on where the pointer was relative to the point. If `atpen` is true, the labels are placed with the bottom left of the string’s box at the pointer.

For the usual `X11` device the identification process is terminated by pressing any mouse button other than the first. For the `quartz` device the process is terminated by pressing either the pop-up menu equivalent (usually second mouse button or `Ctrl`-click) or the `ESC` key.

On most devices which support `identify`, successful selection of a point is indicated by a bell sound unless `options(locatorBell = FALSE)` has been set.

If the window is resized or hidden and then exposed before the identification process has terminated, any labels drawn by `identify` will disappear. These will reappear once the identification process has terminated and the window is resized or hidden and exposed again. This is because the labels drawn by `identify` are not recorded in the device’s display list until the identification process has terminated.

If you interrupt the `identify` call this leaves the graphics device in an undefined state, with points labelled but labels not recorded in the display list. Copying a device in that state will give unpredictable results.

**Value**

If both `pos` and `order` are `FALSE`, an integer vector containing the indices of the identified points.

If either of `pos` or `order` is `TRUE`, a list containing a component `ind`, indicating which points were identified and (if `pos` is `TRUE`) a component `pos`, indicating where the labels were placed relative to the identified points (1=below, 2=left, 3=above, 4=right and 0=no offset, used if `atpen = TRUE`) and (if `order` is `TRUE`) a component `order`, indicating the order in which points were identified.

**Technicalities**

The algorithm used for placing labels is the same as used by `text` if `pos` is specified there, the difference being that the position of the pointer relative the identified point determines `pos` in `identify`.

For labels placed to the left of a point, the right-hand edge of the string’s box is placed `offset` units to the left of the point, and analogously for points to the right. The baseline of the text is placed below the point so as to approximately centre string vertically. For labels placed above or below a point, the string is centered horizontally on the point. For labels placed above, the baseline of the text is placed `offset` units above the point, and for those placed below, the baseline is placed so that the top of the string’s box is approximately `offset` units below the point. If you want more precise placement (e.g., centering) use `plot = FALSE` and plot via `text` or `points`: see the examples.

**References**


**See Also**

`locator`, `text`, `dev.capabilities` to see if it is supported.
## Examples

```r
## A function to use identify to select points, and overplot the
## points with another symbol as they are selected
identifyPch <- function(x, y = NULL, n = length(x), plot = FALSE, pch = 19, ...)
{
  xy <- xy.coords(x, y); x <- xy$x; y <- xy$y
  sel <- rep(FALSE, length(x))
  while(sum(sel) < n) {
    ans <- identify(x[!sel], y[!sel], labels = which(!sel), n = 1, plot = plot, ...)
    if(!length(ans)) break
    ans <- which(!sel)[ans]
    points(x[ans], y[ans], pch = pch)
    sel[ans] <- TRUE
  }
  return(indices of selected points)
}

if(dev.interactive()) { ## use it
  x <- rnorm(50); y <- rnorm(50)
  plot(x,y); identifyPch(x,y) # how fast to get all?
}
```

---

### Display a Color Image

**image**

**Description**

Creates a grid of colored or gray-scale rectangles with colors corresponding to the values in `z`. This can be used to display three-dimensional or spatial data aka images. This is a generic function.

**NOTE:** the grid is drawn as a set of rectangles by default; see the `useRaster` argument to draw the grid as a raster image.

The function `hcl.colors` provides a broad range of sequential color palettes that are suitable for displaying ordered data, with `n` giving the number of colors desired.

**Usage**

```r
image(x, ..., )
```

**Arguments**

- `x, y` locations of grid lines at which the values in `z` are measured. These must be finite, non-missing and in (strictly) ascending order. By default, equally spaced values from 0 to 1 are used. If `x` is a list, its components `x$x` and `x$y` are used for `x` and `y`, respectively. If the list has component `z` this is used for `z`.

---

**Examples**

```r
## A function to use identify to select points, and overplot the
## points with another symbol as they are selected
identifyPch <- function(x, y = NULL, n = length(x), plot = FALSE, pch = 19, ...)
{
  xy <- xy.coords(x, y); x <- xy$x; y <- xy$y
  sel <- rep(FALSE, length(x))
  while(sum(sel) < n) {
    ans <- identify(x[!sel], y[!sel], labels = which(!sel), n = 1, plot = plot, ...)
    if(!length(ans)) break
    ans <- which(!sel)[ans]
    points(x[ans], y[ans], pch = pch)
    sel[ans] <- TRUE
  }
  return(indices of selected points)
}

if(dev.interactive()) { ## use it
  x <- rnorm(50); y <- rnorm(50)
  plot(x,y); identifyPch(x,y) # how fast to get all?
}
```
**image**

z a numeric or logical matrix containing the values to be plotted (NAs are allowed). Note that x can be used instead of z for convenience.

zlim the minimum and maximum z values for which colors should be plotted, defaulting to the range of the finite values of z. Each of the given colors will be used to color an equispaced interval of this range. The midpoints of the intervals cover the range, so that values just outside the range will be plotted.

xlim, ylim ranges for the plotted x and y values, defaulting to the ranges of x and y.

col a list of colors such as that generated by hcl.colors, gray.colors or similar functions.

add logical; if TRUE, add to current plot (and disregard the following four arguments). This is rarely useful because image ‘paints’ over existing graphics.

xaxs, yaxs style of x and y axis. The default "i" is appropriate for images. See par.

xlab, ylab each a character string giving the labels for the x and y axis. Default to the 'call names' of x or y, or to "" if these were unspecified.

breaks a set of finite numeric breakpoints for the colours: must have one more breakpoint than colour and be in increasing order. Unsorted vectors will be sorted, with a warning.

oldstyle logical. If true the midpoints of the colour intervals are equally spaced, and zlim[1] and zlim[2] were taken to be midpoints. The default is to have colour intervals of equal lengths between the limits.

useRaster logical; if TRUE a bitmap raster is used to plot the image instead of polygons. The grid must be regular in that case, otherwise an error is raised. For the behaviour when this is not specified, see ‘Details’.

... graphical parameters for plot may also be passed as arguments to this function, as can the plot aspect ratio asp and axes (see plot.window).

**Details**

The length of x should be equal to the nrow(z)+1 or nrow(z). In the first case x specifies the boundaries between the cells: in the second case x specifies the midpoints of the cells. Similar reasoning applies to y. It probably only makes sense to specify the midpoints of an equally-spaced grid. If you specify just one row or column and a length-one x or y, the whole user area in the corresponding direction is filled. For logarithmic x or y axes the boundaries between cells must be specified.

Rectangles corresponding to missing values are not plotted (and so are transparent and (unless add = TRUE) the default background painted in par("bg") will show through and if that is transparent, the canvas colour will be seen).

If breaks is specified then zlim is unused and the algorithm used follows cut, so intervals are closed on the right and open on the left except for the lowest interval which is closed at both ends. The axes (where plotted) make use of the classes of xlim and ylim (and hence by default the classes of x and y): this will mean that for example dates are labelled as such.

Notice that image interprets the z matrix as a table of f(x[i], y[j]) values, so that the x axis corresponds to row number and the y axis to column number, with column 1 at the bottom, i.e. a 90 degree counter-clockwise rotation of the conventional printed layout of a matrix.

Images for large z on a regular grid are rendered more efficiently with useRaster = TRUE and can prevent rare anti-aliasing artifacts, but may not be supported by all graphics devices. Some devices (such as postscript and X11(type = "Xlib")) which do not support semi-transparent colours may emit missing values as white rather than transparent, and there may be limitations on the size
of a raster image. (Problems with the rendering of raster images have been reported by users of
windows() devices under Remote Desktop, at least under its default settings.)

The graphics files in PDF and PostScript can be much smaller under this option.

If useRaster is not specified, raster images are used when the getOption("preferRaster") is
ture, the grid is regular and either dev.capabilities("rasterImage")$rasterImage is "yes"
or it is "non-missing" and there are no missing values.

Note

Originally based on a function by Thomas Lumley.

See Also

filled.contour or heatmap which can look nicer (but are less modular), contour; The lattice
equivalent of image is levelplot.

hcl.colors, gray.colors, hcl, hsv, par.

dev.capabilities to see if useRaster = TRUE is supported on the current device.

Examples

require("grDevices") # for colours
x <- y <- seq(-4*pi, 4*pi, length.out = 27)
r <- sqrt(outer(x^2, y^2, `+`))
image(z = z <- cos(r^2)*exp(-r/6), col = gray.colors(33))
image(z, axes = FALSE, main = "Math can be beautiful ...",
     xlab = expression(cos(r^2) * e^{-r/6}))
contour(z, add = TRUE, drawlabels = FALSE)

# Visualize as matrix. Need to transpose matrix and then flip it horizontally:
tf <- function(m) t(m)[, nrow(m):1]
imageM <- function(m, grid = max(dim(m)) <= 25, asp = (nrow(m)-1)/(ncol(m)-1), ...) {
  image(tf(m), asp=asp, axes = FALSE, ...)
  mAxis(side, at, ...) # using 'j'
  n <- ncol(m); n1 <- n-1L; j <- 0L:n1; mAxis(1, at= j/n1)
  n <- nrow(m); n1 <- n-1L; j <- 0L:n1; mAxis(2, at=1-j/n1, las=1)
  n <- nrow(m); n1 <- n-1L; j <- 0L:n1; mAxis(2, at=1-j/n1, las=1)
  n <- ncol(m); n1 <- n-1L; j <- 0L:n1; mAxis(1, at= j/n1)
  if(grid) abline(v = (0:n - .5)/n1, col="gray77", lty="dotted")
  if(grid) abline(h = (0:n - .5)/n1, col="gray77", lty="dotted")
}

(m <- outer(1:5, 1:14))
imageM(m, main = "image(<5 x 14 matrix>) with rows and columns")

imageM(volcano)

# A prettier display of the volcano
x <- 10*x1:nrow(volcano))
y <- 10*y1:ncol(volcano))
image(x, y, volcano, col = hcl.colors(100, "terrain"), axes = FALSE)
contour(x, y, volcano, levels = seq(90, 200, by = 5),
    add = TRUE, col = "brown")
axis(1, at = seq(100, 800, by = 100))
axis(2, at = seq(100, 600, by = 100))
box()
title(main = "Maunga Whau Volcano", font.main = 4)
**Description**

`layout` divides the device up into as many rows and columns as there are in matrix `mat`, with the column-widths and the row-heights specified in the respective arguments.

**Usage**

```r
layout(mat, widths = rep.int(1, ncol(mat)),
       heights = rep.int(1, nrow(mat)), respect = FALSE)
layout.show(n = 1)
lcm(x)
```

**Arguments**

- `mat` a matrix object specifying the location of the next `N` figures on the output device. Each value in the matrix must be 0 or a positive integer. If `N` is the largest positive integer in the matrix, then the integers `{1, \ldots, N - 1}` must also appear at least once in the matrix.
- `widths` a vector of values for the widths of columns on the device. Relative widths are specified with numeric values. Absolute widths (in centimetres) are specified with the `lcm()` function (see examples).
- `heights` a vector of values for the heights of rows on the device. Relative and absolute heights can be specified, see `widths` above.
- `respect` either a logical value or a matrix object. If the latter, then it must have the same dimensions as `mat` and each value in the matrix must be either 0 or 1.
- `n` number of figures to plot.
- `x` a dimension to be interpreted as a number of centimetres.

**Details**

Figure `i` is allocated a region composed from a subset of these rows and columns, based on the rows and columns in which `i` occurs in `mat`.

The `respect` argument controls whether a unit column-width is the same physical measurement on the device as a unit row-height.

There is a limit (currently 200) for the numbers of rows and columns in the layout, and also for the total number of cells (10007).

`layout.show(n)` plots (part of) the current layout, namely the outlines of the next `n` figures.

`lcm` is a trivial function, to be used as the interface for specifying absolute dimensions for the `widths` and `heights` arguments of `layout()`.

**Value**

`layout` returns the number of figures, `N`, see above.
Warnings

These functions are totally incompatible with the other mechanisms for arranging plots on a device:
\texttt{par(mfrow)}, \texttt{par(mfcol)} and \texttt{split.screen}.

Author(s)

Paul R. Murrell

References


Chapter 5 of Paul Murrell’s Ph.D. thesis.


See Also

\texttt{par} with arguments \texttt{mfrow}, \texttt{mfcol}, or \texttt{mfg}.

Examples

def.par <- \texttt{par(no.readonly = TRUE)} # save default, for resetting...

## divide the device into two rows and two columns
## allocate figure 1 all of row 1
## allocate figure 2 the intersection of column 2 and row 2
layout(matrix(c(1,1,0,2), 2, 2, byrow = TRUE))
## show the regions that have been allocated to each plot
layout.show(2)

## divide device into two rows and two columns
## allocate figure 1 and figure 2 as above
## respect relations between widths and heights
nf <- layout(matrix(c(1,1,0,2), 2, 2, byrow = TRUE), respect = TRUE)
layout.show(nf)

## create single figure which is 5cm square
nf <- layout(matrix(c(1), 1), widths = lcm(5), heights = lcm(5))
layout.show(nf)

#### Create a scatterplot with marginal histograms -----

x <- pmin(3, pmax(-3, stats::rnorm(50)))
y <- pmin(3, pmax(-3, stats::rnorm(50)))
xhist <- hist(x, breaks = seq(-3,3,0.5), plot = FALSE)
yhist <- hist(y, breaks = seq(-3,3,0.5), plot = FALSE)
top <- max(c(xhist$count, yhist$count))
xrange <- c(-3, 3)
yrange <- c(-3, 3)
nf <- layout(matrix(c(2,0,1,3),2,2,byrow = TRUE), c(3,1), c(1,3), TRUE)
layout.show(nf)

par(mar = c(3,3,1,1))
plot(x, y, xlim = xrange, ylim = yrange, xlab = '', ylab = '')
par(mar = c(0,3,1,1))
barplot(xhist$counts, axes = FALSE, xlim = c(0, top), space = 0)
par(mar = c(3,0,1,1))
barplot(yhist$counts, axes = FALSE, xlim = c(0, top), space = 0, horiz = TRUE)
par(def.par) #- reset to default

---

Add Legends to Plots

**Description**

This function can be used to add legends to plots. Note that a call to the function `locator(1)` can be used in place of the x and y arguments.

**Usage**

```r
legend(x, y = NULL, legend, fill = NULL, col = par("col"),
       border = "black", lty, lwd, pch,
       angle = 45, density = NULL, bty = "o", bg = par("bg"),
       box.lwd = par("lwd"), box.lty = par("lty"), box.col = par("fg"),
       pt.bg = NA, cex = 1, pt.cex = cex, pt.lwd = lwd,
       xjust = 0, yjust = 1, x.intersp = 1, y.intersp = 1,
       adj = c(0, 0.5), text.width = NULL, text.col = par("col"),
       text.font = NULL, merge = do.lines && has.pch, trace = FALSE,
       plot = TRUE, ncol = 1, horiz = FALSE, title = NULL,
       inset = 0, xpd, title.col = text.col[1], title.adj = 0.5,
       title.cex = cex[1], title.font = text.font[1],
       seg.len = 2)
```

**Arguments**

- `x, y` the x and y co-ordinates to be used to position the legend. They can be specified by keyword or in any way which is accepted by `xy.coords`; See ‘Details’.
- `legend` a character or expression vector of length ≥ 1 to appear in the legend. Other objects will be coerced by `as.graphicsAnnot`.
- `fill` if specified, this argument will cause boxes filled with the specified colors (or shaded in the specified colors) to appear beside the legend text.
- `col` the color of points or lines appearing in the legend.
- `border` the border color for the boxes (used only if fill is specified).
- `lty, lwd` the line types and widths for lines appearing in the legend. One of these two must be specified for line drawing.
- `pch` the plotting symbols appearing in the legend, as numeric vector or a vector of 1-character strings (see `points`). Unlike points, this can all be specified as a single multi-character string. Must be specified for symbol drawing.
- `angle` angle of shading lines.
- `density` the density of shading lines, if numeric and positive. If NULL or negative or NA color filling is assumed.
the type of box to be drawn around the legend. The allowed values are "o" (the default) and "n".

the background color for the legend box. (Note that this is only used if bty != "n").

the line type, width and color for the legend box (if bty = "o").

the line type factor corresponding to its argument bg.

character expansion factor relative to current par("cex"). Used for text, and provides the default for pt.cex.

line width for the points, defaults to the one for lines, or if that is not set, to par("lwd").

how the legend is to be justified relative to the legend x location. A value of 0 means left justified, 0.5 means centered and 1 means right justified.

the same as xjust for the legend y location.

character interspacing factor for horizontal (x) spacing between symbol and legend text.

vertical (y) distances (in lines of text shared above/below each legend entry). A vector with one element for each row of the legend can be used.

numeric of length 1 or 2; the string adjustment for legend text. Useful for y-adjustment when labels are plotmath expressions.

the width of the legend text in x ("user") coordinates. (Should be positive even for a reversed x axis.) Can be a single positive numeric value (same width for each column of the legend), a vector (one element for each column of the legend), NULL (default) for computing a proper maximum value of strwidth(legend)), or NA for computing a proper column wise maximum value of strwidth(legend)).

the color used for the legend text.

the font used for the legend text, see text.

logical; if TRUE, merge points and lines but not filled boxes. Defaults to TRUE if there are points and lines.

logical; if TRUE, shows how legend does all its magical computations.

logical. If FALSE, nothing is plotted but the sizes are returned.

the number of columns in which to set the legend items (default is 1, a vertical legend).

logical; if TRUE, set the legend horizontally rather than vertically (specifying horiz overrides the ncol specification).

character string or length-one expression giving a title to be placed at the top of the legend. Other objects will be coerced by as.graphicsAnnot.

inset distance(s) from the margins as a fraction of the plot region when legend is placed by keyword.

if supplied, a value of the graphical parameter xpd to be used while the legend is being drawn.

color for title, defaults to text.col[1].

horizontal adjustment for title; see the help for par("adj").
Arguments \(x, y, \text{legend}\) are interpreted in a non-standard way to allow the coordinates to be specified via one or two arguments. If \text{legend} is missing and \(y\) is not numeric, it is assumed that the second argument is intended to be \text{legend} and that the first argument specifies the coordinates.

The coordinates can be specified in any way which is accepted by \texttt{xy.coords}. If this gives the coordinates of one point, it is used as the top-left coordinate of the rectangle containing the legend. If it gives the coordinates of two points, these specify opposite corners of the rectangle (either pair of corners, in any order).

The location may also be specified by setting \(x\) to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". This places the legend on the inside of the plot frame at the given location. Partial argument matching is used. The optional \texttt{inset} argument specifies how far the legend is inset from the plot margins. If a single value is given, it is used for both margins; if two values are given, the first is used for \(x\)-distance, the second for \(y\)-distance.

Attribute arguments such as \texttt{col}, \texttt{pch}, \texttt{lty}, etc, are recycled if necessary: \texttt{merge} is not. Set entries of \texttt{lty} to 0 or set entries of \texttt{lwd} to NA to suppress lines in corresponding legend entries; set \texttt{pch} values to NA to suppress points.

Points are drawn after lines in order that they can cover the line with their background color \texttt{pt.bg}, if applicable.

See the examples for how to right-justify labels.

Since they are not used for Unicode code points, values \(-31:-1\) are silently omitted, as are NA and "" values.

Value

A list with list components

\texttt{rect} \hspace{1cm} a list with components

\(w, h\) positive numbers giving width and height of the legend’s box.

\texttt{left, top} \hspace{1cm} \(x\) and \(y\) coordinates of upper left corner of the box.

\texttt{text} \hspace{1cm} a list with components

\(x, y\) numeric vectors of length \(\text{length(legend)}\), giving the \(x\) and \(y\) coordinates of the legend’s text(s).

returned invisibly.

References


See Also

\texttt{plot, barplot} which uses \texttt{legend()}, and \texttt{text} for more examples of math expressions.
Examples

```r
## Run the example in '?matplot' or the following:
leg.txt <- c("Setosa Petals", "Setosa Sepals",
"Versicolor Petals", "Versicolor Sepals")
y.leg <- c(4.5, 3, 2.1, 1.4, .7)
cexv <- c(1.2, 1, 4/5, 2/3, 1/2)
matplot(c(1, 8), c(0, 4.5), type = "n", xlab = "Length", ylab = "Width",
main = "Petal and Sepal Dimensions in Iris Blossoms")
for (i in seq(cexv)) {
  text (1, y.leg[i] - 0.1, paste("cex=", formatC(cexv[i]), cex = 0.8, adj = 0)
  legend(3, y.leg[i], leg.txt, pch = "sSvV", col = c(1, 3), cex = cexv[i])
}
## cex *vector* [in R <= 3.5.1 has `if(xc < 0)` w/ length(xc) == 2]
legend("right", leg.txt, pch = "sSvV", col = c(1, 3),
cex = 1+(-1:2)/8, trace = TRUE)# trace: show computed lengths & coords
## 'merge = TRUE' for merging lines & points:
x <- seq(-pi, pi, length.out = 65)
for(reverse in c(FALSE, TRUE)) { ## normal *and* reverse axes:
  F <- if(reverse) rev else identity
  plot(x, sin(x), type = "l", col = 3, lty = 2,
  xlim = F(range(x)), ylim = F(c(-1.2, 1.8)))
  points(x, cos(x), pch = 3, col = 4)
  lines(x, tan(x), type = "b", lty = 1, pch = 4, col = 6)
  title("legend("top", lty = c(2, -1, 1), pch = c(NA, 3, 4), merge = TRUE"),
  cex.main = 1.1)
  legend("top", c("sin", "cos", "tan"), col = c(3, 4, 6),
text.col = "green4", lty = c(2, -1, 1), pch = c(NA, 3, 4),
  merge = TRUE, bg = "gray90", trace=TRUE)
}
## right-justifying a set of labels: thanks to Uwe Ligges
x <- 1:5; y1 <- 1/x; y2 <- 2/x
plot(rep(x, 2), c(y1, y2), type = "n", xlab = "x", ylab = "y")
lines(x, y1); lines(x, y2, lty = 2)
temp <- legend("topright", legend = c(" ", " "),
text.width = strwidth("1,000,000"),
lty = 1:2, xjust = 1, yjust = 1, inset = 1/10,
title = "Line Types", title.cex = 0.5, trace=TRUE)
text(temp$rect$left + temp$rect$w, temp$text$y,
c("1,000", "1,000,000"), pos = 2)
```

```r
##--- log scaled Examples ------------------------------
leg.txt <- c("a one", "a two")
par(mfrow = c(2, 2))
for(ll in c("", "x", "y", "xy")) {
  plot(2:10, log = ll, main = paste0("log = ", ll, ""))
  abline(1, 1)
  lines(2:3, 3:4, col = 2)
  points(2, 2, col = 3)
  rect(2, 3, 3, 2, col = 4)
  text(c(3,3), 2:3, c("rect(2,3,3,2,col=4)",
  "text(c(3,3),2:3,\"c(rect(...)\")"), adj = c(0, 0.3))
```
legend(list(x = 2, y = 8), legend = leg.txt, col = 2:3, pch = 1:2,
   lty = 1) #, trace = TRUE)
) # ^^^^^^^ to force lines -> automatic merge=TRUE
par(mfrow = c(1,1))

###-- Math expressions: ------------------------------
x <- seq(-pi, pi, length.out = 65)
plot(x, sin(x), type = "l", col = 2, xlab = expression(phi),
   ylab = expression(f(phi)))
abline(h = -1:1, v = pi/2*(-6:6), col = "gray90")
lines(x, cos(x), col = 3, lty = 2)
ex.cs1 <- expression(plain(sin) * phi, paste("cos", phi)) # 2 ways
utils::str(legend(-3, .9, ex.cs1, lty = 1:2, plot = FALSE,
   adj = c(0, 0.6))) # adj y！
legend(-3, 0.9, ex.cs1, lty = 1:2, col = 2:3, adj = c(0, 0.6))

require(stats)
x <- rexp(100, rate = .5)
hist(x, main = "Mean and Median of a Skewed Distribution")
abline(v = mean(x), col = 2, lty = 2, lwd = 2)
abline(v = median(x), col = 3, lty = 3, lwd = 2)
ex12 <- expression(bar(x) == sum(over(x[i], n), i == 1, n),
   hat(x) == median(x[i], i == 1, n))
utils::str(legend(4.1, 30, ex12, col = 2:3, lty = 2:3, lwd = 2))

## 'filled' boxes -- see also example(barplot) which may call legend(*, fill=)
barplot(VADeaths)
legend("topright", rownames(VADeaths), fill = gray.colors(nrow(VADeaths)))

## Using 'ncol'
x <- 0:64/64
for(R in c(identity, rev)) { # normal *and* reverse x-axis works fine:
x1 <- R(range(x)); x1 <- x1[1]
matplot(x, outer(x, 1:7, function(x, k) sin(k * pi * x)), xlim=x1,
   type = "o", col = 1:7, ylim = c(-1, 1.5), pch = "*")
op <- par(bg = "antiquewhite1")
legend(x1, 1.5, paste("sin", 1:7, "pi * x"), col = 1:7, lty = 1:7,
   pch = "x", ncol = 4, cex = 0.8)
legend("bottomright", paste("sin", 1:7, "pi * x"), col = 1:7, lty = 1:7,
   pch = "x", cex = 0.8)
legend(x1, -.4, paste("sin", 5:7, "pi * x"), col = 4:6, pch = 24,
   ncol = 2, cex = 1.5, lwd = 2, pt.bg = "pink", pt.cex = 1.3)
par(op)
} # for(..)

## point covering line :
y <- sin(3*pi*x)
plot(x, y, type = "l", col = "blue",
   main = "points with bg & legend(*, pt.bg")
points(x, y, pch = 21, bg = "white")
legend(.4,1, "sin(c x)", pch = 21, bg = "white", lty = 1, col = "blue")

## legends with titles at different locations
plot(x, y, type = "n")
legend("bottomright", "(x,y)", pch=1, title= "bottomright")
legend("bottom", "(x,y)", pch=1, title= "bottom")
legend("bottomleft", "(x,y)", pch=1, title= "bottomleft")
legend("left", "(x,y)", pch=1, title= "left")
legend("topleft", "(x,y)", pch=1, title= "topleft, inset = .05", inset = .05)
legend("top", "(x,y)", pch=1, title= "top")
legend("topright", "(x,y)", pch=1, title= "topright, inset = .02", inset = .02)
legend("right", "(x,y)", pch=1, title= "right")
legend("center", "(x,y)", pch=1, title= "center")

# using text.font (and text.col):
op <- par(mfrow = c(2, 2), mar = rep(2.1, 4))
c6 <- terrain.colors(10)[1:6]
for(i in 1:4) {
  plot(1, type = "n", axes = FALSE, ann = FALSE); title(paste("text.font =",i))
  legend("top", legend = LETTERS[1:6], col = c6,
         ncol = 2, cex = 2, lwd = 3, text.font = i, text.col = c6)
}
par(op)

# using text.width for several columns
plot(1, type="n")
legend("topleft", c("This legend", "has", "equally sized", "columns."),
      pch = 1:4, ncol = 4)
legend("bottomleft", c("This legend", "has", "optimally sized", "columns."),
      pch = 1:4, ncol = 4, text.width = NA)
legend("right", letters[1:4], pch = 1:4, ncol = 4,
       text.width = 1:4 / 50)

---

**lines**

**Add Connected Line Segments to a Plot**

**Description**

A generic function taking coordinates given in various ways and joining the corresponding points with line segments.

**Usage**

```r
lines(x, ...)
```

### Default S3 method:
```r
lines(x, y = NULL, type = "l", ...) # lines(x, y = NULL, type = "l", ...)# # Default S3 method:
```

**Arguments**

- `x, y` coordinate vectors of points to join.
- `type` character indicating the type of plotting; actually any of the types as in `plot.default`.
- `...` Further graphical parameters (see `par`) may also be supplied as arguments, particularly, line type, `lty`, line width, `lwd`, color, `col` and for `type = "b"`, `pch`. Also the line characteristics `lend`, `ljoin` and `lmitre`.
**locator**

**Graphical Input**

**Description**

Reads the position of the graphics cursor when the (first) mouse button is pressed.

**Usage**

`locator(n = 512, type = "n", ...)`

**Arguments**

- `n` the maximum number of points to locate. Valid values start at 1.
- `type` One of "n", "p", "l" or "o". If "p" or "o" the points are plotted; if "l" or "o" they are joined by lines.
- `...` additional graphics parameters used if type != "n" for plotting the locations.

**Details**

The coordinates can be passed in a plotting structure (a list with x and y components), a two-column matrix, a time series, ... See `xy.coords`. If supplied separately, they must be of the same length.

The coordinates can contain NA values. If a point contains NA in either its x or y value, it is omitted from the plot, and lines are not drawn to or from such points. Thus missing values can be used to achieve breaks in lines.

For type = "h", col can be a vector and will be recycled as needed.

lwd can be a vector: its first element will apply to lines but the whole vector to symbols (recycled as necessary).

**References**


**See Also**

- `lines.formula` for the formula method; `points`, particularly for type %in% c("p","b","o"), `plot`, and the workhorse function `plot.xy`.
- `abline` for drawing (single) straight lines.
- `par` for line type (lty) specification and how to specify colors.

**Examples**

```r
# draw a smooth line through a scatter plot
plot(cars, main = "Stopping Distance versus Speed")
lines(stats::lowess(cars))
```

---

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- `abline` for drawing (single) straight lines.
- `par` for line type (lty) specification and how to specify colors.

**Examples**

```r
# draw a smooth line through a scatter plot
plot(cars, main = "Stopping Distance versus Speed")
lines(stats::lowess(cars))
```
Details

locator is only supported on screen devices such as X11, windows and quartz. On other devices
the call will do nothing.

Unless the process is terminated prematurely by the user (see below) at most n positions are deter-
mined.

For the usual X11 device the identification process is terminated by pressing any mouse button other
than the first. For the quartz device the process is terminated by pressing the ESC key.

The current graphics parameters apply just as if plot.default has been called with the same value
of type. The plotting of the points and lines is subject to clipping, but locations outside the current
clipping rectangle will be returned.

On most devices which support locator, successful selection of a point is indicated by a bell sound
unless options(locatorBell = FALSE) has been set.

If the window is resized or hidden and then exposed before the input process has terminated, any
lines or points drawn by locator will disappear. These will reappear once the input process has
terminated and the window is resized or hidden and exposed again. This is because the points and
lines drawn by locator are not recorded in the device’s display list until the input process has
terminated.

Value

A list containing x and y components which are the coordinates of the identified points in the user
coordinate system, i.e., the one specified by par("usr").

References

Brooks/Cole.

See Also

identify, grid.locator is the corresponding grid package function.

dev.capabilities to see if it is supported.

matplot

Plot Columns of Matrices

Description

Plot the columns of one matrix against the columns of another (which often is just a vector treated
as 1-column matrix).

Usage

matplot(x, y, type = "p", lty = 1:5, lwd = 1, lend = par("lend"),
          pch = NULL,
          col = 1:6, cex = NULL, bg = NA,
          xlab = NULL, ylab = NULL, xlim = NULL, ylim = NULL,
          log = "", ..., add = FALSE, verbose = getOption("verbose"))
Arguments

- **x, y**: vectors or matrices of data for plotting. The number of rows should match. If one of them is missing, the other is taken as y and an x vector of 1:n is used. Missing values (NA) are allowed. Typically, `class()`es of x and y such as "Date" are preserved.
- **type**: character string (length 1 vector) or vector of 1-character strings indicating the type of plot for each column of y, see `plot` for all possible types. The first character of type defines the first plot, the second character the second, etc. Characters in type are cycled through; e.g., "pl" alternately plots points and lines.
- **lty, lwd, lend**: vector of line types, widths, and end styles. The first element is for the first column, the second element for the second column, etc., even if lines are not plotted for all columns. Line types will be used cyclically until all plots are drawn.
- **pch**: character string or vector of 1-characters or integers for plotting characters, see `points` for details. The first character is the plotting-character for the first plot, the second for the second, etc. The default is the digits (1 through 9, 0) then the lowercase and uppercase letters.
- **col**: vector of colors. Colors are used cyclically.
- **cex**: vector of character expansion sizes, used cyclically. This works as a multiple of `par("cex")`. NULL is equivalent to 1.0.
- **bg**: vector of background (fill) colors for the open plot symbols given by `pch = 21:25` as in `points`. The default NA corresponds to the one of the underlying function `plot.xy`.
- **xlab, ylab**: titles for x and y axes, as in `plot`.
- **xlim, ylim**: ranges of x and y axes, as in `plot`.
- **log, ...**: Graphical parameters (see `par`) and any further arguments of `plot`, typically `plot.default`, may also be supplied as arguments to this function; even `panel.first` etc now work. Hence, the high-level graphics control arguments described under `par` and the arguments to `title` may be supplied to this function.
- **add**: logical. If TRUE, plots are added to current one, using `points` and `lines`.
- **verbose**: logical. If TRUE, write one line of what is done.

Details

`matplot(x,y, ..)` is basically a wrapper for

1. calling (the generic function) `plot(x[,1], y[,1], ..)` for the first columns (only if `add = TRUE`).
2. calling (the generic) `lines(x[,j], y[,j], ..)` for subsequent columns.
Care is taken to keep the `class()` of `x` and `y`, such that the corresponding `plot()` and `lines()` methods will be called.

Points involving missing values are not plotted.

The first column of `x` is plotted against the first column of `y`, the second column of `x` against the second column of `y`, etc. If one matrix has fewer columns, plotting will cycle back through the columns again. (In particular, either `x` or `y` may be a vector, against which all columns of the other argument will be plotted.)

The first element of `col`, `cex`, `lty`, `lwd` is used to plot the axes as well as the first line.

Because plotting symbols are drawn with lines and because these functions may be changing the line style, you should probably specify `lty = 1` when using plotting symbols.

**Side Effects**

Function `matplot` generates a new plot; `matpoints` and `matlines` add to the current one.

**References**


**See Also**

`plot`, `points`, `lines`, `matrix`, `par`.

**Examples**

```r
require(grDevices)
matplot(((-4:5)^2, main = "Quadratic") # almost identical to plot(*)
sines <- outer(1:20, 1:4, function(x, y) sin(x / 20 * pi * y))
matplot(sines, pch = 1:4, type = "o", col = rainbow(ncol(sines)))
matplot(sines, type = "b", pch = 21:23, col = 2:5, bg = 2:5,
        main = "matplot(...., pch = 21:23, bg = 2:5)"

x <- 0:50/50
matplot(x, outer(x, 1:8, function(x, k) sin(k*pi * x)),
        ylim = c(-2,2), type = "plobcsSh",
        main = "matplot(type = \"plobcsSh\")")
## pch & type = vector of 1-chars :
matplot(x, outer(x, 1:4, function(x, k) sin(k*pi * x)),
        pch = letters[1:4], type = c("b","p","o"))

lends <- c("round","butt","square")
matplot(matrix(1:12, 4), type="c", lty=1, lwd=10, lend=lends)
text(cbind(2.5, 2*c(1,3,5)-.4), lends, col= 1:3, cex = 1.5)
table(iris$Species) # is data.frame with 'Species' factor
iS <- iris$Species == "setosa"
iV <- iris$Species == "versicolor"
op <- par(bg = "bisque")
matplot(c(1, 8), c(0, 4.5), type = "n", xlab = "Length", ylab = "Width",
        main = "Petal and Sepal Dimensions in Iris Blossoms")
matpoints(iS,c(1,3)), iS,c(2,4)), pch = "sS", col = c(2,4))
matpoints(iV,c(1,3)), iV,c(2,4)), pch = "vV", col = c(2,4))
legend(1, 4, c(" Setosa Petals", " Setosa Sepals",
```
mosaicplot

"Versicolor Petals", "Versicolor Sepals"),
pch = "sSvV", col = rep(c(2,4), 2))

nam.var <- colnames(iris)[-5]
nam.spec <- as.character(iris[1:50*0:2, "Species"])
iris.S <- array(NA, dim = c(50,4,3),
               dimnames = list(NULL, nam.var, nam.spec))
for(i in 1:3) iris.S[,i] <- data.matrix(iris[1:50*50*(i-1), -5])

matplot(iris.S[, "Petal.Length"], iris.S[, "Petal.Width"], pch = "SCV",
col = rainbow(3, start = 0.8, end = 0.1),
sub = paste(c("S", "C", "V"), dimnames(iris.S)[[3]],
            sep = "="), collapse= " ",
main = "Fisher's Iris Data")

par(op)

## 'x' a "Date" vector:
nd <- length(dv <- seq(as.Date("1959-02-21"), by = "weeks", length.out = 100))
mSC <- cbind(I=1, sin=sin(pi*(1:nd)/8), cos=cos(pi*(1:nd)/8))
matplot(dv, mSC, type = "b", main = "matplot(<Date>, y)"

## 'x' a "POSIXct" date-time vector:
ct <- seq(c(ISODate(2000,3,20)), by = "15 mins", length.out = 100)
matplot(ct, mSC, type = "b", main = "matplot(<POSIXct>, y)"
## or the same with even more axis flexibility:
matplot(ct, mSC, type = "b", main = "matplot(<POSIXct>, y)", xaxt="n")
Axis(ct, side=1, at = ct[1+4*(0:24)])

## Also works for data frame columns:
matplot(iris[1:50,1:4])

mosaicplot

Mosaic Plots

Description
Plots a mosaic on the current graphics device.

Usage
mosaicplot(x, ...)

## Default S3 method:
mosaicplot(x, main = deparse1(substitute(x)),
           sub = NULL, xlab = NULL, ylab = NULL,
           sort = NULL, off = NULL, dir = NULL,
           color = NULL, shade = FALSE, margin = NULL,
           cex.axis = 0.66, las = par("las"), border = NULL,
           type = c("pearson", "deviance", "FT"), ...)  

## S3 method for class 'formula'
mosaicplot(formula, data = NULL, ...,
           main = deparse1(substitute(data)), subset,
           na.action = stats::na.omit)
### mosaicplot

**Arguments**

- **x**
  - A contingency table in array form, with optional category labels specified in the `dimnames(x)` attribute. The table is best created by the `table()` command.

- **main**
  - Character string for the mosaic title.

- **sub**
  - Character string for the mosaic sub-title (at bottom).

- **xlab, ylab**
  - X- and y-axis labels used for the plot; by default, the first and second element of `names(dimnames(X))` (i.e., the name of the first and second variable in X).

- **sort**
  - Vector ordering of the variables, containing a permutation of the integers `1:length(dim(x))` (the default).

- **off**
  - Vector of offsets to determine percentage spacing at each level of the mosaic (appropriate values are between 0 and 20, and the default is 20 times the number of splits for 2-dimensional tables, and 10 otherwise). Rescaled to maximally 50, and recycled if necessary.

- **dir**
  - Vector of split directions ("v" for vertical and "h" for horizontal) for each level of the mosaic, one direction for each dimension of the contingency table. The default consists of alternating directions, beginning with a vertical split.

- **color**
  - Logical or (recycling) vector of colors for color shading, used only when shade is `FALSE`, or `NULL` (default). By default, grey boxes are drawn. `color = TRUE` uses `grey.colors` for a gamma-corrected grey palette. `color = FALSE` gives empty boxes with no shading.

- **shade**
  - A logical indicating whether to produce extended mosaic plots, or a numeric vector of at most 5 distinct positive numbers giving the absolute values of the cut points for the residuals. By default, shade is `FALSE`, and simple mosaics are created. Using `shade = TRUE` cuts absolute values at 2 and 4.

- **margin**
  - A list of vectors with the marginal totals to be fit in the log-linear model. By default, an independence model is fitted. See `loglin` for further information.

- **cex.axis**
  - The magnification to be used for axis annotation, as a multiple of `par("cex")`.

- **las**
  - Numeric; the style of axis labels, see `par`.

- **border**
  - Colour of borders of cells: see `polygon`.

- **type**
  - A character string indicating the type of residual to be represented. Must be one of "pearson" (giving components of Pearson's \( \chi^2 \)), "deviance" (giving components of the likelihood ratio \( \chi^2 \)), or "FT" for the Freeman-Tukey residuals. The value of this argument can be abbreviated.

- **formula**
  - A formula, such as \( y \sim x \).

- **data**
  - A data frame (or list), or a contingency table from which the variables in formula should be taken.

- **...**
  - Further arguments to be passed to or from methods.

- **subset**
  - An optional vector specifying a subset of observations in the data frame to be used for plotting.

- **na.action**
  - A function which indicates what should happen when the data contains variables to be cross-tabulated, and these variables contain NAs. The default is to omit cases which have an NA in any variable. Since the tabulation will omit all cases containing missing values, this will only be useful if the na.action function replaces missing values.
mosaicplot

Details

This is a generic function. It currently has a default method (mosaicplot.default) and a formula interface (mosaicplot.formula).

Extended mosaic displays visualize standardized residuals of a loglinear model for the table by color and outline of the mosaic’s tiles. (Standardized residuals are often referred to a standard normal distribution.) Cells representing negative residuals are drawn in shaded of red and with broken borders; positive ones are drawn in blue with solid borders.

For the formula method, if data is an object inheriting from class "table" or class "ftable" or an array with more than 2 dimensions, it is taken as a contingency table, and hence all entries should be non-negative. In this case the left-hand side of formula should be empty and the variables on the right-hand side should be taken from the names of the dimnames attribute of the contingency table. A marginal table of these variables is computed, and a mosaic plot of that table is produced. Otherwise, data should be a data frame or matrix, list or environment containing the variables to be cross-tabulated. In this case, after possibly selecting a subset of the data as specified by the subset argument, a contingency table is computed from the variables given in formula, and a mosaic is produced from this.

See Emerson (1998) for more information and a case study with television viewer data from Nielsen Media Research.

Missing values are not supported except via an na.action function when data contains variables to be cross-tabulated.

A more flexible and extensible implementation of mosaic plots written in the grid graphics system is provided in the function mosaic in the contributed package vcd (Meyer, Zeileis and Hornik, 2006).

Author(s)

S-PLUS original by John Emerson <john.emerson@yale.edu>. Originally modified and enhanced for R by Kurt Hornik.

References


See Also

assocplot, loglin.

Examples

```r
require(stats)
mosaicplot(Titanic, main = "Survival on the Titanic", color = TRUE)
## Formula interface for tabulated data:
mosaicplot(~ Sex + Age + Survived, data = Titanic, color = TRUE)
```
mosaicplot(HairEyeColor, shade = TRUE)
## Independence model of hair and eye color and sex. Indicates that
## there are more blue eyed blonde females than expected in the case
## of independence and too few brown eyed blonde females.
## The corresponding model is:
fm <- loglin(HairEyeColor, list(1, 2, 3))
pchisq(fm$pearson, fm$df, lower.tail = FALSE)

mosaicplot(HairEyeColor, shade = TRUE, margin = list(1:2, 3))
## Model of joint independence of sex from hair and eye color. Males
## are underrepresented among people with brown hair and eyes, and are
## overrepresented among people with brown hair and blue eyes.
## The corresponding model is:
fm <- loglin(HairEyeColor, list(1:2, 3))
pchisq(fm$pearson, fm$df, lower.tail = FALSE)

## Formula interface for raw data: visualize cross-tabulation of numbers
## of gears and carburettors in Motor Trend car data.
mosaicplot(~ gear + carb, data = mtcars, color = TRUE, las = 1)
# color recycling
mosaicplot(~ gear + carb, data = mtcars, color = 2:3, las = 1)

---

mtext

**Write Text into the Margins of a Plot**

### Description

Text is written in one of the four margins of the current figure region or one of the outer margins of the device region.

### Usage

```r
mtext(text, side = 3, line = 0, outer = FALSE, at = NA,
      adj = NA, padj = NA, cex = NA, col = NA, font = NA, ...)
```

### Arguments

- **text**: a character or expression vector specifying the text to be written. Other objects are coerced by `as.graphicsAnnot`.
- **side**: on which side of the plot (1=bottom, 2=left, 3=top, 4=right).
- **line**: on which margin line, starting at 0 counting outwards.
- **outer**: use outer margins if available.
- **at**: give location of each string in user coordinates. If the component of `at` corresponding to a particular text item is not a finite value (the default), the location will be determined by `adj`.
- **adj**: adjustment for each string in reading direction. For strings parallel to the axes, `adj = 0` means left or bottom alignment, and `adj = 1` means right or top alignment.

If `adj` is not a finite value (the default), the value of `par("las")` determines the adjustment. For strings plotted parallel to the axis the default is to centre the string.
mtext

- **padj**: adjustment for each string perpendicular to the reading direction (which is controlled by `adj`). For strings parallel to the axes, `padj = 0` means left or bottom alignment, and `padj = 1` means right or top alignment (relative to the line). If `padj` is not a finite value (the default), the value of `par("las")` determines the adjustment. For strings plotted perpendicular to the axis the default is to centre the string.

- **cex**: character expansion factor. `NULL` and `NA` are equivalent to `1.0`. This is an absolute measure, not scaled by `par("cex")` or by setting `par("mfrow")` or `par("mfcol")`. Can be a vector.

- **col**: color to use. Can be a vector. `NA` values (the default) mean use `par("col")`.

- **font**: font for text. Can be a vector. `NA` values (the default) mean use `par("font")`.

- **...**: Further graphical parameters (see `par`), including `family`, `las` and `xpd`. (The latter defaults to the figure region unless `outer = TRUE`, otherwise the device region. It can only be increased.)

**Details**

The user coordinates in the outer margins always range from zero to one, and are not affected by the user coordinates in the figure region(s) — R differs here from other implementations of S.

All of the named arguments can be vectors, and recycling will take place to plot as many strings as the longest of the vector arguments.

Note that a vector `adj` has a different meaning from `text`. `adj = 0.5` will centre the string, but for `outer = TRUE` on the device region rather than the plot region.

Parameter `las` will determine the orientation of the string(s). For strings plotted perpendicular to the axis the default justification is to place the end of the string nearest the axis on the specified line. (Note that this differs from S, which uses `srt` if `at` is supplied and `las` if it is not. Parameter `srt` is ignored in R.)

Note that if the text is to be plotted perpendicular to the axis, `adj` determines the justification of the string and the position along the axis unless `at` is specified.

Graphics parameter "ylbias" (see `par`) determines how the text baseline is placed relative to the nominal line.

**Side Effects**

The given text is written onto the current plot.

**References**


**See Also**

`title`, `text`, `plot`, `par`; `plotmath` for details on mathematical annotation.

**Examples**

```r
plot(1:10, (-4:5)^2, main = "Parabola Points", xlab = "xlab")
mtext("10 of them")
for(s in 1:4)
  mtext(paste("mtext(..., line=-1, \{side, col, font\} = ", s,
```
Description
A matrix of scatterplots is produced.

Usage
pairs(x, ...)

## S3 method for class 'formula'
pairs(formula, data = NULL, ..., subset,
       na.action = stats::na.pass)

## Default S3 method:
pairs(x, labels, panel = points, ...,
       horInd = 1:nc, verInd = 1:nc,
       lower.panel = panel, upper.panel = panel,
       diag.panel = NULL, text.panel = textPanel,
       label.pos = 0.5 + has.diag/3, line.main = 3,
       cex.labels = NULL, font.labels = 1,
       row1attop = TRUE, gap = 1, log = "",
       horOdd = !row1attop, verOdd = !row1attop)

Arguments
x
the coordinates of points given as numeric columns of a matrix or data frame. Logical and factor columns are converted to numeric in the same way that data.matrix does.

formula
a formula, such as ~ x + y + z. Each term will give a separate variable in the pairs plot, so terms should be numeric vectors. (A response will be interpreted as another variable, but not treated specially, so it is confusing to use one.)

data
a data.frame (or list) from which the variables in formula should be taken.

subset
an optional vector specifying a subset of observations to be used for plotting.

na.action
a function which indicates what should happen when the data contain NAs. The default is to pass missing values on to the panel functions, but na.action = na.omit will cause cases with missing values in any of the variables to be ommitted entirely.

labels
the names of the variables.

panel
function(x, y, ...) which is used to plot the contents of each panel of the display.
pairs arguments to be passed to or from methods. Also, graphical parameters can be given as can arguments to plot such as main.par("oma") will be set appropriately unless specified.

horInd, verInd The (numerical) indices of the variables to be plotted on the horizontal and vertical axes respectively.

lower.panel, upper.panel separate panel functions (or NULL) to be used below and above the diagonal respectively.

diag.panel optional function(x, ...) to be applied on the diagonals.

text.panel optional function(x, y, labels, cex, font, ...) to be applied on the diagonals.

label.pos y position of labels in the text panel.

line.main if main is specified, line.main gives the line argument to mtext() which draws the title. You may want to specify oma when changing line.main.

cex.labels, font.labels graphics parameters for the text panel.

row1attop logical. Should the layout be matrix-like with row 1 at the top, or graph-like with row 1 at the bottom? The latter (non default) leads to a basically symmetric scatterplot matrix.

gap distance between subplots, in margin lines.

log a character string indicating if logarithmic axes are to be used, see plot.default or a numeric vector of indices specifying the indices of those variables where logarithmic axes should be used for both x and y. log = "xy" specifies logarithmic axes for all variables.

horOdd, verOdd logical (or integer) determining how the horizontal and vertical axis labeling happens. If true, the axis labelling starts at the first (from top left) row or column, respectively.

Details

The $ij$th scatterplot contains $x[,i]$ plotted against $x[,j]$. The scatterplot can be customised by setting panel functions to appear as something completely different. The off-diagonal panel functions are passed the appropriate columns of x as x and y: the diagonal panel function (if any) is passed a single column, and the text.panel function is passed a single $(x, y)$ location and the column name. Setting some of these panel functions to NULL is equivalent to not drawing anything there.

The graphical parameters pch and col can be used to specify a vector of plotting symbols and colors to be used in the plots.

The graphical parameter oma will be set by pairs.default unless supplied as an argument.

A panel function should not attempt to start a new plot, but just plot within a given coordinate system: thus plot and boxplot are not panel functions.

By default, missing values are passed to the panel functions and will often be ignored within a panel. However, for the formula method and na.action = na.omit, all cases which contain a missing values for any of the variables are omitted completely (including when the scales are selected).

Arguments horInd and verInd were introduced in R 3.2.0. If given the same value they can be used to select or re-order variables: with different ranges of consecutive values they can be used to plot rectangular windows of a full pairs plot; in the latter case 'diagonal' refers to the diagonal of the full plot.
Enhancements for R 1.0.0 contributed by Dr. Jens Oehlschlägel-Akiyoshi and R-core members.

References


Examples

```r
pairs(iris[1:4], main = "Anderson's Iris Data -- 3 species", pch = 21, bg = c("red", "green3", "blue")[unclass(iris$Species)])

## formula method, "graph" layout (row 1 at bottom):
pairs(~ Fertility + Education + Catholic, data = swiss, row1attop=FALSE, subset = Education < 20, main = "Swiss data, Education < 20")

pairs(USJudgeRatings, gap=1/10) # (gap: not wasting plotting area)
## show only lower triangle (and suppress labeling for whatever reason):
pairs(USJudgeRatings, text.panel = NULL, upper.panel = NULL)

## put histograms on the diagonal
panel.hist <- function(x, ...) {
  usr <- par("usr")
  par(usr = c(usr[1:2], 0, 1.5))
  h <- hist(x, plot = FALSE)
  breaks <- h$breaks; nB <- length(breaks)
  y <- h$counts; y <- y/max(y)
  rect(breaks[-nB], 0, breaks[-1], y, col = "cyan", ...)
}

pairs(USJudgeRatings[1:5], panel = panel.smooth, cex = 1.5, pch = 24, bg = "light blue", horOdd=TRUE, diag.panel = panel.hist, cex.labels = 2, font.labels = 2)

## put (absolute) correlations on the upper panels,
## with size proportional to the correlations.
panel.cor <- function(x, y, digits = 2, prefix = ",", cex.cor, ...) {
  par(usr = c(0, 1, 0, 1))
  r <- abs(cor(x, y))
  txt <- format(c(r, 0.123456789), digits = digits)[1]
  txt <- paste0(prefix, txt)
  if(missing(cex.cor)) cex.cor <- 0.8/strwidth(txt)
  text(0.5, 0.5, txt, cex = cex.cor * r)
}

pairs(USJudgeRatings, lower.panel = panel.smooth, upper.panel = panel.cor, gap=0, row1attop=FALSE)

pairs(iris[-5], log = "xy") # plot all variables on log scale
pairs(iris, log = 1:4, # log the first four
      main = "Lengths and Widths in [log]", line.main=1.5, oma=c(2,2,3,2))
```
Description

An example of a simple useful panel function to be used as argument in e.g., `coplot` or `pairs`.

Usage

```r
panel.smooth(x, y, col = par("col"), bg = NA, pch = par("pch"),
             cex = 1, col.smooth = 2, span = 2/3, iter = 3,
             ...)```

Arguments

- `x, y` numeric vectors of the same length
- `col, bg, pch, cex` numeric or character codes for the color(s), point type and size of points; see also `par`.
- `col.smooth` color to be used by `lines` for drawing the smooths.
- `span` smoothing parameter \( f \) for `lowess`, see there.
- `iter` number of robustness iterations for `lowess`.
- `...` further arguments to `lines`.

See Also

`coplot` and `pairs` where `panel.smooth` is typically used; `lowess` which does the smoothing.

Examples

```r
pairs(swiss, panel = panel.smooth, pch = ".") # emphasize the smooths
pairs(swiss, panel = panel.smooth, lwd = 2, cex = 1.5, col = 4) # hmm...
```

par

Description

par can be used to set or query graphical parameters. Parameters can be set by specifying them as arguments to `par` in `tag = value` form, or by passing them as a list of tagged values.

Usage

```r
par(...., no.readonly = FALSE)

<highlevel plot> (...., <tag> = <value>)```
Arguments

... arguments in tag = value form, a single list of tagged values, or character vectors of parameter names. Supported parameters are described in the ‘Graphical Parameters’ section.

no.readonly logical; if TRUE and there are no other arguments, only parameters are returned which can be set by a subsequent par() call on the same device.

Details

Each device has its own set of graphical parameters. If the current device is the null device, par will open a new device before querying/setting parameters. (What device is controlled by options("device").)

Parameters are queried by giving one or more character vectors of parameter names to par.

par() (no arguments) or par(no.readonly = TRUE) is used to get all the graphical parameters (as a named list). Their names are currently taken from the unexported variable graphics::.Pars.

R.O. indicates read-only arguments: These may only be used in queries and cannot be set. ("cin", "cra", "csi", "cxy", "din" and "page" are always read-only.)

Several parameters can only be set by a call to par():

- "ask",
- "fig", "fin",
- "lheight",
- "mai", "mar", "mex", "mfcol", "mfrow", "mfg",
- "new",
- "oma", "omd", "omi",
- "pin", "plt", "ps", "pty",
- "usr",
- "xlog", "ylog",
- "ylbias"

The remaining parameters can also be set as arguments (often via ...) to high-level plot functions such as plot.default, plot.window, points, lines, abline, axis, title, text, mtext, segments, symbols, arrows, polygon, rect, box, contour, filled.contour and image. Such settings will be active during the execution of the function, only. However, see the comments on bg, cex, col, lty, lwd and pch which may be taken as arguments to certain plot functions rather than as graphical parameters.

The meaning of ‘character size’ is not well-defined: this is set up for the device taking pointsize into account but often not the actual font family in use. Internally the corresponding pars (cra, cin, cxy and csi) are used only to set the inter-line spacing used to convert mar and oma to physical margins. (The same inter-line spacing multiplied by lheight is used for multi-line strings in text and strheight.)

Note that graphical parameters are suggestions: plotting functions and devices need not make use of them (and this is particularly true of non-default methods for e.g. plot).
**Value**

When parameters are set, their previous values are returned in an invisible named list. Such a list can be passed as an argument to `par` to restore the parameter values. Use `par(no.readonly = TRUE)` for the full list of parameters that can be restored. However, restoring all of these is not wise: see the ‘Note’ section.

When just one parameter is queried, the value of that parameter is returned as (atomic) vector. When two or more parameters are queried, their values are returned in a list, with the list names giving the parameters.

Note the inconsistency: setting one parameter returns a list, but querying one parameter returns a vector.

**Graphical Parameters**

- **adj** The value of `adj` determines the way in which text strings are justified in `text`, `mtext`, and `title`. A value of 0 produces left-justified text, 0.5 (the default) centered text and 1 right-justified text. (Any value in [0, 1] is allowed, and on most devices values outside that interval will also work.)

  Note that the `adj` argument of `text` also allows `adj = c(x, y)` for different adjustment in x- and y- directions. Note that whereas for `text` it refers to positioning of text about a point, for `mtext` and `title` it controls placement within the plot or device region.

- **ann** If set to `FALSE`, high-level plotting functions calling `plot.default` do not annotate the plots they produce with axis titles and overall titles. The default is to do annotation.

  This not really a graphics parameter, and its use is deprecated in favour of `devAskNewPage`.

- **bg** The color to be used for the background of the device region. When called from `par()` it also sets `new = FALSE`. See section ‘Color Specification’ for suitable values. For many devices the initial value is set from the `bg` argument of the device, and for the rest it is normally "white".

  Note that some graphics functions such as `plot.default` and `points` have an argument of this name with a different meaning.

- **bty** A character string which determined the type of `box` which is drawn about plots. If `bty` is one of "o" (the default), "l", "7", "c", "u", or "]\" the resulting box resembles the corresponding upper case letter. A value of "n" suppresses the box.

- **cex** A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default. This starts as 1 when a device is opened, and is reset when the layout is changed, e.g., by setting `mfrow`.

  Note that some graphics functions such as `plot.default` have an argument of this name which multiplies this graphical parameter, and some functions such as `points` and `text` accept a vector of values which are recycled.

- **cex.axis** The magnification to be used for axis annotation relative to the current setting of `cex`.

- **cex.lab** The magnification to be used for x and y labels relative to the current setting of `cex`.

- **cex.main** The magnification to be used for main titles relative to the current setting of `cex`.

- **cex.sub** The magnification to be used for sub-titles relative to the current setting of `cex`.

- **cin** `R.O.`; character size (width, height) in inches. These are the same measurements as `cra`, expressed in different units.
col  A specification for the default plotting color. See section ‘Color Specification’.
Some functions such as `lines` and `text` accept a vector of values which are recycled and may be interpreted slightly differently.

col.axis  The color to be used for axis annotation. Defaults to "black".
col.lab  The color to be used for x and y labels. Defaults to "black".
col.main  The color to be used for plot main titles. Defaults to "black".
col.sub  The color to be used for plot sub-titles. Defaults to "black".

cra  **R.O.**; size of default character (width, height) in ‘rasters’ (pixels). Some devices have no concept of pixels and so must assume an arbitrary pixel size, usually 1/72 inch. These are the same measurements as `cin`, expressed in different units.

crt  A numerical value specifying (in degrees) how single characters should be rotated. It is unwise to expect values other than multiples of 90 to work. Compare with `srt` which does string rotation.

csi  **R.O.**; height of (default-sized) characters in inches. The same as `par("cin")[2]`.

cxy  **R.O.**; size of default character (width, height) in user coordinate units. `par("cxy")` is `par("cin")/par("pin")` scaled to user coordinates. Note that `c(strwidth(ch), strheight(ch))` for a given string `ch` is usually much more precise.

din  **R.O.**; the device dimensions, (width, height), in inches. See also `dev.size`, which is updated immediately when an on-screen device window is re-sized.

err  (Unimplemented; R is silent when points outside the plot region are not plotted.) The degree of error reporting desired.

family  The name of a font family for drawing text. The maximum allowed length is 200 bytes. This name gets mapped by each graphics device to a device-specific font description. The default value is "" which means that the default device fonts will be used (and what those are should be listed on the help page for the device). Standard values are "serif", "sans" and "mono", and the Hershey font families are also available. (Devices may define others, and some devices will ignore this setting completely. Names starting with "Hershey" are treated specially and should only be used for the built-in Hershey font families.) This can be specified inline for `text`.

fg  The color to be used for the foreground of plots. This is the default color used for things like axes and boxes around plots. When called from `par()` this also sets parameter `col` to the same value. See section ‘Color Specification’. A few devices have an argument to set the initial value, which is otherwise "black".

fig  A numerical vector of the form `c(x1, x2, y1, y2)` which gives the (NDC) coordinates of the figure region in the display region of the device. If you set this, unlike S, you start a new plot, so to add to an existing plot use `new = TRUE` as well.

fin  The figure region dimensions, (width, height), in inches. If you set this, unlike S, you start a new plot.

font  An integer which specifies which font to use for text. If possible, device drivers arrange so that 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic. Also, font 5 is expected to be the symbol font, in Adobe symbol encoding. On some devices fonts can be selected by `family` to choose different sets of 5 fonts.

text  The font to be used for axis annotation.

text.lab  The font to be used for x and y labels.
text.main  The font to be used for plot main titles.
text.sub  The font to be used for plot sub-titles.
A numerical vector of the form $c(x, y, 1en)$ which modifies the default way that axes are annotated. The values of $x$ and $y$ give the (approximate) number of tickmarks on the x and y axes and $1en$ specifies the label length. The default is $c(5, 5, 7)$. $1en$ is unimplemented in R.

The style of axis labels.

0: always parallel to the axis [default],
1: always horizontal,
2: always perpendicular to the axis,
3: always vertical.

Also supported by mtext. Note that string/character rotation via argument srt to par does not affect the axis labels.

The line end style. This can be specified as an integer or string:

0 and "round" mean rounded line caps [default];
1 and "butt" mean butt line caps;
2 and "square" mean square line caps.

The line height multiplier. The height of a line of text (used to vertically space multi-line text) is found by multiplying the character height both by the current character expansion and by the line height multiplier. Default value is 1. Used in text and strheight.

The line join style. This can be specified as an integer or string:

0 and "round" mean rounded line joins [default];
1 and "mitre" mean mitred line joins;
2 and "bevel" mean bevelled line joins.

The line mitre limit. This controls when mitred line joins are automatically converted into bevelled line joins. The value must be larger than 1 and the default is 10. Not all devices will honour this setting.

The line type. Line types can either be specified as an integer (0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "blank", "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash", where "blank" uses 'invisible lines' (i.e., does not draw them).

Alternatively, a string of up to 8 characters (from c(1:9, "A":"F")) may be given, giving the length of line segments which are alternatively drawn and skipped. See section 'Line Type Specification'.

Functions such as lines and segments accept a vector of values which are recycled.

The line width, a positive number, defaulting to 1. The interpretation is device-specific, and some devices do not implement line widths less than one. (See the help on the device for details of the interpretation.)

Functions such as lines and segments accept a vector of values which are recycled: in such uses lines corresponding to values NA or NaN are omitted. The interpretation of 0 is device-specific.

A numerical vector of the form $c(bottom, left, top, right)$ which gives the margin size specified in inches.
mar A numerical vector of the form c(bottom, left, top, right) which gives the number of
lines of margin to be specified on the four sides of the plot. The default is c(5, 4, 4, 2) +
0.1.

mex mex is a character size expansion factor which is used to describe coordinates in the margins
of plots. Note that this does not change the font size, rather specifies the size of font (as a
multiple of csi) used to convert between mar and mai, and between oma and omi.
This starts as 1 when the device is opened, and is reset when the layout is changed (alongside
resetting cex).

mfcol, mfrow A vector of the form c(nr, nc). Subsequent figures will be drawn in an nr-by-nc
array on the device by columns (mfcol), or rows (mfrow), respectively.
In a layout with exactly two rows and columns the base value of "cex" is reduced by a factor
of 0.83: if there are three or more of either rows or columns, the reduction factor is 0.66.
Setting a layout resets the base value of cex and that of mex to 1.
If either of these is queried it will give the current layout, so querying cannot tell you the order
in which the array will be filled.
Consider the alternatives, layout and split.screen.

mfg A numerical vector of the form c(i, j) where i and j indicate which figure in an array of
figures is to be drawn next (if setting) or is being drawn (if enquiring). The array must already
have been set by mfcol or mfrow.
For compatibility with S, the form c(i, j, nr, nc) is also accepted, when
nr and nc should be the current number of rows and number of columns. Mismatches will be ignored, with a
warning.

mgp The margin line (in mex units) for the axis title, axis labels and axis line. Note that mgp[1]
affects title whereas mgp[2:3] affect axis. The default is c(3, 1, 0).

mkh The height in inches of symbols to be drawn when the value of pch is an integer. Completely
ignored in R.

new logical, defaulting to FALSE. If set to TRUE, the next high-level plotting command (actually
plot.new) should not clean the frame before drawing as if it were on a new device. It is an
error (ignored with a warning) to try to use new = TRUE on a device that does not currently
contain a high-level plot.

oma A vector of the form c(bottom, left, top, right) giving the size of the outer margins in
lines of text.
omd A vector of the form \(c(x_1, x_2, y_1, y_2)\) giving the region inside outer margins in NDC (= normalized device coordinates), i.e., as a fraction (in [0, 1]) of the device region.

omi A vector of the form \(c(bottom, left, top, right)\) giving the size of the outer margins in inches.

page R.O.; A boolean value indicating whether the next call to plot.new is going to start a new page. This value may be FALSE if there are multiple figures on the page.

pch Either an integer specifying a symbol or a single character to be used as the default in plotting points. See points for possible values and their interpretation. Note that only integers and single-character strings can be set as a graphics parameter (and not NA nor NULL).

Some functions such as points accept a vector of values which are recycled.

pin The current plot dimensions, \((width, height)\), in inches.

plt A vector of the form \(c(x_1, x_2, y_1, y_2)\) giving the coordinates of the plot region as fractions of the current figure region.

ps integer; the point size of text (but not symbols). Unlike the pointsize argument of most devices, this does not change the relationship between mar and mai (nor oma and omi).

What is meant by ‘point size’ is device-specific, but most devices mean a multiple of 1bp, that is 1/72 of an inch.

pty A character specifying the type of plot region to be used; "s" generates a square plotting region and "m" generates the maximal plotting region.

smo \((Unimplemented)\) a value which indicates how smooth circles and circular arcs should be.

tsrt The string rotation in degrees. See the comment about crt. Only supported by text.

tck The length of tick marks as a fraction of the smaller of the width or height of the plotting region. If tck >= 0.5 it is interpreted as a fraction of the relevant side, so if tck = 1 grid lines are drawn. The default setting (tck = NA) is to use tcl = -0.5.

tcl The length of tick marks as a fraction of the height of a line of text. The default value is -0.5; setting tcl = NA sets tck = -0.01 which is S’ default.

usr A vector of the form \(c(x_1, x_2, y_1, y_2)\) giving the extremes of the user coordinates of the plotting region. When a logarithmic scale is in use (i.e., par("xlog") is true, see below), then the x-limits will be \(10^{\text{par("usr")}[1:2]}\). Similarly for the y-axis.
xaxp A vector of the form c(x1, x2, n) giving the coordinates of the extreme tick marks and the number of intervals between tick-marks when par("xlog") is false. Otherwise, when log coordinates are active, the three values have a different meaning: For a small range, n is negative, and the ticks are as in the linear case, otherwise, n is in 1:3, specifying a case number, and x1 and x2 are the lowest and highest power of 10 inside the user coordinates, 10 ^ par("usr")[1:2]. (The "usr" coordinates are log10-transformed here!)

n = 1 will produce tick marks at 10^j for integer j,

n = 2 gives marks k10^j with k \in \{1, 5\},

n = 3 gives marks k10^j with k \in \{1, 2, 5\}.

See axTicks() for a pure R implementation of this.

This parameter is reset when a user coordinate system is set up, for example by starting a new page or by calling plot.window or setting par("usr"): n is taken from par("lab"). It affects the default behaviour of subsequent calls to axis for sides 1 or 3.

It is only relevant to default numeric axis systems, and not for example to dates.

xaxs The style of axis interval calculation to be used for the x-axis. Possible values are "r", "i", "e", "s", "d". The styles are generally controlled by the range of data or xlim, if given.

Style "r" (regular) first extends the data range by 4 percent at each end and then finds an axis with pretty labels that fits within the extended range.

Style "i" (internal) just finds an axis with pretty labels that fits within the original data range.

Style "s" (standard) finds an axis with pretty labels within which the original data range fits.

Style "e" (extended) is like style "s", except that it also ensures that there is room for plotting symbols within the bounding box.

Style "d" (direct) specifies that the current axis should be used on subsequent plots.

(Only "r" and "i" styles have been implemented in R.)

xaxt A character which specifies the x axis type. Specifying "n" suppresses plotting of the axis.

The standard value is "s": for compatibility with S values "l" and "t" are accepted but are equivalent to "s": any value other than "n" implies plotting.

xlog A logical value (see log in plot.default). If TRUE, a logarithmic scale is in use (e.g., after plot(*, log = "x")). For a new device, it defaults to FALSE, i.e., linear scale.

xpd A logical value or NA. If FALSE, all plotting is clipped to the plot region, if TRUE, all plotting is clipped to the figure region, and if NA, all plotting is clipped to the device region. See also clip.

yaxp A vector of the form c(y1, y2, n) giving the coordinates of the extreme tick marks and the number of intervals between tick-marks unless for log coordinates, see xaxp above.

yaxs The style of axis interval calculation to be used for the y-axis. See xaxs above.

yaxt A character which specifies the y axis type. Specifying "n" suppresses plotting.

ylbias A positive real value used in the positioning of text in the margins by axis and mtext. The default is in principle device-specific, but currently 0.2 for all of R’s own devices. Set this to 0.2 for compatibility with R < 2.14.0 on x11 and windows() devices.

ylog A logical value; see xlog above.

Color Specification

Colors can be specified in several different ways. The simplest way is with a character string giving the color name (e.g., "red"). A list of the possible colors can be obtained with the function colors. Alternatively, colors can be specified directly in terms of their RGB components with a string of the form "#RRGGBB" where each of the pairs RR, GG, BB consist of two hexadecimal digits giving a value in the range 00 to FF. Colors can also be specified by giving an index into a small table of colors, the palette: indices wrap round so with the default palette of size 8, 10 is the same as 2. This
par provides compatibility with S. Index 0 corresponds to the background color. Note that the palette (apart from 0 which is per-device) is a per-session setting.

Negative integer colours are errors.

Additionally, "transparent" is transparent, useful for filled areas (such as the background!), and just invisible for things like lines or text. In most circumstances (integer) NA is equivalent to "transparent" (but not for text and mtext).

Semi-transparent colors are available for use on devices that support them.

The functions rgb, hsv, hcl, gray and rainbow provide additional ways of generating colors.

Line Type Specification

Line types can either be specified by giving an index into a small built-in table of line types (1 = solid, 2 = dashed, etc, see lty above) or directly as the lengths of on/off stretches of line. This is done with a string of an even number (up to eight) of characters, namely non-zero (hexadecimal) digits which give the lengths in consecutive positions in the string. For example, the string "33" specifies three units on followed by three off and "3313" specifies three units on followed by three off followed by one on and finally three off. The ‘units’ here are (on most devices) proportional to lwd, and with lwd = 1 are in pixels or points or 1/96 inch.

The five standard dash-dot line types (lty = 2:6) correspond to c("44", "13", "1343", "73", "2262").

Note that NA is not a valid value for lty.

Note

The effect of restoring all the (settable) graphics parameters as in the examples is hard to predict if the device has been resized. Several of them are attempting to set the same things in different ways, and those last in the alphabet will win. In particular, the settings of mai, mar, pin, plt and pty interact, as do the outer margin settings, the figure layout and figure region size.

References


See Also

plot.default for some high-level plotting parameters; colors; clip; options for other setup parameters; graphic devices x11, postscript and setting up device regions by layout and split.screen.

Examples

op <- par(mfrow = c(2, 2), # 2 x 2 pictures on one plot
pty = "s") # square plotting region,
# independent of device size

## At end of plotting, reset to previous settings:
par(op)

## Alternatively,
op <- par(no.readonly = TRUE) # the whole list of settable par’s.
## do lots of plotting and par(.) calls, then reset:
par(op)
## Note this is not in general good practice
par("ylog") # FALSE
plot(1:12, log = "y")
par("ylog") # TRUE

plot(1:2, xaxs = "i") # 'inner axis' w/o extra space
par(c("usr", "xaxp"))

c(prof.pilots = 16, lawyers = 11, farmers = 10, salesmen = 9, physicians = 9,
mechanics = 6, policemen = 6, managers = 6, engineers = 5, teachers = 4,
housewives = 3, students = 3, armed.forces = 1))
par(las = 3)
barplot(rbind(nr.prof)) # R 0.63.2: shows alignment problem
par(las = 0) # reset to default

require(grDevices) # for gray
## 'fg' use:
plot(1:12, type = "b", main = "fg : axes, ticks and box in gray",
fg = gray(0.7), bty = "7", sub = R.version.string)
ex <- function() {
  old.par <- par(no.readonly = TRUE) # all par settings which
  # could be changed.
  on.exit(par(old.par))
  ## ...  
  ## ... do lots of par() settings and plots
  ## ... invisible() #-- now, par(old.par) will be executed
}
ex()

## Line types
showLty <- function(ltys, xoff = 0, ...) {
  stopifnot((n <- length(ltys)) >= 1)
  op <- par(mar = rep(.5, 4)); on.exit(par(op))
  plot(0:1, 0:1, type = "n", axes = FALSE, ann = FALSE)
  y <- (n:1)/(n+1)
  clty <- as.character(ltys)
  mytext <- function(x, y, txt) {text(x, y, txt, adj = c(0, -.3), cex = 0.8, ...)
    abline(h = y, lty = ltys, ...); mytext(xoff, y, clty)
  y <- y - 1/(3*(n+1))
  abline(h = y, lty = ltys, lwd = 2, ...)
  mytext(1/8+xoff, y, paste(clty," lwd = 2"))
}
showLty(c("solid", "dashed", "dotted", "dotdash", "longdash", "twodash"))
par(new = TRUE) # the same:
showLty(c("solid", "44", "13", "1343", "73", "2262"), xoff = .2, col = 2)
showLty(c("11", "22", "33", "44", "12", "13", "14", "21", "31"))
Description

This function draws perspective plots of a surface over the x–y plane. persp is a generic function.

Usage

persp(x, ...)

## Default S3 method:
persp(x = seq(0, 1, length.out = nrow(z)),
y = seq(0, 1, length.out = ncol(z)),
z, xlab = NULL, ylab = NULL, zlab = NULL,
theta = 0, phi = 15, r = sqrt(3), d = 1,
scale = TRUE, expand = 1,
col = "white", border = NULL, shade = NA, box = TRUE, axes = TRUE, nticks = 5,
ticktype = "simple", ...)

Arguments

x, y
locations of grid lines at which the values in z are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If x is a list, its components x$x and x$y are used for x and y, respectively.

z
a matrix containing the values to be plotted (NAs are allowed). Note that x can be used instead of z for convenience.

xlim, ylim, zlim
x-, y- and z-limits. These should be chosen to cover the range of values of the surface: see ‘Details’.

xlab, ylab, zlab
titles for the axes. N.B. These must be character strings; expressions are not accepted. Numbers will be coerced to character strings.

main, sub
main title and subtitle, as for title.

theta, phi
angles defining the viewing direction. theta gives the azimuthal direction and phi the colatitude.

r
the distance of the eyepoint from the centre of the plotting box.

d
a value which can be used to vary the strength of the perspective transformation. Values of d greater than 1 will lessen the perspective effect and values less and 1 will exaggerate it.

scale
before viewing the x, y and z coordinates of the points defining the surface are transformed to the interval [0,1]. If scale is TRUE the x, y and z coordinates are transformed separately. If scale is FALSE the coordinates are scaled so that aspect ratios are retained. This is useful for rendering things like DEM information.

expand
a expansion factor applied to the z coordinates. Often used with 0 < expand < 1 to shrink the plotting box in the z direction.

col
the color(s) of the surface facets. Transparent colours are ignored. This is recycled to the \((nx - 1)(ny - 1)\) facets.
border  the color of the line drawn around the surface facets. The default, NULL, corresponds to par("fg"). A value of NA will disable the drawing of borders: this is sometimes useful when the surface is shaded.

ltheta, lphi  if finite values are specified for ltheta and lphi, the surface is shaded as though it was being illuminated from the direction specified by azimuth ltheta and colatitude lphi.

shade  the shade at a surface facet is computed as ((1+d)/2)^shade, where d is the dot product of a unit vector normal to the facet and a unit vector in the direction of a light source. Values of shade close to one yield shading similar to a point light source model and values close to zero produce no shading. Values in the range 0.5 to 0.75 provide an approximation to daylight illumination.

box  should the bounding box for the surface be displayed. The default is TRUE.

axes  should ticks and labels be added to the box. The default is TRUE. If box is FALSE then no ticks or labels are drawn.

ticktype  character: "simple" draws just an arrow parallel to the axis to indicate direction of increase; "detailed" draws normal ticks as per 2D plots.

nticks  the (approximate) number of tick marks to draw on the axes. Has no effect if ticktype is "simple".

...  additional graphical parameters (see par).

Details

The plots are produced by first transforming the (x,y,z) coordinates to the interval [0,1] using the limits supplied or computed from the range of the data. The surface is then viewed by looking at the origin from a direction defined by theta and phi. If theta and phi are both zero the viewing direction is directly down the negative y axis. Changing theta will vary the azimuth and changing phi the colatitude.

There is a hook called "persp" (see setHook) called after the plot is completed, which is used in the testing code to annotate the plot page. The hook function(s) are called with no argument.

Notice that persp interprets the z matrix as a table of f(x[i], y[j]) values, so that the x axis corresponds to row number and the y axis to column number, with column 1 at the bottom, so that with the standard rotation angles, the top left corner of the matrix is displayed at the left hand side, closest to the user.

The sizes and fonts of the axis labels and the annotations for ticktype = "detailed" are controlled by graphics parameters "cex.lab"/"font.lab" and "cex.axis"/"font.axis" respectively.

The bounding box is drawn with edges of faces facing away from the viewer (and hence at the back of the box) with solid lines and other edges dashed and on top of the surface. This (and the plotting of the axes) assumes that the axis limits are chosen so that the surface is within the box, and the function will warn if this is not the case.

Value

persp() returns the viewing transformation matrix, say VT, a 4 × 4 matrix suitable for projecting 3D coordinates (x, y, z) into the 2D plane using homogeneous 4D coordinates (x, y, z, t). It can be used to superimpose additional graphical elements on the 3D plot, by lines() or points(), using the function trans3d().

References

See Also

contour and image; trans3d.

Rotatable 3D plots can be produced by package rgl: other ways to produce static perspective plots are available in packages lattice and scatterplot3d.

Examples

```
require(grDevices) # for trans3d
## More examples in demo(persp) !!

# (1) The Obligatory Mathematical surface.
# Rotated sinc function.
x <- seq(-10, 10, length.out = 30)
y <- x
f <- function(x, y) { r <- sqrt(x^2+y^2); 10 * sin(r)/r }
z <- outer(x, y, f)
op <- par(bg = "white")
persp(x, y, z, theta = 30, phi = 30, expand = 0.5, col = "lightblue")
persp(x, y, z, theta = 30, phi = 30, expand = 0.5, col = "lightblue",
      ltheta = 120, shade = 0.75, ticktype = "detailed",
      xlab = "X", ylab = "Y", zlab = "Sinc( r )", cex.axis = 0.8)
) -> res
round(res, 3)

# (2) Add to existing persp plot - using trans3d():
xE <- c(-10,10); xy <- expand.grid(xE, xE)
points(trans3d(xy[,1], xy[,2], 6, pmat = res), col = 2, pch = 16)
lines (trans3d(x, y = 10, z = 6 + sin(x), pmat = res), col = 3)
phi <- seq(0, 2*pi, length.out = 201)
r1 <- 7.725 # radius of 2nd maximum
xr <- r1 * cos(phi)
yr <- r1 * sin(phi)
lines(trans3d(xr,yr, f(xr,yr), res), col = "pink", lwd = 2)
## (no hidden lines)

# (3) Visualizing a simple DEM model
z <- 2 * volcano # Exaggerate the relief
x <- 10 * (1:nrow(z)) # 10 meter spacing (S to N)
y <- 10 * (1:ncol(z)) # 10 meter spacing (E to W)
## Don't draw the grid lines: border = NA
par(bg = "slategray")
persp(x, y, z, theta = 135, phi = 30, col = "green3", scale = FALSE,
      ltheta = -120, shade = 0.75, border = NA, box = FALSE)

# (4) Surface colours corresponding to z-values
par(bg = "white")
x <- seq(-1.95, 1.95, length.out = 30)
y <- seq(-1.95, 1.95, length.out = 35)
z <- outer(x, y, function(a, b) a+b^2)
nrz <- nrow(z)
```

ncz <- ncol(z)
# Create a function interpolating colors in the range of specified colors
jet.colors <- colorRampPalette( c("blue", "green") )
# Generate the desired number of colors from this palette
ncol <- 100
color <- jet.colors(ncol)
# Compute the z-value at the facet centres
zfacet <- z[-1, -1] + z[-1, -ncz] + z[-nrz, -1] + z[-nrz, -ncz]
# Recode facet z-values into color indices
facetcol <- cut(zfacet, ncol)
persp(x, y, z, col = color[facetcol], phi = 30, theta = -30)
par(op)

pie

Pie Charts

Description

Draw a pie chart.

Usage

pie(x, labels = names(x), edges = 200, radius = 0.8,
clockwise = FALSE, init.angle = if(clockwise) 90 else 0,
density = NULL, angle = 45, col = NULL, border = NULL,
lty = NULL, main = NULL, ...)

Arguments

x

a vector of non-negative numerical quantities. The values in x are displayed as the areas of pie slices.

labels

one or more expressions or character strings giving names for the slices. Other objects are coerced by \texttt{as.graphicsAnnot}. For empty or NA (after coercion to character) labels, no label nor pointing line is drawn.

edges

the circular outline of the pie is approximated by a polygon with this many edges.

radius

the pie is drawn centered in a square box whose sides range from $-1$ to 1. If the character strings labeling the slices are long it may be necessary to use a smaller radius.

clockwise

logical indicating if slices are drawn clockwise or counter clockwise (i.e., mathematically positive direction), the latter is default.

init.angle

number specifying the starting angle (in degrees) for the slices. Defaults to 0 (i.e., '3 o'clock') unless clockwise is true where \texttt{init.angle} defaults to 90 (degrees), (i.e., '12 o'clock').

density

the density of shading lines, in lines per inch. The default value of \texttt{NULL} means that no shading lines are drawn. Non-positive values of density also inhibit the drawing of shading lines.

angle

the slope of shading lines, given as an angle in degrees (counter-clockwise).
Pie charts are a very bad way of displaying information. The eye is good at judging linear measures and bad at judging relative areas. A bar chart or dot chart is a preferable way of displaying this type of data.

Cleveland (1985), page 264: “Data that can be shown by pie charts always can be shown by a dot chart. This means that judgements of position along a common scale can be made instead of the less accurate angle judgements.” This statement is based on the empirical investigations of Cleveland and McGill as well as investigations by perceptual psychologists.

### References


### See Also

dotchart.

### Examples

```r
require(grDevices)
pie(rep(1, 24), col = rainbow(24), radius = 0.9)

pie.sales <- c(0.12, 0.3, 0.26, 0.16, 0.04, 0.12)
names(pie.sales) <- c("Blueberry", "Cherry", "Apple", "Boston Cream", "Other", "Vanilla Cream")
pie(pie.sales) # default colours

pie(pie.sales, col = c("purple", "violetred1", "green3", "cornsilk", "cyan", "white"))
pie(pie.sales, density = 10, angle = 15 + 10 * 1:6)
pie(pie.sales, clockwise = TRUE, main = "pie(*, clockwise = TRUE)")
segments(0, 0, 0, 1, col = "red", lwd = 2)

n <- 200
pie(rep(1, n), labels = "", col = rainbow(n), border = NA,
    main = "pie(*, labels="", col=rainbow(n), border=NA,..")

## Another case showing pie() is rather fun than science:
## (original by FinalBackwardsGlance on http://imgur.com/gallery/wWrpU4X)
pie(c(Sky = 78, "Sunny side of pyramid" = 17, "Shady side of pyramid" = 5),
    init.angle = 315, col = c("deepskyblue", "yellow", "yellow3"), border = FALSE)
```
plot.data.frame

Plot Method for Data Frames

Description

plot.data.frame, a method for the plot generic. It is designed for a quick look at numeric data frames.

Usage

## S3 method for class 'data.frame'
plot(x, ...)

Arguments

x

object of class data.frame.

...

further arguments to stripchart, plot.default or pairs.

Details

This is intended for data frames with numeric columns. For more than two columns it first calls data.matrix to convert the data frame to a numeric matrix and then calls pairs to produce a scatterplot matrix. This can fail and may well be inappropriate: for example numerical conversion of dates will lose their special meaning and a warning will be given.

For a two-column data frame it plots the second column against the first by the most appropriate method for the first column.

For a single numeric column it uses stripchart, and for other single-column data frames tries to find a plot method for the single column.

See Also

data.frame

Examples

plot(OrchardSprays[1], method = "jitter")
plot(OrchardSprays[c(4,1)])
plot(OrchardSprays)

plot(iris)
plot(iris[5:4])
plot(women)
The Default Scatterplot Function

Description

Draw a scatter plot with decorations such as axes and titles in the active graphics window.

Usage

```r
## Default S3 method:
plot(x, y = NULL, type = "p", xlim = NULL, ylim = NULL,
    log = "", main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
    ann = par("ann"), axes = TRUE, frame.plot = axes,
    panel.first = NULL, panel.last = NULL, asp = NA,
    xgap.axis = NA, ygap.axis = NA,
    ...)```

Arguments

- `x, y`: the x and y arguments provide the x and y coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function `xy.coords` for details. If supplied separately, they must be of the same length.

- `type`: a 1-character string giving the type of plot desired. The following values are possible, for details, see `plot`: "p" for points, "l" for lines, "b" for both points and lines, "c" for empty points joined by lines, "o" for overplotted points and lines, "s" and "S" for stair steps and "h" for histogram-like vertical lines. Finally, "n" does not produce any points or lines.

- `xlim`: the x limits (x1, x2) of the plot. Note that x1 > x2 is allowed and leads to a 'reversed axis'. The default value, NULL, indicates that the range of the finite values to be plotted should be used.

- `ylim`: the y limits of the plot.

- `log`: a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic.

- `main`: a main title for the plot, see also `title`.

- `sub`: a subtitle for the plot.

- `xlab`: a label for the x axis, defaults to a description of x.

- `ylab`: a label for the y axis, defaults to a description of y.

- `ann`: a logical value indicating whether the default annotation (title and x and y axis labels) should appear on the plot.

- `axes`: a logical value indicating whether both axes should be drawn on the plot. Use graphical parameter "xaxt" or "yaxt" to suppress just one of the axes.

- `frame.plot`: a logical indicating whether a box should be drawn around the plot.

- `panel.first`: an 'expression' to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids or scatterplot smooths. Note that this works by lazy evaluation: passing this argument from other `plot` methods may well not work since it may be evaluated too early.
plot.default

panel.last  an expression to be evaluated after plotting has taken place but before the axes, title and box are added. See the comments about panel.first.

asp  the y/x aspect ratio, see plot.window.

xgap.axis, ygap.axis  the x/y axis gap factors, passed as gap.axis to the two axis() calls (when axes is true, as per default).

...  other graphical parameters (see par and section 'Details' below).

Details

Commonly used graphical parameters are:

col  The colors for lines and points. Multiple colors can be specified so that each point can be given its own color. If there are fewer colors than points they are recycled in the standard fashion. Lines will all be plotted in the first colour specified.

dg  a vector of background colors for open plot symbols, see points. Note: this is not the same setting as par("bg").

pch  a vector of plotting characters or symbols: see points.

cex  a numerical vector giving the amount by which plotting characters and symbols should be scaled relative to the default. This works as a multiple of par("cex"). NULL and NA are equivalent to 1.0. Note that this does not affect annotation: see below.

lty  a vector of line types, see par.

cex.main, col.lab, font.sub, etc  settings for main- and sub-title and axis annotation, see title and par.

lwd  a vector of line widths, see par.

Note

The presence of panel.first and panel.last is a historical anomaly: default plots do not have 'panels', unlike e.g. pairs plots. For more control, use lower-level plotting functions: plot.default calls in turn some of plot.new, plot.window, plot.xy, axis, box and title, and plots can be built up by calling these individually, or by calling plot(type = "n") and adding further elements.

The plot generic was moved from the graphics package to the base package in R 4.0.0. It is currently re-exported from the graphics namespace to allow packages importing it from there to continue working, but this may change in future versions of R.

References


See Also

plot, plot.window, xy.coords. For thousands of points, consider using smoothScatter instead.
Examples

```r
Speed <- cars$speed
distance <- cars$dist
plot(Speed, Distance, panel.first = grid(8, 8),
pch = 0, cex = 1.2, col = "blue")
plot(Speed, Distance,
panel.first = lines(stats::lowess(Speed, Distance), lty = "dashed"),
pch = 0, cex = 1.2, col = "blue")
```

### Show the different plot types

```r
x <- 0:12
y <- sin(pi/5 * x)
op <- par(mfrow = c(3,3), mar = .1+ c(2,2,3,1))
for (tp in c("p","l","b", "c","o","h", "s","S","n")) {
  plot(y ~ x, type = tp, main = paste0("plot(*, type = ", tp, ")")
  if(tp == "S") {
    lines(x, y, type = "s", col = "red", lty = 2)
    mtext("lines(*, type = "s", ...)", col = "red", cex = 0.8)
  }
}
par(op)
```

###--- Log-Log Plot with custom axes

```r
lx <- seq(1, 5, length.out = 41)
yl <- expression(e^{-frac(1,2) * {log[10](x)}^2})
y <- exp(-.5*lx^2)
op <- par(mfrow = c(2,1), mar = par("mar")-c(1,0,2,0), mgp = c(2, .7, 0))
plot(10^lx, y, log = "xy", type = "l", col = "purple",
     main = "Log-Log plot", ylab = yl, xlab = "x")
plot(10^lx, y, log = "xy", type = "o", pch = ".", col = "forestgreen",
     main = "Log-Log plot with custom axes", ylab = yl, xlab = "x",
     axes = FALSE, frame.plot = TRUE)
my.at <- 10^((1:5)
axis(1, at = my.at, labels = formatC(my.at, format = "fg"))
e.y <- -5:-1 ; at.y <- 10^e.y
axis(2, at = at.y, col.axis = "red", las = 1,
     labels = as.expression(lapply(e.y, function(E) bquote(10^.(E)))))
par(op)
```

---

**plot.design**  
*Plot Univariate Effects of a Design or Model*

**Description**

Plot univariate effects of one or more **factors**, typically for a designed experiment as analyzed by `aov()`.

**Usage**

```r
plot.design(x, y = NULL, fun = mean, data = NULL, ...,
            ylim = NULL, xlab = "Factors", ylab = NULL,
            main = NULL, ask = NULL, xaxt = par("xaxt"),
            axes = TRUE, xtick = FALSE)
```
Arguments

- **x**: either a data frame containing the design factors and optionally the response, or a formula or terms object.
- **y**: the response, if not given in x.
- **fun**: a function (or name of one) to be applied to each subset. It must return one number for a numeric (vector) input.
- **data**: data frame containing the variables referenced by x when that is formula-like.
- **...**: graphical parameters such as col, see par.
- **ylim**: range of y values, as in plot.default.
- **xlab**: x axis label, see title.
- **ylab**: y axis label with a ‘smart’ default.
- **main**: main title, see title.
- **ask**: logical indicating if the user should be asked before a new page is started – in the case of multiple y’s.
- **xaxt**: character giving the type of x axis.
- **axes**: logical indicating if axes should be drawn.
- **xtick**: logical indicating if ticks (one per factor) should be drawn on the x axis.

Details

The supplied function will be called once for each level of each factor in the design and the plot will show these summary values. The levels of a particular factor are shown along a vertical line, and the overall value of fun() for the response is drawn as a horizontal line.

Note

A big effort was taken to make this closely compatible to the S version. However, col (and fg) specifications have different effects.

In S this was a method of the plot generic function for design objects.

Author(s)

Roberto Frisullo and Martin Maechler

References


See Also

interaction.plot for a ‘standard graphic’ of designed experiments.
Examples

require(stats)
plot.design(warpbreaks)  # automatic for data frame with one numeric var.

Form <- breaks ~ wool + tension
summary(fm1 <- aov(Form, data = warpbreaks))
plot.design(    Form, data = warpbreaks, col = 2)  # same as above

## More than one y :
utils::str(esoph)
plot.design(esoph) ## two plots; if interactive you are "ask"ed

## or rather, compare mean and median:
op <- par(mfcol = 1:2)
plot.design(ncases/ncontrols ~ ., data = esoph, ylim = c(0, 0.8))
plot.design(ncases/ncontrols ~ ., data = esoph, ylim = c(0, 0.8),
             fun = median)
par(op)

plot.factor  

Plotting Factor Variables

Description

This functions implements a scatterplot method for factor arguments of the generic plot function. If y is missing barplot is produced. For numeric y a boxplot is used, and for a factor y a spineplot is shown. For any other type of y the next plot method is called, normally plot.default.

Usage

## S3 method for class 'factor'
plot(x, y, legend.text = NULL, ...)

Arguments

x, y numeric or factor. y may be missing.
legend.text character vector for annotation of y axis in the case of a factor y: defaults to levels(y). This sets the yaxlabels argument of spineplot.
...

Further arguments to barplot, boxplot, spineplot or plot as appropriate. All of these accept graphical parameters (see par) and annotation arguments passed to title and axes = FALSE. None accept type.

See Also

plot.default, plot.formula, barplot, boxplot, spineplot.
Examples

```r
require(grDevices)

plot(weight ~ group, data = PlantGrowth) # numeric vector ~ factor
plot(cut(weight, 2) ~ group, data = PlantGrowth) # factor ~ factor
## passing "..." to spineplot() eventually:
plot(cut(weight, 3) ~ group, data = PlantGrowth,
     col = hcl(c(0, 120, 240), 50, 70))

plot(PlantGrowth$group, axes = FALSE, main = "no axes") # extremely silly
```

---

**plot.formula**  
*Formula Notation for Scatterplots*

**Description**  
Specify a scatterplot or add points, lines, or text via a formula.

**Usage**

```r
## S3 method for class 'formula'
plot(formula, data = parent.frame(), ..., subset,
     ylab = varnames[response], ask = dev.interactive())

## S3 method for class 'formula'
points(formula, data = parent.frame(), ..., subset)

## S3 method for class 'formula'
lines(formula, data = parent.frame(), ..., subset)

## S3 method for class 'formula'
text(formula, data = parent.frame(), ..., subset)
```

**Arguments**

- **formula**  
a formula, such as y ~ x.
- **data**  
a data.frame (or list) from which the variables in formula should be taken. A matrix is converted to a data frame.
- **...**  
Arguments to be passed to or from other methods. `horizontal = TRUE` is also accepted.
- **subset**  
an optional vector specifying a subset of observations to be used in the fitting process.
- **ylab**  
the y label of the plot(s).
- **ask**  
logical, see `par`.
plot.histogram

Details

For the lines, points and text methods the formula should be of the form \( y \sim x \) or \( y \sim 1 \) with a left-hand side and a single term on the right-hand side. The plot method accepts other forms discussed later in this section.

Both the terms in the formula and the ... arguments are evaluated in data enclosed in parent.frame() if data is a list or a data frame. The terms of the formula and those arguments in ... that are of the same length as data are subjected to the subsetting specified in subset. A plot against the running index can be specified as plot(\( y \sim 1 \)).

If the formula in the plot method contains more than one term on the right-hand side, a series of plots is produced of the response against each non-response term.

For the plot method the formula can be of the form \( y \sim z + y + z \): the variables specified on the right-hand side are collected into a data frame, subsetted if specified, and displayed by plot.data.frame.

Missing values are not considered in these methods, and in particular cases with missing values are not removed.

If \( y \) is an object (i.e., has a class attribute) then plot.formula looks for a plot method for that class first. Otherwise, the class of \( x \) will determine the type of the plot. For factors this will be a parallel boxplot, and argument horizontal = TRUE can be specified (see boxplot).

Note that some arguments will need to be protected from premature evaluation by enclosing them in quote: currently this is done automatically for main, sub and xlab. For example, it is needed for the panel.first and panel.last arguments passed to plot.default.

Value

These functions are invoked for their side effect of drawing on the active graphics device.

See Also

plot.default, points, lines, plot.factor.

Examples

op <- par(mfrow = c(2,1))
plot(Ozone ~ Wind, data = airquality, pch = as.character(Month))
plot(Ozone ~ Wind, data = airquality, pch = as.character(Month),
     subset = Month != 7)
par(op)

## text.formula() can be very natural:
w <- within(warpbreaks, {
    time <- seq_along(breaks); W.T <- wool:tension })
plot(breaks ~ time, data = wb, type = "b")
text(breaks ~ time, data = wb, labels = W.T, col = 1+as.integer(wool))

plot.histogram

Plot Histograms

Description

Plotting methods for objects of class "histogram", typically produced by hist.
Usage

### S3 method for class 'histogram'

```r
plot(x, freq = equidist, density = NULL, angle = 45,
    col = "lightgray", border = NULL, lty = NULL,
    main = paste("Histogram of", paste(x$xname, collapse = "\n")),
    sub = NULL, xlab = x$xname, ylab,
    xlim = range(x$breaks), ylim = NULL,
    axes = TRUE, labels = FALSE, add = FALSE,
    ann = TRUE, ...)```

### S3 method for class 'histogram'

```r
lines(x, ...)```

Arguments

- **x**
  - A histogram object, or a `list` with components `density`, `mid`, etc, see `hist` for information about the components of `x`.

- **freq**
  - Logical; if `TRUE`, the histogram graphic is to present a representation of frequencies, i.e., `x$counts`; if `FALSE`, relative frequencies (probabilities), i.e., `x$density`, are plotted. The default is true for equidistant breaks and false otherwise.

- **col**
  - A colour to be used to fill the bars. The default has been changed from `NULL` (unfilled bars) only as from R 4.2.0.

- **border**
  - The color of the border around the bars.

- **angle, density**
  - Select shading of bars by lines: see `rect`.

- **lty**
  - The line type used for the bars, see also `lines`.

- **main, sub, xlab, ylab**
  - These arguments to `title` have useful defaults here.

- **xlim, ylim**
  - The range of x and y values with sensible defaults.

- **axes**
  - Logical, indicating if axes should be drawn.

- **labels**
  - Logical or character. Additionally draw labels on top of bars, if not `FALSE`; if `TRUE`, draw the counts or rounded densities; if `labels` is a character, draw itself.

- **add**
  - Logical. If `TRUE`, only the bars are added to the current plot. This is what `lines.histogram(*)` does.

- **ann**
  - Logical. Should annotations (titles and axis titles) be plotted?

- **...**
  - Further graphical parameters to `title` and `axis`.

Details

`lines.histogram(*)` is the same as `plot.histogram(*, add = TRUE)`.

See Also

`hist`, `stem`, `density`.
Examples

```r
(wwt <- hist(women$weight, nclass = 7, plot = FALSE))
plot(wwt, labels = TRUE) # default main & xlab using wwt$xname
plot(wwt, border = "dark blue", col = "light blue",
     main = "Histogram of 15 women’s weights", xlab = "weight [pounds]")
```

```r
## Fake "lines" example, using non-default labels:
w2 <- wwt; w2$counts <- w2$counts - 1
lines(w2, col = "Midnight Blue", labels = ifelse(w2$counts, "> 1", "1"))
```

---

**plot.raster**

*Plotting Raster Images*

**Description**

This function implements a `plot` method for raster images.

**Usage**

```r
## S3 method for class 'raster'
plot(x, y,
     xlim = c(0, ncol(x)), ylim = c(0, nrow(x)),
     xaxs = "i", yaxs = "i",
     asp = 1, add = FALSE, ...)
```

**Arguments**

- `x, y` : raster. `y` will be ignored.
- `xlim, ylim` : Limits on the plot region (default from dimensions of the raster).
- `xaxs, yaxs` : Axis interval calculation style (default means that raster fills plot region).
- `asp` : Aspect ratio (default retains aspect ratio of the raster).
- `add` : Logical indicating whether to simply add raster to an existing plot.
- `...` : Further arguments to the `rasterImage` function.

**See Also**

`plot.default, rasterImage`.

**Examples**

```r
require(grDevices)
r <- as.raster(c(0.5, 1, 0.5))
plot(r)
# additional arguments to rasterImage()
plot(r, interpolate=FALSE)
# distort
plot(r, asp=NA)
# fill page
op <- par(mar=rep(0, 4))
plot(r, asp=NA)
par(op)
```
# normal annotations work
plot(r, asp=NA)
box()
title(main="This is my raster")
# add to existing plot
plot()
plot(r, add=TRUE)

plot.table  
Plot Methods for table Objects

Description
This is a method of the generic plot function for (contingency) table objects. Whereas for two- and more dimensional tables, a mosaicplot is drawn, one-dimensional ones are plotted as bars.

Usage
## S3 method for class 'table'
plot(x, type = "h", ylim = c(0, max(x)), lwd = 2,
xlab = NULL, ylab = NULL, frame.plot = is.num, ...)
## S3 method for class 'table'
points(x, y = NULL, type = "h", lwd = 2, ...)
## S3 method for class 'table'
lines(x, y = NULL, type = "h", lwd = 2, ...)

Arguments
- x a table (like) object.
- y Must be NULL: there to protect against incorrect calls.
- type plotting type.
- ylim range of y-axis.
- lwd line width for bars when type = "h" is used in the 1D case.
- xlab, ylab x- and y-axis labels.
- frame.plot logical indicating if a frame (box) should be drawn in the 1D case. Defaults to true when x has dimnames coerce-able to numbers.
- ... further graphical arguments, see plot.default. axes = FALSE is accepted.

See Also
plot.factor, the plot method for factors.

Examples
## 1-d tables
(Poiss.tab <- table(N = stats::rpois(200, lambda = 5)))
plot(Poiss.tab, main = "plot(table(rpois(200, lambda = 5))")
plot(table(state.division))
## 4-D :
plot(Titanic, main ="plot(Titanic, main= *)")
plot.window

Set up World Coordinates for Graphics Window

Description

This function sets up the world coordinate system for a graphics window. It is called by higher level functions such as `plot.default` *(after plot.new)*.

Usage

`plot.window(xlim, ylim, log = "", asp = NA, ...)`

Arguments

- `xlim, ylim`: numeric vectors of length 2, giving the x and y coordinates ranges.
- `log`: character; indicating which axes should be in log scale.
- `asp`: numeric, giving the aspect ratio y/x, see ‘Details’.
- `...`: further graphical parameters as in `par`. The relevant ones are `xaxs`, `yaxs` and `lab`.

Details

- `asp`: If `asp` is a finite positive value then the window is set up so that one data unit in the y direction is equal in length to `asp × one data unit in the x direction`.
  - Note that in this case, `par("usr")` is no longer determined by, e.g., `par("xaxs")`, but rather by `asp` and the device’s aspect ratio. (See what happens if you interactively resize the plot device after running the example below!)
  - The special case `asp == 1` produces plots where distances between points are represented accurately on screen. Values with `asp > 1` can be used to produce more accurate maps when using latitude and longitude.

Note that the coordinate ranges will be extended by 4% if the appropriate graphical parameter `xaxs` or `yaxs` has value "r" (which is the default).

To reverse an axis, use `xlim` or `ylim` of the form `c(hi, lo)`.

The function attempts to produce a plausible set of scales if one or both of `xlim` and `ylim` is of length one or the two values given are identical, but it is better to avoid that case.

Usually, one should rather use the higher-level functions such as `plot`, `hist`, `image`, ..., instead and refer to their help pages for explanation of the arguments.

A side-effect of the call is to set up the `usr`, `xaxp` and `yaxp` graphical parameters. (It is for the latter two that `lab` is used.)

See Also

- `xy.coords`, `plot.xy`, `plot.default`
- `par` for the graphical parameters mentioned.
Examples

```r
#--- An example for the use of 'asp':
require(stats)  # normally loaded
loc <- cmdscale(eurodist)
rx <- range(x <- loc[,1])
ry <- range(y <- -loc[,2])
plot(x, y, type = "n", asp = 1, xlab = "", ylab = "")
abline(h = pretty(rx, 10), v = pretty(ry, 10), col = "lightgray")
text(x, y, labels(eurodist), cex = 0.8)
```

---

**plot.xy**

### Basic Internal Plot Function

#### Description

This is the internal function that does the basic plotting of points and lines. Usually, one should rather use the higher level functions instead and refer to their help pages for explanation of the arguments.

#### Usage

```r
plot.xy(xy, type, pch = par("pch"), lty = par("lty"),
        col = par("col"), bg = NA,
        cex = 1, lwd = par("lwd"), ...)  
```

#### Arguments

- **xy**
  A four-element list as results from `xy.coords`.
- **type**
  A 1 character code: see `plot.default`. NULL is accepted as a synonym for "p".
- **pch**
  Character or integer code for kind of points, see `points.default`.
- **lty**
  Line type code, see `lines`.
- **col**
  Color code or name, see `colors, palette`. Here NULL means colour 0.
- **bg**
  Background (fill) color for the open plot symbols 21:25: see `points.default`.
- **cex**
  Character expansion.
- **lwd**
  Line width, also used for (non-filled) plot symbols, see `lines` and `points`.
- **...**
  Further graphical parameters such as xpd, lend, ljoin and lmitre.

#### Details

The arguments `pch`, `col`, `bg`, `cex`, `lwd` may be vectors and may be recycled, depending on `type`: see `points` and `lines` for specifics. In particular note that `lwd` is treated as a vector for points and as a single (first) value for lines.

`cex` is a numeric factor in addition to `par("cex")` which affects symbols and characters as drawn by type "p", "o", "b" and "c".

#### See Also

`plot, plot.default, points, lines.`
Points

Examples

```r
points.default # to see how it calls "plot.xy(xy.coords(x, y), ...)"
```

Description

points is a generic function to draw a sequence of points at the specified coordinates. The specified character(s) are plotted, centered at the coordinates.

Usage

```r
points(x, ...)
```

## Default S3 method:
```r
points(x, y = NULL, type = "p", ...)
```

Arguments

- **x, y**: coordinate vectors of points to plot.
- **type**: character indicating the type of plotting; actually any of the types as in `plot.default`.
- **...**: Further graphical parameters may also be supplied as arguments. See ‘Details’.

Details

The coordinates can be passed in a plotting structure (a list with `x` and `y` components), a two-column matrix, a time series, .... See `xy.coords`. If supplied separately, they must be of the same length.

Graphical parameters commonly used are

- **pch**: plotting 'character', i.e., symbol to use. This can either be a single character or an integer code for one of a set of graphics symbols. The full set of S symbols is available with `pch = 0:18`, see the examples below. (NB: R uses circles instead of the octagons used in S.)
  
  Value `pch = "."` (equivalently `pch = 46`) is handled specially. It is a rectangle of side 0.01 inch (scaled by `cex`). In addition, if `cex = 1` (the default), each side is at least one pixel (1/72 inch on the pdf, postscript and xfig devices).

  For other text symbols, `cex = 1` corresponds to the default fontsize of the device, often specified by an argument `pointsize`. For `pch` in `0:25` the default size is about 75% of the character height (see `par("cin")`).

- **col**: color code or name, see `par`.

- **bg**: background (fill) color for the open plot symbols given by `pch = 21:25`.

- **cex**: character (or symbol) expansion: a numerical vector. This works as a multiple of `par("cex")`.

- **lwd**: line width for drawing symbols see `par`.

Others less commonly used are `lty` and `lwd` for types such as "b" and "l".

The graphical parameters `pch`, `col`, `bg`, `cex` and `lwd` can be vectors (which will be recycled as needed) giving a value for each point plotted. If lines are to be plotted (e.g., for `type = "b"`) the first element of `lwd` is used.

Points whose `x`, `y`, `pch`, `col` or `cex` value is `NA` are omitted from the plot.
'pch' values

Values of `pch` are stored internally as integers. The interpretation is

- **NA_integer_**: no symbol.
- `0:18`: S-compatible vector symbols.
- `19:25`: further R vector symbols.
- `26:31`: unused (and ignored).
- `32:127`: ASCII characters.
- `128:255`: native characters only in a single-byte locale and for the symbol font. (128:159 are only used on Windows.)
- `-32...`: Unicode code point (where supported).

Note that unlike S (which uses octagons), symbols 1, 10, 13 and 16 use circles. The filled shapes 15:18 do not include a border.

```
 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
 □ ◇ △ □ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇ ◇
Note

A single-byte encoding may include the characters in \( \text{pch} = 128:255 \), and if it does, a font may not include all (or even any) of them.

Not all negative numbers are valid as Unicode code points, and no check is done. A display device is likely to use a rectangle for (or omit) Unicode code points which are invalid or for which it does not have a glyph in the font used.

What happens for very small or zero values of \( \text{cex} \) is device-dependent: symbols or characters may become invisible or they may be plotted at a fixed minimum size. Circles of zero radius will not be plotted.

References


See Also

points.formula for the formula method; plot, lines, and the underlying workhorse function plot.xy.

Examples

```r
require(stats) # for rnorm
plot(-4:4, -4:4, type = "n") # setting up coord. system
points(rnorm(200), rnorm(200), col = "red")
points(rnorm(100)/2, rnorm(100)/2, col = "blue", cex = 1.5)

op <- par(bg = "light blue")
x <- seq(0, 2*pi, length.out = 51)
## something "between type='b' and type='o'":
plot(x, sin(x), type = "o", pch = 21, bg = par("bg"), col = "blue", cex = .6,
    main = "plot(..., type='o', pch=21, bg=par("bg"))")
par(op)

## Not run:
## The figure was produced by calls like
png("pch.png", height = 0.7, width = 7, res = 100, units = "in")
par(mar = rep(0,4))
plot(c(-1, 26), 0:1, type = "n", axes = FALSE)
text(0:25, 0.6, 0:25, cex = 0.5)
points(0:25, rep(0.3, 26), pch = 0:25, bg = "grey")

## End(Not run)

##-------- Showing all the extra & some char graphics symbols --------

pchShow <-
function(extras = c("*", ".", "o", "O", "0", "+", "-", "|", "%", ","),
    cex = 3, ## good for both .Device="postscript" and "x11"
    col = "red3", bg = "gold", coltext = "brown", cextext = 1.2,
    main = paste("plot symbols: points (... pch = *, cex =",
    cex,"))
{
    nex <- length(extras)
    np <- 26 + nex
    ipch <- 0:(np-1)
```
polygon

Polygon Drawing

Description

polygon draws the polygons whose vertices are given in x and y.

Usage

polygon(x, y = NULL, density = NULL, angle = 45,
border = NULL, col = NA, lty = par("lty"),
..., fillOddEven = FALSE)

Arguments

\[x, y\] vectors containing the coordinates of the vertices of the polygon.

\[\text{density}\] the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn. A zero value of density means no shading nor filling whereas negative values and NA suppress shading (and so allow color filling).

\[\text{angle}\] the slope of shading lines, given as an angle in degrees (counter-clockwise).

\[\text{col}\] the color for filling the polygon. The default, NA, is to leave polygons unfilled, unless density is specified. (For back-compatibility, NULL is equivalent to NA.) If density is specified with a positive value this gives the color of the shading lines.

\[\text{border}\] the color to draw the border. The default, NULL, means to use \texttt{par("fg")}. Use \texttt{border = NA} to omit borders.

\[\text{lty}\] the line type to be used, as in \texttt{par}.

... graphical parameters such as \texttt{xpd}, \texttt{lend}, \texttt{ljoin} and \texttt{lmitre} can be given as arguments.

\[\text{fillOddEven}\] logical controlling the polygon shading mode: see below for details. Default FALSE.

Details

The coordinates can be passed in a plotting structure (a list with \(x\) and \(y\) components), a two-column matrix, .... See \texttt{xy.coords}.

It is assumed that the polygon is to be closed by joining the last point to the first point.

The coordinates can contain missing values. The behaviour is similar to that of \texttt{lines}, except that instead of breaking a line into several lines, NA values break the polygon into several complete polygons (including closing the last point to the first point). See the examples below.

When multiple polygons are produced, the values of density, angle, col, border, and lty are recycled in the usual manner.

Shading of polygons is only implemented for linear plots: if either axis is on log scale then shading is omitted, with a warning.

Bugs

Self-intersecting polygons may be filled using either the “odd-even” or “non-zero” rule. These fill a region if the polygon border encircles it an odd or non-zero number of times, respectively. Shading lines are handled internally by \texttt{R} according to the \texttt{fillOddEven} argument, but device-based solid fills depend on the graphics device. The \texttt{windows}, \texttt{pdf} and \texttt{postscript} devices have their own \texttt{fillOddEven} argument to control this.

Author(s)

The code implementing polygon shading was donated by Kevin Buhr <buhr@stat.wisc.edu>.
References


See Also

segments for even more flexibility, lines, rect, box, abline.
par for how to specify colors.

Examples

```r
x <- c(1:9, 8:1)
y <- c(1, 2*(5:3), 2, -1, 17, 9, 8, 2:9)
op <- par(mfcol = c(3, 1))
for(xpd in c(FALSE, TRUE, NA)) {
  plot(1:10, main = paste("xpd =", xpd))
  box("figure", col = "pink", lwd = 3)
  polygon(x, y, xpd = xpd, col = "orange", lty = 2, lwd = 2, border = "red")
}
par(op)

n <- 100
xx <- c(0:n, n:0)
yy <- c(c(0, cumsum(stats::rnorm(n))), rev(c(0, cumsum(stats::rnorm(n)))))
plot (xx, yy, type = "n", xlab = "Time", ylab = "Distance")
polygon(xx, yy, col = "gray", border = "red")
title("Distance Between Brownian Motions")

# Multiple polygons from NA values
# and recycling of col, border, and lty
op <- par(mfrow = c(2, 1))
plot(c(1, 9), 1:2, type = "n")
polygon(1:9, c(2,1,2,1,1,2,1,2,1),
  col = c("red", "blue"),
  border = c("green", "yellow"),
  lwd = 3, lty = c("dashed", "solid"))
plot(c(1, 9), 1:2, type = "n")
polygon(1:9, c(2,1,2,1,NA,2,1,2,1),
  col = c("red", "blue"),
  border = c("green", "yellow"),
  lwd = 3, lty = c("dashed", "solid"))
par(op)

# Line-shaded polygons
plot(c(1, 9), 1:2, type = "n")
polygon(1:9, c(2,1,2,1,NA,2,1,2,1),
  density = c(10, 20), angle = c(-45, 45))
```

polyPath

Path Drawing
Description

path draws a path whose vertices are given in x and y.

Usage

polypath(x, y = NULL, border = NULL, col = NA, lty = par("lty"), rule = "winding", ...)

Arguments

x, y vectors containing the coordinates of the vertices of the path.

col the color for filling the path. The default, NA, is to leave paths unfilled.

border the color to draw the border. The default, NULL, means to use par("fg"). Use border = NA to omit borders.

For compatibility with S, border can also be logical, in which case FALSE is equivalent to NA (borders omitted) and TRUE is equivalent to NULL (use the foreground colour),

lty the line type to be used, as in par.

rule character value specifying the path fill mode: either "winding" or "evenodd".

... graphical parameters such as xpd, lend, ljoin and lmitre can be given as arguments.

Details

The coordinates can be passed in a plotting structure (a list with x and y components), a two-column matrix, .... See xy.coords.

It is assumed that the path is to be closed by joining the last point to the first point.

The coordinates can contain missing values. The behaviour is similar to that of polygon, except that instead of breaking a polygon into several polygons, NA values break the path into several sub-paths (including closing the last point to the first point in each sub-path). See the examples below.

The distinction between a path and a polygon is that the former can contain holes, as interpreted by the fill rule; these fill a region if the path border encircles it an odd or non-zero number of times, respectively.

Hatched shading (as implemented for polygon()) is not (currently) supported.

Not all graphics devices support this function: for example xfig and pictex do not.

References


See Also

segments for even more flexibility, lines, rect, box, polygon.
par for how to specify colors.
Examples

```
plotPath <- function(x, y, col = "grey", rule = "winding") {
  plot.new()
  plot.window(range(x, na.rm = TRUE), range(y, na.rm = TRUE))
  polypath(x, y, col = col, rule = rule)
  if (!is.na(col))
    mtext(paste("Rule: ", rule), side = 1, line = 0)
}

plotRules <- function(x, y, title) {
  plotPath(x, y)
  plotPath(x, y, rule = "evenodd")
  mtext(title, side = 3, line = 0)
  plotPath(x, y, col = NA)
}

op <- par(mfrow = c(5, 3), mar = c(2, 1, 1, 1))

plotRules(c(.1, .1, .9, .9, NA, .2, .2, .8, .8),
  c(.1, .9, .9, .1, NA, .2, .8, .8, .2),
  "Nested rectangles, both clockwise")
plotRules(c(.1, .1, .9, .9, NA, .2, .8, .8, .2),
  c(.1, .9, .9, .1, NA, .2, .2, .8, .8),
  "Nested rectangles, outer clockwise, inner anti-clockwise")
plotRules(c(.1, .1, .4, .4, NA, .6, .9, .9, .6),
  c(.1, .4, .4, .1, NA, .6, .6, .9, .9),
  "Disjoint rectangles")
plotRules(c(.1, .1, .6, .6, NA, .4, .4, .9, .9),
  c(.1, .6, .6, .1, NA, .4, .9, .9, .4),
  "Overlapping rectangles, both clockwise")
plotRules(c(.1, .1, .6, .6, NA, .4, .9, .9, .4),
  c(.1, .6, .6, .1, NA, .4, .4, .9, .9),
  "Overlapping rectangles, one clockwise, other anti-clockwise")

par(op)
```

---

**rasterImage**

*Draw One or More Raster Images*

**Description**

*rasterImage* draws a raster image at the given locations and sizes.

**Usage**

```
rasterImage(image,
  xleft, ybottom, xright, ytop,
  angle = 0, interpolate = TRUE, ...)
```

**Arguments**

- **image**
  A raster object, or an object that can be coerced to one by *as.raster*.

- **xleft**
  A vector (or scalar) of left x positions.
rect

**Description**

`rect` draws a rectangle (or sequence of rectangles) with the given coordinates, fill and border colors.

**Details**

The positions supplied, i.e., `xleft`, ..., are relative to the current plotting region. If the x-axis goes from 100 to 200 then `xleft` should be larger than 100 and `xright` should be less than 200. The position vectors will be recycled to the length of the longest.

Plotting raster images is not supported on all devices and may have limitations where supported, for example (e.g., for `postscript` and `X11(type = "Xlib")` is restricted to opaque colors). Problems with the rendering of raster images have been reported by users of `windows()` devices under Remote Desktop, at least under its default settings.

You should not expect a raster image to be re-sized when an on-screen device is re-sized: whether it is is device-dependent.

**See Also**

`rect`, `polygon`, and `segments` and others for flexible ways to draw shapes.

`dev.capabilities` to see if it is supported.

**Examples**

```r
require(grDevices)
## set up the plot region:
op <- par(bg = "thistle")
plot(c(100, 250), c(300, 450), type = "n", xlab = "", ylab = "")
image <- as.raster(matrix(0:1, ncol = 5, nrow = 3))
rasterImage(image, 100, 300, 150, 350, interpolate = FALSE)
rasterImage(image, 100, 400, 150, 450)
rasterImage(image, 200, 300, 200 + xinch(.5), 300 + yinch(.3),
            interpolate = FALSE)
rasterImage(image, 200, 400, 250, 450, angle = 15, interpolate = FALSE)
par(op)
```

---

**rect**

**Draw One or More Rectangles**

**Description**

`rect` draws a rectangle (or sequence of rectangles) with the given coordinates, fill and border colors.
Usage

rect(xleft, ybottom, xright, ytop, density = NULL, angle = 45,
    col = NA, border = NULL, lty = par("lty"), lwd = par("lwd"),
    ...)  

Arguments

xleft  a vector (or scalar) of left x positions.
ybottom  a vector (or scalar) of bottom y positions.
xright  a vector (or scalar) of right x positions.
ytop  a vector (or scalar) of top y positions.
density  the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn. A zero value of density means no shading lines whereas negative values (and NA) suppress shading (and so allow color filling).
angle  angle (in degrees) of the shading lines.
col  color(s) to fill or shade the rectangle(s) with. The default NA (or also NULL) means do not fill, i.e., draw transparent rectangles, unless density is specified.
border  color for rectangle border(s). The default means par("fg"). Use border = NA to omit borders. If there are shading lines, border = TRUE means use the same colour for the border as for the shading lines.
lty  line type for borders and shading; defaults to "solid".
lwd  line width for borders and shading. Note that the use of lwd = 0 (as in the examples) is device-dependent.
...  graphical parameters such as xpd, lend, ljoin and lmitre can be given as arguments.

Details

The positions supplied, i.e., xleft, ..., are relative to the current plotting region. If the x-axis goes from 100 to 200 then xleft must be larger than 100 and xright must be less than 200. The position vectors will be recycled to the length of the longest.

It is a graphics primitive used in hist, barplot, legend, etc.

See Also

box for the standard box around the plot; polygon and segments for flexible line drawing.
par for how to specify colors.

Examples

require(grDevices)
## set up the plot region:
op <- par(bg = "thistle")
plot(c(100, 250), c(300, 450), type = "n", xlab = "", ylab = "",
    main = "2 x 11 rectangles; 'rect(100+i,300+i, 150+i,380+i)'")
i <- 4*(0:10)
## draw rectangles with bottom left (100, 300)+i
## and top right (150, 380)+i
rect(100+i, 300+i, 150+i, 380+i, col = rainbow(11, start = 0.7, end = 0.1))
rect(240-i, 320+i, 250-i, 410+i, col = heat.colors(11), lwd = i/5)
## Background alternating ( transparent / "bg" ):

```r
j <- 10*(0:5)
rect(125+j, 360+j, 141+j, 405+j/2, col = c(NA,0),
     border = "gold", lwd = 2)
rect(125+j, 296+j/2, 141+j, 331+j/5, col = c(NA,"midnightblue"))
mtext("+ 2 x 6 rect(*, col = c(NA,0)) and col = c(NA,"m..blue")")
```

## an example showing colouring and shading

```r
plot(c(100, 200), c(300, 450), type= "n", xlab = "", ylab = ")
rect(100, 300, 125, 350) # transparent
rect(100, 400, 125, 450, col = "green", border = "blue") # coloured
rect(115, 375, 150, 425, col = par("bg"), border = "transparent")
rect(150, 300, 175, 350, density = 10, border = "red")
rect(150, 400, 175, 450, density = 30, col = "blue",
     angle = -30, border = "transparent")

legend(180, 450, legend = 1:4, fill = c(NA, "green", par("fg"), "blue"),
      density = c(NA, NA, 10, 30), angle = c(NA, NA, 30, -30))

par(op)
```

---

**rug**

Add a Rug to a Plot

**Description**

Adds a rug representation (1-d plot) of the data to the plot.

**Usage**

```r
rug(x, ticksize = 0.03, side = 1, lwd = 0.5, col = par("fg"),
    quiet = getOption("warn") < 0, ...)```

**Arguments**

- `x` A numeric vector
- `ticksize` The length of the ticks making up the ‘rug’. Positive lengths give inwards ticks.
- `side` On which side of the plot box the rug will be plotted. Normally 1 (bottom) or 3 (top).
- `lwd` The line width of the ticks. Some devices will round the default width up to 1.
- `col` The colour the ticks are plotted in.
- `quiet` logical indicating if there should be a warning about clipped values.
- `...` further arguments, passed to `axis`, such as `line` or `pos` for specifying the location of the rug.

**Details**

Because of the way rug is implemented, only values of `x` that fall within the plot region are included. There will be a warning if any finite values are omitted, but non-finite values are omitted silently.
screen

References


See Also

`jitter` which you may want for ties in `x`.

Examples

```r
require(stats)  # both 'density' and its default method
with(faithful, {
  plot(density(eruptions, bw = 0.15))
  rug(eruptions)
  rug(jitter(eruptions, amount = 0.01), side = 3, col = "light blue")
})
```

Description

`split.screen` defines a number of regions within the current device which can, to some extent, be treated as separate graphics devices. It is useful for generating multiple plots on a single device. Screens can themselves be split, allowing for quite complex arrangements of plots.

`screen` is used to select which screen to draw in.

`erase.screen` is used to clear a single screen, which it does by filling with the background colour.

`close.screen` removes the specified screen definition(s).

Usage

```r
split.screen(figs, screen, erase = TRUE)
screen(n = , new = TRUE)
erase.screen(n = )
close.screen(n, all.screens = FALSE)
```

Arguments

- **figs** a two-element vector describing the number of rows and the number of columns in a screen matrix or a matrix with 4 columns. If a matrix, then each row describes a screen with values for the left, right, bottom, and top of the screen (in that order) in NDC units, that is 0 at the lower left corner of the device surface, and 1 at the upper right corner.
- **screen** a number giving the screen to be split. It defaults to the current screen if there is one, otherwise the whole device region.
- **erase** logical: should the selected screen be cleared?
- **n** a number indicating which screen to prepare for drawing (`screen`), erase (`erase.screen`), or close (`close.screen`). (`close.screen` will accept a vector of screen numbers.)
- **new** logical value indicating whether the screen should be erased as part of the preparation for drawing in the screen.
- **all.screens** logical value indicating whether all of the screens should be closed.
Details

The first call to `split.screen` places R into split-screen mode. The other split-screen functions only work within this mode. While in this mode, certain other commands should be avoided (see the Warnings section below). Split-screen mode is exited by the command `close.screen(all = TRUE).

If the current screen is closed, `close.screen` sets the current screen to be the next larger screen number if there is one, otherwise to the first available screen.

Value

`split.screen(*)` returns a vector of screen numbers for the newly-created screens. With no arguments, `split.screen()` returns a vector of valid screen numbers.

`screen(n)` invisibly returns `n`, the number of the selected screen. With no arguments, `screen()` returns the number of the current screen.

`close.screen()` returns a vector of valid screen numbers.

`screen`, `erase.screen`, and `close.screen` all return `FALSE` if R is not in split-screen mode.

Warnings

The recommended way to use these functions is to completely draw a plot and all additions (i.e., points and lines) to the base plot, prior to selecting and plotting on another screen. The behavior associated with returning to a screen to add to an existing plot is unpredictable and may result in problems that are not readily visible.

These functions are totally incompatible with the other mechanisms for arranging plots on a device: `par(mfrow), par(mfcol)` and `layout()`.

The functions are also incompatible with some plotting functions, such as `coplot`, which make use of these other mechanisms.

`erase.screen` will appear not to work if the background colour is transparent (as it is by default on most devices).

References


See Also

`par, layout, Devices, dev.*`

Examples

```r
if (interactive()) {
  par(bg = "white") # default is likely to be transparent
  split.screen(c(2, 1)) # split display into two screens
  split.screen(c(1, 3), screen = 2) # now split the bottom half into 3
  screen(1) # prepare screen 1 for output
  plot(1:10)
  screen(4) # prepare screen 4 for output
  plot(1:10)
  close.screen(all = TRUE) # exit split-screen mode
```
segments

Add Line Segments to a Plot

Description

Draw line segments between pairs of points.

Usage

segments(x0, y0, x1 = x0, y1 = y0, 
col = par("fg"), lty = par("lty"), lwd = par("lwd"), 
...)  

Arguments

x0, y0 coordinates of points from which to draw.

x1, y1 coordinates of points to which to draw. At least one must be supplied.

col, lty, lwd graphical parameters as in par, possibly vectors. NA values in col cause the segment to be omitted.

... further graphical parameters (from par), such as xpd and the line characteristics lend, ljoin and lmitre.

Details

For each i, a line segment is drawn between the point (x0[i], y0[i]) and the point (x1[i], y1[i]). The coordinate vectors will be recycled to the length of the longest.

The graphical parameters col, lty and lwd can be vectors of length greater than one and will be recycled if necessary.

References

smoothScatter

Scatterplots with Smoothed Densities Color Representation

Description

smoothScatter produces a smoothed color density representation of a scatterplot, obtained through a (2D) kernel density estimate.

Usage

smoothScatter(x, y = NULL, nbin = 128, bandwidth,
               colramp = colorRampPalette(c("white", blues9)),
               nrpoints = 100, ret.selection = FALSE,
               pch = ".", cex = 1, col = "black",
               transformation = function(x) x^.25,
               postPlotHook = box,
               xlab = NULL, ylab = NULL, xlim, ylim,
               xaxs = par("xaxs"), yaxs = par("yaxs"), ...)

Arguments

x, y the x and y coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function xy.coords for details. If supplied separately, they must be of the same length.

nbin numeric vector of length one (for both directions) or two (for x and y separately) specifying the number of equally spaced grid points for the density estimation; directly used as gridsize in bkde2D().

bandwidth numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. bandwidth is subsequently passed to function bkde2D.

colramp function accepting an integer n as an argument and returning n colors.

nrpoints number of points to be superimposed on the density image. The first nrpoints points from those areas of lowest regional densities will be plotted. Adding points to the plot allows for the identification of outliers. If all points are to be plotted, choose nrpoints = Inf.

Examples

```r
x <- stats::runif(12); y <- stats::rnorm(12)
i <- order(x, y); x <- x[i]; y <- y[i]
plot(x, y, main = "arrows(.) and segments(.)")
## draw arrows from point to point :
s <- seq(length(x)-1) # one shorter than data
arrows(x[s], y[s], x[s+1], y[s+1], col= 1:3)
s <- s[-length(s)]
segments(x[s], y[s], x[s+2], y[s+2], col='pink')
```

See Also

arrows, polygon for slightly easier and less flexible line drawing, and lines for the usual polygons.
smoothScatter produces a smoothed version of a scatter plot. Two dimensional (kernel density) smoothing is performed by `bkde2D` from package **KernSmooth**. See the examples for how to use this function together with `pairs`.

Value

If `ret.selection` is true, a vector of integers of length `nrpoints` (or smaller, if there are less finite points inside `xlim` and `ylim`) with the indices of the low-density points drawn, ordered with lowest density first.

Author(s)

Florian Hahne at FHCRC, originally

See Also

`bkde2D` from package **KernSmooth**; `densCols` which uses the same smoothing computations and `blues9` in package **grDevices**.

`scatter.smooth` adds a loess regression smoother to a scatter plot.

Examples

```r
## A largish data set
n <- 10000
x1 <- matrix(rnorm(n), ncol = 2)
x2 <- matrix(rnorm(n, mean = 3, sd = 1.5), ncol = 2)
x <- rbind(x1, x2)
oldpar <- par(mfrow = c(2, 2), mar=.1+c(3,3,1,1), mgp = c(1.5, 0.5, 0))
smoothScatter(x, nrpoints = 0)
smoothScatter(x)

## a different color scheme:
Lab.palette <- colorRampPalette(c("blue", "orange", "red"), space = "Lab")
i.s <- smoothScatter(x, colramp = Lab.palette,
  ## pch=NA: do not draw them
  nrpoints = 250, ret.selection=TRUE)
## label the 20 very lowest-density points, the "outliers" (with obs.number):
i.20 <- i.s[1:20]
text(x[i.20,], labels = i.20, cex = 0.75)
```
somewhat similar, using identical smoothing computations, but considerably *less* efficient for really large data:

```r
plot(x, col = densCols(x), pch = 20)
```

use with pairs:

```r
par(mfrow = c(1, 1))
y <- matrix(rnorm(40000), ncol = 4) + 3*rnorm(10000)
y[, c(2,4)] <- -y[, c(2,4)]
pairs(y, panel = function(...) smoothScatter(..., nrpoints = 0, add = TRUE),
gap = 0.2)
```

```r
par(oldpar)
```

---

**spineplot**

**Spine Plots and Spinograms**

**Description**

Spine plots are a special cases of mosaic plots, and can be seen as a generalization of stacked (or highlighted) bar plots. Analogously, spinograms are an extension of histograms.

**Usage**

```r
spineplot(x, ...)  
```

**Arguments**

- **x**
  - an object, the default method expects either a single variable (interpreted to be the explanatory variable) or a 2-way table. See details.
- **y**
  - a "factor" interpreted to be the dependent variable
- **formula**
  - a "formula" of type `y ~ x` with a single dependent "factor" and a single explanatory variable.
- **data**
  - an optional data frame.
spineplot

breaks  if the explanatory variable is numeric, this controls how it is discretized. breaks is passed to `hist` and can be a list of arguments.

tol.ylab  convenience tolerance parameter for y-axis annotation. If the distance between two labels drops under this threshold, they are plotted equidistantly.

off  vertical offset between the bars (in per cent). It is fixed to 0 for spinograms and defaults to 2 for spine plots.

ylevels  a character or numeric vector specifying in which order the levels of the dependent variable should be plotted.

col  a vector of fill colors of the same length as `levels(y)`. The default is to call `gray.colors`.

main, xlab, ylab  character strings for annotation

xaxlabels, yaxlabels  character vectors for annotation of x and y axis. Default to `levels(y)` and `levels(x)`, respectively for the spine plot. For `xaxlabels` in the spinogram, the breaks are used.

xlim, ylim  the range of x and y values with sensible defaults.

axes  logical. If `FALSE` all axes (including those giving level names) are suppressed.

weights  numeric. A vector of frequency weights for each observation in the data. If `NULL` all weights are implicitly assumed to be 1. If `x` is already a 2-way table, the weights are ignored.

...  additional arguments passed to `rect`.

subset  an optional vector specifying a subset of observations to be used for plotting.

drop.unused.levels  should factors have unused levels dropped? Defaults to `FALSE`.

Details

spineplot creates either a spinogram or a spine plot. It can be called via `spineplot(x, y)` or `spineplot(y ~ x)` where `y` is interpreted to be the dependent variable (and has to be categorical) and `x` the explanatory variable. `x` can be either categorical (then a spine plot is created) or numerical (then a spinogram is plotted). Additionally, spineplot can also be called with only a single argument which then has to be a 2-way table, interpreted to correspond to `table(x, y)`.

Both, spine plots and spinograms, are essentially mosaic plots with special formatting of spacing and shading. Conceptually, they plot $P(y|x)$ against $P(x)$. For the spine plot (where both `x` and `y` are categorical), both quantities are approximated by the corresponding empirical relative frequencies. For the spinogram (where `x` is numerical), `x` is first discretized (by calling `hist` with `breaks` argument) and then empirical relative frequencies are taken.

Thus, spine plots can also be seen as a generalization of stacked bar plots where not the heights but the widths of the bars corresponds to the relative frequencies of `x`. The heights of the bars then correspond to the conditional relative frequencies of `y` in every `x` group. Analogously, spinograms extend stacked histograms.

Value

The table visualized is returned invisibly.

Author(s)

Achim Zeileis <Achim.Zeileis@R-project.org>
**References**


**See Also**

`mosaicplot`, `hist`, `cdplot`

**Examples**

```r
## treatment and improvement of patients with rheumatoid arthritis
Treatment <- factor(rep(c(1, 2), c(43, 41)), levels = c(1, 2),
labels = c("placebo", "treated"))
Improved <- factor(rep(c(1, 2, 3, 1, 2, 3), c(29, 7, 7, 13, 7, 21)),
levels = c(1, 2, 3),
labels = c("none", "some", "marked"))

## (dependence on a categorical variable)
(spineplot(Improved ~ Treatment))

## applications and admissions by department at UC Berkeley
## (two-way tables)
(spineplot(marginSums(UCBAdmissions, c(3, 2)),
main = "Applications at UCB"))
(spineplot(marginSums(UCBAdmissions, c(3, 1)),
main = "Admissions at UCB"))

## NASA space shuttle o-ring failures
Fail <- factor(c(2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1),
levels = c(1, 2), labels = c("no", "yes"))
Temperature <- c(53, 57, 58, 63, 66, 67, 67, 67, 68, 69, 70, 70, 70, 72, 73, 75, 75, 75, 75, 75, 76, 76, 78, 78, 79, 81)

## (dependence on a numerical variable)
(spineplot(Fail ~ Temperature))
(spineplot(Fail ~ Temperature, breaks = 3))
(spineplot(Fail ~ Temperature, breaks = quantile(Temperature)))

## highlighting for failures
spineplot(Fail ~ Temperature, ylevels = 2:1)
```
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stars

Description
Draw star plots or segment diagrams of a multivariate data set. With one single location, also draws
‘spider’ (or ‘radar’) plots.
Usage
stars(x, full = TRUE, scale = TRUE, radius = TRUE,
labels = dimnames(x)[[1]], locations = NULL,
nrow = NULL, ncol = NULL, len = 1,
key.loc = NULL, key.labels = dimnames(x)[[2]],
key.xpd = TRUE,
xlim = NULL, ylim = NULL, flip.labels = NULL,
draw.segments = FALSE,
col.segments = 1:n.seg, col.stars = NA, col.lines = NA,
axes = FALSE, frame.plot = axes,
main = NULL, sub = NULL, xlab = "", ylab = "",
cex = 0.8, lwd = 0.25, lty = par("lty"), xpd = FALSE,
mar = pmin(par("mar"),
1.1+ c(2*axes+ (xlab != ""),
2*axes+ (ylab != ""), 1, 0)),
add = FALSE, plot = TRUE, ...)
Arguments
x

matrix or data frame of data. One star or segment plot will be produced for each
row of x. Missing values (NA) are allowed, but they are treated as if they were 0
(after scaling, if relevant).

full

logical flag: if TRUE, the segment plots will occupy a full circle. Otherwise, they
occupy the (upper) semicircle only.

scale

logical flag: if TRUE, the columns of the data matrix are scaled independently so
that the maximum value in each column is 1 and the minimum is 0. If FALSE,
the presumption is that the data have been scaled by some other algorithm to the
range [0, 1].

radius

logical flag: in TRUE, the radii corresponding to each variable in the data will be
drawn.

labels

vector of character strings for labeling the plots. Unlike the S function stars,
no attempt is made to construct labels if labels = NULL.

locations

Either two column matrix with the x and y coordinates used to place each of the
segment plots; or numeric of length 2 when all plots should be superimposed
(for a ‘spider plot’). By default, locations = NULL, the segment plots will be
placed in a rectangular grid.

nrow, ncol

integers giving the number of rows and columns to use when locations is NULL.
By default, nrow == ncol, a square layout will be used.

len

scale factor for the length of radii or segments.

key.loc

vector with x and y coordinates of the unit key.

key.labels

vector of character strings for labeling the segments of the unit key. If omitted,
the second component of dimnames(x) is used, if available.

key.xpd

clipping switch for the unit key (drawing and labeling), see par("xpd").

xlim

vector with the range of x coordinates to plot.


stars

ylim vector with the range of y coordinates to plot.

flip.labels logical indicating if the label locations should flip up and down from diagram to diagram. Defaults to a somewhat smart heuristic.

draw.segments logical. If TRUE draw a segment diagram.

col.segments color vector (integer or character, see par), each specifying a color for one of the segments (variables). Ignored if draw.segments = FALSE.

col.stars color vector (integer or character, see par), each specifying a color for one of the stars (cases). Ignored if draw.segments = TRUE.

col.lines color vector (integer or character, see par), each specifying a color for one of the lines (cases). Ignored if draw.segments = TRUE.

axes logical flag: if TRUE axes are added to the plot.

frame.plot logical flag: if TRUE, the plot region is framed.

main a main title for the plot.

sub a subtitle for the plot.

xlab a label for the x axis.

ylab a label for the y axis.

cex character expansion factor for the labels.

lwd line width used for drawing.

lty line type used for drawing.

xpd logical or NA indicating if clipping should be done, see par(xpd = ).

mar argument to par(mar = *), typically choosing smaller margins than by default.

... further arguments, passed to the first call of plot(), see plot.default and to box() if frame.plot is true.

add logical, if TRUE add stars to current plot.

plot logical, if FALSE, nothing is plotted.

Details

Missing values are treated as 0.

Each star plot or segment diagram represents one row of the input x. Variables (columns) start on the right and wind counterclockwise around the circle. The size of the (scaled) column is shown by the distance from the center to the point on the star or the radius of the segment representing the variable.

Only one page of output is produced.

Value

Returns the locations of the plots in a two column matrix, invisibly when plot = TRUE.

Note

This code started life as spatial star plots by David A. Andrews.

Prior to R 1.4.1, scaling only shifted the maximum to 1, although documented as here.

Author(s)

Thomas S. Dye
References


See Also

`symbols` for another way to draw stars and other symbols.

Examples

```r
require(grDevices)
stars(mtcars[, 1:7], key.loc = c(14, 2),
     main = "Motor Trend Cars : stars(*, full = F)", full = FALSE)
stars(mtcars[, 1:7], key.loc = c(14, 1.5),
     main = "Motor Trend Cars : full stars()", flip.labels = FALSE)

## 'Spider' or 'Radar' plot:
stars(mtcars[, 1:7], locations = c(0, 0), radius = FALSE,
      key.loc = c(0, 0), main = "Motor Trend Cars", lty = 2)

## Segment Diagrams:
palette(rainbow(12, s = 0.6, v = 0.75))
stars(mtcars[, 1:7], len = 0.8, key.loc = c(12, 1.5),
      main = "Motor Trend Cars", draw.segments = TRUE)
stars(mtcars[, 1:7], len = 0.6, key.loc = c(1.5, 0),
      main = "Motor Trend Cars", draw.segments = TRUE,
      frame.plot = TRUE, nrow = 4, cex = .7)

## scale linearly (not affinely) to [0, 1]
USJudge <- apply(USJudgeRatings, 2, function(x) x/max(x))
Jnam <- row.names(USJudgeRatings)
Snam <- abbreviate(substring(Jnam, 1, regexpr("[,."],Jnam) - 1), 7)
stars(USJudge, labels = Jnam, scale = FALSE,
      key.loc = c(13, 1.5), main = "Judge not ...", len = 0.8)
stars(USJudge, labels = Snam, scale = FALSE,
      key.loc = c(13, 1.5), radius = FALSE)

loc <- stars(USJudge, labels = NULL, scale = FALSE,
             radius = FALSE, frame.plot = TRUE,
             key.loc = c(13, 1.5), main = "Judge not ...", len = 1.2)
text(loc, Snam, col = "blue", cex = 0.8, xpd = TRUE)

## 'Segments':
stars(USJudge, draw.segments = TRUE, scale = FALSE, key.loc = c(13,1.5))

## 'Spider':
stars(USJudgeRatings, locations = c(0, 0), scale = FALSE, radius = FALSE,
       col.stars = 1:10, key.loc = c(0, 0), main = "US Judges rated")

## Same as above, but with colored lines instead of filled polygons.
stars(USJudgeRatings, locations = c(0, 0), scale = FALSE, radius = FALSE,
       col.lines = 1:10, key.loc = c(0, 0), main = "US Judges rated")

## 'Radar-Segments'
stars(USJudgeRatings[,1:10,], locations = 0:1, scale = FALSE,
       draw.segments = TRUE, col.segments = 0, col.stars = 1:10, key.loc = 0:1,
       main = "US Judges 1-10")
palette("default")
```
stem

```r
stars(cbind(1:16, 10*(16:1)), draw.segments = TRUE,
     main = "A Joke -- do *not* use symbols on 2D data!"
```

---

**stem**

**Stem-and-Leaf Plots**

**Description**

stem produces a stem-and-leaf plot of the values in x. The parameter scale can be used to expand the scale of the plot. A value of scale = 2 will cause the plot to be roughly twice as long as the default.

**Usage**

```r
stem(x, scale = 1, width = 80, atom = 1e-08)
```

**Arguments**

- `x` a numeric vector.
- `scale` This controls the plot length.
- `width` The desired width of plot.
- `atom` a tolerance.

**Details**

Infinite and missing values in x are discarded.

**References**


**Examples**

```r
stem(islands)
stem(log10(islands))
```

---

**stripchart**

**1-D Scatter Plots**

**Description**

stripchart produces one dimensional scatter plots (or dot plots) of the given data. These plots are a good alternative to boxplots when sample sizes are small.

```r
```
Usage

```r
stripchart(x, ...)  
```

## S3 method for class 'formula'

```r
stripchart(x, data = NULL, dlab = NULL, ...,  
subset, na.action = NULL)
```

## Default S3 method:

```r
stripchart(x, method = "overplot", jitter = 0.1, offset = 1/3,  
vertical = FALSE, group.names, add = FALSE,  
at = NULL, xlim = NULL, ylim = NULL,  
ylab = NULL, xlab = NULL, dlab = "", glab = "",  
log = "", pch = 0, col = par("fg"), cex = par("cex"),  
axes = TRUE, frame.plot = axes, ...)
```

Arguments

- **x**: the data from which the plots are to be produced. In the default method the data can be specified as a single numeric vector, or as list of numeric vectors, each corresponding to a component plot. In the *formula* method, a symbolic specification of the form `y ~ g` can be given, indicating the observations in the vector `y` are to be grouped according to the levels of the factor `g`. NAs are allowed in the data.

- **data**: a data.frame (or list) from which the variables in `x` should be taken.

- **subset**: an optional vector specifying a subset of observations to be used for plotting.

- **na.action**: a function which indicates what should happen when the data contain NAs. The default is to ignore missing values in either the response or the group.

- **...**: additional parameters passed to the default method, or by it to `plot.window`, `points`, `axis` and `title` to control the appearance of the plot.

- **method**: the method to be used to separate coincident points. The default method "overplot" causes such points to be overplotted, but it is also possible to specify "jitter" to jitter the points, or "stack" have coincident points stacked. The last method only makes sense for very granular data.

- **jitter**: when `method = "jitter"` is used, jitter gives the amount of jittering applied.

- **offset**: when stacking is used, points are stacked this many line-heights (symbol widths) apart.

- **vertical**: when `vertical` is `TRUE` the plots are drawn vertically rather than the default horizontal.

- **group.names**: group labels which will be printed alongside (or underneath) each plot.

- **add**: logical, if true `add` the chart to the current plot.

- **at**: numeric vector giving the locations where the charts should be drawn, particularly when `add = TRUE`; defaults to `1:n` where `n` is the number of boxes.

- **ylab, xlab**: labels: see `title`.

- **dlab, glab**: alternate way to specify axis labels: see "Details".

- **xlim, ylim**: plot limits: see `plot.window`.

- **log**: on which axes to use a log scale: see `plot.default`
**strwidth**

Graphical parameters: see `par`.

Axis control: see `plot.default`.

**Details**

Extensive examples of the use of this kind of plot can be found in Box, Hunter and Hunter or Seber and Wild.

The `dlab` and `glab` labels may be used instead of `xlab` and `ylab` if those are not specified. `dlab` applies to the continuous data axis (the X axis unless `vertical` is `TRUE`), `glab` to the group axis.

**Examples**

```r
x <- stats::rnorm(50)
xr <- round(x, 1)
stripchart(x); m <- mean(par("usr")[1:2])
  text(m, 1.04, "stripchart(x, \"overplot\")")
stripchart(xr, method = "stack", add = TRUE, at = 1.2)
  text(m, 1.35, "stripchart(round(x,1), \"stack\")")
stripchart(xr, method = "jitter", add = TRUE, at = 0.7)
  text(m, 0.85, "stripchart(round(x,1), \"jitter\")")

stripchart(decrease ~ treatment,
  main = "stripchart(OrchardSprays)",
  vertical = TRUE, log = "y", data = OrchardSprays)

stripchart(decrease ~ treatment, at = c(1:8)^2,
  main = "stripchart(OrchardSprays)",
  vertical = TRUE, log = "y", data = OrchardSprays)
```

**strwidth**

Plotting Dimensions of Character Strings and Math Expressions

**Description**

These functions compute the width or height, respectively, of the given strings or mathematical expressions `s[i]` on the current plotting device in `user` coordinates, `inches` or as fraction of the figure width `par("fin")`.

**Usage**

```r
strwidth(s, units = "user", cex = NULL, font = NULL, vfont = NULL, ...)
strheight(s, units = "user", cex = NULL, font = NULL, vfont = NULL, ...)
```

**Arguments**

- `s` a character or expression vector whose dimensions are to be determined. Other objects are coerced by `as.graphicsAnnot`.
- `units` character indicating in which units `s` is measured; should be one of "user", "inches", "figure"; partial matching is performed.
- `cex` numeric character expansion factor; multiplied by `par("cex")` yields the final character size; the default NULL is equivalent to 1.
font, vfont, ...

additional information about the font, possibly including the graphics parameter "family": see text.

Details

Note that the ‘height’ of a string is determined only by the number of linefeeds ("\n", aka “newline”)s it contains: it is the (number of linefeeds - 1) times the line spacing plus the height of "M" in the selected font. For an expression it is the height of the bounding box as computed by plotmath. Thus in both cases it is an estimate of how far above the final baseline the typeset object extends. (It may also extend below the baseline.) The inter-line spacing is controlled by cex, par("lheight") and the ‘point size’ (but not the actual font in use).

Measurements in "user" units (the default) are only available after plot.new has been called – otherwise an error is thrown.

Value

Numeric vector with the same length as s, giving the estimate of width or height for each s[i]. NA strings are given width and height 0 (as they are not plotted).

See Also

text, nchar

Examples

str.ex <- c("W","w","I",".","WwI.")
op <- par(pty = "s"); plot(1:100, 1:100, type = "n")
sw <- strwidth(str.ex); sw
all.equal(sum(sw[1:4]), sw[5])
#- since the last string contains the others

sw.i <- strwidth(str.ex, "inches"); 25.4 * sw.i # width in [mm]
unique(sw / sw.i)
# constant factor: 1 value
mean(sw.i / strwidth(str.ex, "fig")) / par("fin")[1] # = 1: are the same

## See how letters fall in classes
## -- depending on graphics device and font!
all.lett <- c(letters, LETTERS)
shL <- strheight(all.lett, units = "inches") * 72 # 'big points'
table(shL) # all have same heights ...
mean(shL)/par("cin")[2] # around 0.6

(swL <- strwidth(all.lett, units = "inches") * 72) # 'big points'
split(all.lett, factor(round(swL, 2)))

sumex <- expression(sum(x[i], i=1,n), e^{i * pi} == -1)
strwidth(sumex)
strheight(sumex)

par(op) #- reset to previous setting
Sunflowerplot

Produce a Sunflower Scatter Plot

Description

Multiple points are plotted as ‘sunflowers’ with multiple leaves (‘petals’) such that overplotting is visualized instead of accidental and invisible.

Usage

sunflowerplot(x, ...)

## Default S3 method:
sunflowerplot(x, y = NULL, number, log = "", digits = 6,
xlab = NULL, ylab = NULL, xlim = NULL, ylim = NULL,
add = FALSE, rotate = FALSE,
pch = 16, cex = 0.8, cex.fact = 1.5,
col = par("col"), bg = NA, size = 1/8, seg.col = 2,
seg.lwd = 1.5, ...)

## S3 method for class 'formula'
sunflowerplot(formula, data = NULL, xlab = NULL, ylab = NULL, ...,
subset, na.action = NULL)

Arguments

x numeric vector of x-coordinates of length n, say, or another valid plotting structure, as for plot.default, see also xy.coords.

y numeric vector of y-coordinates of length n.

number integer vector of length n. number[i] = number of replicates for (x[i], y[i]), may be 0. Default (missing(number)): compute the exact multiplicity of the points x[], y[], via xyTable().

log character indicating log coordinate scale, see plot.default.

digits when number is computed (i.e., not specified), x and y are rounded to digits significant digits before multiplicities are computed.

xlab, ylab character label for x-, or y-axis, respectively.

xlim, ylim numeric(2) limiting the extents of the x-, or y-axis.

add logical; should the plot be added on a previous one? Default is FALSE.

rotate logical; if TRUE, randomly rotate the sunflowers (preventing artefacts).

pch plotting character to be used for points (number[i]==1) and center of sunflowers.

cex numeric; character size expansion of center points (s. pch).

cex.fact numeric shrinking factor to be used for the center points when there are flower leaves, i.e., cex / cex.fact is used for these.

col, bg colors for the plot symbols, passed to plot.default.
size of sunflower leaves in inches, \(1\text{[in]} := 2.54\text{[cm]}\). Default: \(1/8\text{"}, approximately 3.2\text{mm}.

seg.col color to be used for the segments which make the sunflowers leaves, see \texttt{par(col=)}; \texttt{col = "gold"} reminds of real sunflowers.

seg.lwd numeric; the line width for the leaves’ segments.

... further arguments to \texttt{plot [if add = FALSE]}, or to be passed to or from another method.

formula a \texttt{formula}, such as \(y \sim x\).

data a \texttt{data.frame (or list) from which the variables in formula should be taken.}

subset an optional vector specifying a subset of observations to be used in the fitting process.

na.action a function which indicates what should happen when the data contain NAs. The default is to ignore case with missing values.

Details

This is a generic function with default and formula methods.

For \texttt{number[1] == 1}, a (slightly enlarged) usual plotting symbol (\texttt{pch}) is drawn. For \texttt{number[1] > 1}, a small plotting symbol is drawn and \texttt{number[1]} equi-angular ‘rays’ emanate from it.

If \texttt{rotate = TRUE} and \texttt{number[1] >= 2}, a random direction is chosen (instead of the y-axis) for the first ray. The goal is to \texttt{jitter} the orientations of the sunflowers in order to prevent artefactual visual impressions.

Value

A list with three components of same length,

\begin{tabular}{ll}
\texttt{x} & x coordinates \\
\texttt{y} & y coordinates \\
\texttt{number} & number
\end{tabular}

Use \texttt{xyTable()} (from package \texttt{grDevices}) if you are only interested in this return value.

Side Effects

A scatter plot is drawn with ‘sunflowers’ as symbols.

Author(s)

Andreas Ruckstuhl, Werner Stahel, Martin Maechler, Tim Hesterberg, 1989–1993. Port to \texttt{R} by Martin Maechler <maechler@stat.math.ethz.ch>.

References


symbols

Draw Symbols (Circles, Squares, Stars, Thermometers, Boxplots)

Description

This function draws symbols on a plot. One of six symbols; circles, squares, rectangles, stars, thermometers, and boxplots, can be plotted at a specified set of x and y coordinates. Specific aspects of the symbols, such as relative size, can be customized by additional parameters.

Usage

symbols(x, y = NULL, circles, squares, rectangles, stars, thermometers, boxplots, inches = TRUE, add = FALSE, fg = par("col"), bg = NA, xlab = NULL, ylab = NULL, main = NULL, xlim = NULL, ylim = NULL, ...)

Arguments

x, y the x and y co-ordinates for the centres of the symbols. They can be specified in any way which is accepted by xy.coords.
circles a vector giving the radii of the circles.

See Also
density, xyTable

Examples

require(stats) # for rnorm
require(grDevices)

## 'number' is computed automatically:
sunflowerplot(iris[, 3:4])
## Imitating Chambers et al, p.109, closely:
sunflowerplot(iris[, 3:4], cex = .2, cex.fact = 1, size = .035, seg.lwd = .8)
## or
sunflowerplot(Petal.Width ~ Petal.Length, data = iris,
cex = .2, cex.fact = 1, size = .035, seg.lwd = .8)

sunflowerplot(x = sort(2*round(rnorm(100))), y = round(rnorm(100), 0),
main = "Sunflower Plot of Rounded N(0,1)"
## Similarly using a "xyTable" argument:
xyT <- xyTable(x = sort(2*round(rnorm(100))), y = round(rnorm(100), 0),
digits = 3)
utils::str(xyT, vec.len = 20)
sunflowerplot(xyT, main = "2nd Sunflower Plot of Rounded N(0,1)"

## A 'marked point process' (explicit 'number' argument):
sunflowerplot(rnorm(100), rnorm(100), number = rpois(n = 100, lambda = 2),
main = "Sunflower plot (marked point process)",
rotate = TRUE, col = "blue4")
squares
a vector giving the length of the sides of the squares.
rectangles
a matrix with two columns. The first column gives widths and the second the heights of rectangles.
stars
a matrix with three or more columns giving the lengths of the rays from the center of the stars. NA values are replaced by zeroes.
thermometers
a matrix with three or four columns. The first two columns give the width and height of the thermometer symbols. If there are three columns, the third is taken as a proportion: the thermometers are filled (using colour fg) from their base to this proportion of their height. If there are four columns, the third and fourth columns are taken as proportions and the thermometers are filled between these two proportions of their heights. The part of the box not filled in fg will be filled in the background colour (default transparent) given by bg.
boxplots
a matrix with five columns. The first two columns give the width and height of the boxes, the next two columns give the lengths of the lower and upper whiskers and the fifth the proportion (with a warning if not in [0,1]) of the way up the box that the median line is drawn.
inches
TRUE, FALSE or a positive number. See ‘Details’.
add
if add is TRUE, the symbols are added to an existing plot, otherwise a new plot is created.
fg
colour(s) the symbols are to be drawn in.
bg
if specified, the symbols are filled with colour(s), the vector bg being recycled to the number of symbols. The default is to leave the symbols unfilled.
xlab
the x label of the plot if add is not true. Defaults to the deparse d expression used for x.
ylab
the y label of the plot. Unused if add = TRUE.
main
a main title for the plot. Unused if add = TRUE.
xlim
numeric vector of length 2 giving the x limits for the plot. Unused if add = TRUE.
ylim
numeric vector of length 2 giving the y limits for the plot. Unused if add = TRUE.
... graphics parameters can also be passed to this function, as can the plot aspect ratio asp (see plot.window).

Details

Observations which have missing coordinates or missing size parameters are not plotted. The exception to this is stars. In that case, the length of any ray which is NA is reset to zero.

Argument inches controls the sizes of the symbols. If TRUE (the default), the symbols are scaled so that the largest dimension of any symbol is one inch. If a positive number is given the symbols are scaled to make largest dimension this size in inches (so TRUE and 1 are equivalent). If inches is FALSE, the units are taken to be those of the appropriate axes. (For circles, squares and stars the units of the x axis are used. For boxplots, the lengths of the whiskers are regarded as dimensions alongside width and height when scaling by inches, and are otherwise interpreted in the units of the y axis.)

Circles of radius zero are plotted at radius one pixel (which is device-dependent). Circles of a very small non-zero radius may or may not be visible, and may be smaller than circles of radius zero. On windows devices circles are plotted at radius at least one pixel as some Windows versions omit smaller circles.
References


See Also

`symbols` for drawing stars with a bit more flexibility.

If you are thinking about doing ‘bubble plots’ by `symbols(*, circles=*)`, you should really consider using `sunflowerplot` instead.

Examples

```r
require(stats); require(grDevices)
x <- 1:10
y <- sort(10*runif(10))
z <- runif(10)
z3 <- cbind(z, 2*runif(10), runif(10))
symbols(x, y, thermometers = cbind(.5, 1, z), inches = .5, fg = 1:10)
symbols(x, y, thermometers = z3, inches = FALSE)
text(x, y, apply(format(round(z3, digits = 2)), 1, paste, collapse = ""),
     adj = c(-.2,0), cex = .75, col = "purple", xpd = NA)
## Note that example(trees) shows more sensible plots!
N <- nrow(trees)
with(trees, {
## Girth is diameter in inches
  symbols(Height, Volume, circles = Girth/24, inches = FALSE,
          main = "Trees' Girth") # xlab and ylab automatically
## Colours too:
  op <- palette(rainbow(N, end = 0.9))
  symbols(Height, Volume, circles = Girth/16, inches = FALSE, bg = 1:N,
          fg = "gray30", main = "symbols(*, circles = Girth/16, bg = 1:N")
  palette(op)
})
```

---

**Description**

`text` draws the strings given in the vector `labels` at the coordinates given by `x` and `y`. `y` may be missing since `xy.coords(x, y)` is used for construction of the coordinates.

**Usage**

```r
text(x, ..., 
## Default S3 method:
  text(x, y = NULL, labels = seq_along(x$x), adj = NULL,
       pos = NULL, offset = 0.5, vfont = NULL,
       cex = 1, col = NULL, font = NULL, ...)```
Arguments

- **x, y**: numeric vectors of coordinates where the text labels should be written. If the length of x and y differs, the shorter one is recycled.
- **labels**: a character vector or expression specifying the text to be written. An attempt is made to coerce other language objects (names and calls) to expressions, and vectors and other classed objects to character vectors by `as.character`. If `labels` is longer than x and y, the coordinates are recycled to the length of `labels`.
- **adj**: one or two values in [0, 1] which specify the x (and optionally y) adjustment (‘justification’) of the labels, with 0 for left/bottom, 1 for right/top, and 0.5 for centered. On most devices values outside [0, 1] will also work. See below.
- **pos**: a position specifier for the text. If specified this overrides any `adj` value given. Values of 1, 2, 3 and 4, respectively indicate positions below, to the left of, above and to the right of the specified (x,y) coordinates.
- **offset**: when `pos` is specified, this value controls the distance (‘offset’) of the text label from the specified coordinate in fractions of a character width.
- **vfont**: NULL for the current font family, or a character vector of length 2 for Hershey vector fonts. The first element of the vector selects a typeface and the second element selects a style. Ignored if `labels` is an expression.
- **cex**: numeric character expansion factor; multiplied by `par("cex")` yields the final character size. NULL and NA are equivalent to 1.0.
- **col, font**: the color and (if `vfont = NULL`) font to be used, possibly vectors. These default to the values of the global graphical parameters in `par()`.
- **...**: further graphical parameters (from `par`), such as `srt`, `family` and `xpd`.

Details

labels must be of type `character` or `expression` (or be coercible to such a type). In the latter case, quite a bit of mathematical notation is available such as sub- and superscripts, greek letters, fractions, etc.

adj allows adjustment of the text position with respect to (x, y). Values of 0, 0.5, and 1 specify that (x, y) should align with the left/bottom, middle and right/top of the text, respectively. The default is for centered text, i.e., `adj = c(0.5, NA)`. Accurate vertical centering needs character metric information on individual characters which is only available on some devices. Vertical alignment is done slightly differently for character strings and for expressions: `adj = c(0, 0)` means to left-justify and to align on the baseline for strings but on the bottom of the bounding box for expressions. This also affects vertical centering: for strings the centering excludes any descenders whereas for expressions it includes them. Using NA for strings centers them, including descenders.

The `pos` and `offset` arguments can be used in conjunction with values returned by `identify` to recreate an interactively labelled plot.

Text can be rotated by using graphical parameters `srt` (see `par`). When adj is specified, a non-zero `srt` rotates the label about (x, y). If `pos` is specified, `srt` rotates the text about the point on its bounding box which is closest to (x, y): top center for `pos = 1`, right center for `pos = 2`, bottom center for `pos = 3`, and left center for `pos = 4`. The pos interface is not as useful for rotated text because the result is no longer centered vertically or horizontally with respect to (x, y). At present there is no interface in the `graphics` package for directly rotating text about its center which is achievable however by fiddling with `adj` and `srt` simultaneously.

Graphical parameters `col`, `cex` and `font` can be vectors and will then be applied cyclically to the `labels` (and extra values will be ignored). NA values of `font` are replaced by `par("font")`, and similarly for `col`.
Labels whose x, y or labels value is NA are omitted from the plot.

What happens when font = 5 (the symbol font) is selected can be both device- and locale-dependent. Most often labels will be interpreted in the Adobe symbol encoding, so e.g. "d" is delta, and "\300" is aleph.

**Euro symbol**

The Euro symbol may not be available in older fonts. In current versions of Adobe symbol fonts it is character 160, so text(x, y, "\xA0", font = 5) may work. People using Western European locales on Unix-alikes can probably select ISO-8895-15 (Latin-9) which has the Euro as character 165: this can also be used for *postscript* and *pdf*. It is ‘\u20ac’ in Unicode, which can be used in UTF-8 locales.

The Euro should be rendered correctly by X11 in UTF-8 locales, but the corresponding single-byte encoding in *postscript* and *pdf* will need to be selected as ISOLatin9.enc (and the font will need to contain the Euro glyph, which for example older printers may not).

**References**


**See Also**

text.formula for the formula method; mtext, title, Hershey for details on Hershey vector fonts, plotmath for details and more examples on mathematical annotation.

**Examples**

```r
plot(-1:1, -1:1, type = "n", xlab = "Re", ylab = "Im")
K <- 16; text(exp(1i * 2 * pi * (1:K) / K), col = 2)

## The following two examples use latin1 characters: these may not
## appear correctly (or be omitted entirely).
plot(1:10, 1:10, main = "text(...) examples\n~~~~~~~~~~~~~~", 
     sub = "R is GNU ©, but not ®...")
mtext("<Latin-1 accented chars>: éè øØ å<Å æ<Æ", side = 3)
points(c(6,2), c(2,1), pch = 3, cex = 4, col = "red")
text(6, 2, "the text is CENTERED around (x,y) = (6,2) by default",
     cex = .8)
text(2, 1, "or Left/Bottom - JUSTIFIED at (2,1) by \'adj = c(0,0)\'",
     adj = c(0,0))
text(4, 9, expression(hat(beta) == (X^t * X)^{-1} * X^t * y))
text(4, 8.4, "expression(hat(beta) == (X^t * X)^{-1} * X^t * y)",
     cex = .75)
text(4, 7, expression(bar(x) == sum(frac(x[i], n), i==1, n)))

## Two more latin1 examples

text(5, 10.2,
     "Le français, c'est facile: Règles, Liberté, Egalité, Fraternité...")
text(5, 9.8,
     "Jetz no chli züritüütsch: (noch ein bißchen Zürcher deutsch)")
```
Description

This function can be used to add labels to a plot. Its first four principal arguments can also be used as arguments in most high-level plotting functions. They must be of type character or expression. In the latter case, quite a bit of mathematical notation is available such as sub- and superscripts, greek letters, fractions, etc: see plotmath

Usage

```r
title(main = NULL, sub = NULL, xlab = NULL, ylab = NULL, line = NA, outer = FALSE, ...)
```

Arguments

- `main` The main title (on top) using font, size (character expansion) and color `par(c("font.main", "cex.main", "col.main")).`
- `sub` Sub-title (at bottom) using font, size and color `par(c("font.sub", "cex.sub", "col.sub")).`
- `xlab` X axis label using font, size and color `par(c("font.lab", "cex.lab", "col.lab")).`
- `ylab` Y axis label, same font attributes as `xlab`.
- `line` specifying a value for `line` overrides the default placement of labels, and places them this many lines outwards from the plot edge.
- `outer` a logical value. If TRUE, the titles are placed in the outer margins of the plot.
- `...` further graphical parameters from `par`. Use e.g., `col.main` or `cex.sub` instead of just `col` or `cex`. `adj` controls the justification of the titles. `xpd` can be used to set the clipping region: this defaults to the figure region unless `outer = TRUE`, otherwise the device region and can only be increased. `mgp` controls the default placing of the axis titles.

Details

The labels passed to `title` can be character strings or language objects (names, calls or expressions), or a list containing the string to be plotted, and a selection of the optional modifying graphical parameters `cex=, col= and font=`. Other objects will be coerced by `as.graphicsAnnot`.

The position of `main` defaults to being vertically centered in (outer) margin 3 and justified horizontally according to `par("adj")` on the plot region (device region for `outer = TRUE`).

The positions of `xlab`, `ylab` and `sub` are `line` (default for `xlab` and `ylab` being `par("mgp")[1]` and increased by 1 for `sub`) lines (of height `par("mex")`) into the appropriate margin, justified in the text direction according to `par("adj")` on the plot/device region.

References

See Also

mtext, text; plotmath for details on mathematical annotation.

Examples

```r
plot(cars, main = "") # here, could use main directly
title(main = "Stopping Distance versus Speed")

plot(cars, main = "")
title(main = list("Stopping Distance versus Speed", cex = 1.5,
                   col = "red", font = 3))

## Specifying "...":
plot(1, col.axis = "sky blue", col.lab = "thistle")
title(text = "Main Title", sub = "subtitle",
      cex.main = 2, font.main = 4, col.main = "blue",
      cex.sub = 0.75, font.sub = 3, col.sub = "red")
```

```r
x <- seq(-4, 4, length.out = 101)
y <- cbind(sin(x), cos(x))
matplot(x, y, type = "l", xaxt = "n",
        main = expression(paste(plain(sin) * phi, " and ",
                             plain(cos) * phi)),
        ylab = expression("sin" * phi, "cos" * phi), # only 1st is taken
        xlab = expression("Phase Angle ", phi),
        col.main = "blue")
axis(1, at = c(-pi, -pi/2, 0, pi/2, pi),
     labels = expression(-pi, -pi/2, 0, pi/2, pi))
abline(h = 0, v = pi/2 * c(-1,1), lty = 2, lwd = .1, col = "gray70")
```

---

Description

xinch and yinch convert the specified number of inches given as their arguments into the correct units for plotting with graphics functions. Usually, this only makes sense when normal coordinates are used, i.e., no log scale (see the log argument to par).

xyinch does the same for a pair of numbers xy, simultaneously.

Usage

```r
xinch(x = 1, warn.log = TRUE)
yinch(y = 1, warn.log = TRUE)
xyinch(xy = 1, warn.log = TRUE)
```

Arguments

- `x, y` numeric vector
- `xy` numeric of length 1 or 2.
- `warn.log` logical; if TRUE, a warning is printed in case of active log scale.
Examples

```r
all(c(xinch(), yinch()) == xyinch()) # TRUE
xyinch()
xyinch # to see that is really delta("usr") / "pin"

## plot labels offset 0.12 inches to the right
## of plotted symbols in a plot
with(mtcars, {
  plot(mpg, disp, pch = 19, main = "Motor Trend Cars")
  text(mpg + xinch(0.12), disp, row.names(mtcars),
       adj = 0, cex = .7, col = "blue")
})
```

xspline

Draw an X-spline

Description

Draw an X-spline, a curve drawn relative to control points.

Usage

```r
xspline(x, y = NULL, shape = 0, open = TRUE, repEnds = TRUE,
draw = TRUE, border = par("fg"), col = NA, ...)
```

Arguments

- `x, y`: vectors containing the coordinates of the vertices of the polygon. See `xy.coords` for alternatives.
- `shape`: A numeric vector of values between -1 and 1, which control the shape of the spline relative to the control points.
- `open`: A logical value indicating whether the spline is an open or a closed shape.
- `repEnds`: For open X-splines, a logical value indicating whether the first and last control points should be replicated for drawing the curve. Ignored for closed X-splines.
- `draw`: logical: should the X-spline be drawn? If false, a set of line segments to draw the curve is returned, and nothing is drawn.
- `border`: the color to draw the curve. Use `border = NA` to omit borders.
- `col`: the color for filling the shape. The default, `NA`, is to leave unfilled.
- `...`: graphical parameters such as `lty`, `xpd`, `lend`, `ljoin` and `lmitre` can be given as arguments.

Details

An X-spline is a line drawn relative to control points. For each control point, the line may pass through (interpolate) the control point or it may only approach (approximate) the control point; the behaviour is determined by a shape parameter for each control point.

If the shape parameter is greater than zero, the spline approximates the control points (and is very similar to a cubic B-spline when the shape is 1). If the shape parameter is less than zero, the spline
interpolates the control points (and is very similar to a Catmull-Rom spline when the shape is -1). If the shape parameter is 0, the spline forms a sharp corner at that control point.

For open X-splines, the start and end control points must have a shape of 0 (and non-zero values are silently converted to zero).

For open X-splines, by default the start and end control points are replicated before the curve is drawn. A curve is drawn between (interpolating or approximating) the second and third of each set of four control points, so this default behaviour ensures that the resulting curve starts at the first control point you have specified and ends at the last control point. The default behaviour can be turned off via the repEnds argument.

**Value**

If draw = TRUE, NULL otherwise a list with elements x and y which could be passed to lines, polygon and so on.

Invisible in both cases.

**Note**

Two-dimensional splines need to be created in an isotropic coordinate system. Device coordinates are used (with an anisotropy correction if needed.)

**References**


**See Also**

polygon.

par for how to specify colors.

**Examples**

```r
## based on examples in ?grid.xspline
xsplineTest <- function(s, open = TRUE, 
                        x = c(1,1,3,3)/4, 
                        y = c(1,3,3,1)/4, ...) {
  plot(c(0,1), c(0,1), type = "n", axes = FALSE, xlab = "", ylab = "")
  points(x, y, pch = 19)
  xspline(x, y, s, open, ...)
  text(x+0.05*c(-1,-1,1,1), y+0.05*c(-1,1,1,-1), s)
}

op <- par(mfrow = c(3,3), mar = rep(0,4), oma = c(0,0,2,0))
xplineTest(c(0, -1, -1, 0))
xplineTest(c(0, -1, 0, 0))
xplineTest(c(0, -1, 1, 0))
xplineTest(c(0, 0, -1, 0))
xplineTest(c(0, 0, 0, 0))
xplineTest(c(0, 0, 1, 0))
xplineTest(c(0, 1, -1, 0))
xplineTest(c(0, 1, 0, 0))
xplineTest(c(0, 1, 1, 0))
title("Open X-splines", outer = TRUE)
```
xsplineTest(c(0, -1, -1, 0), FALSE, col = "grey80")
xsplinelTest(c(0, -1, 0, 0), FALSE, col = "grey80")
xsplinelTest(c(0, -1, 1, 0), FALSE, col = "grey80")
xsplinelTest(c(0, 0, -1, 0), FALSE, col = "grey80")
xsplinelTest(c(0, 0, 0, 0), FALSE, col = "grey80")
xsplinelTest(c(0, 0, 1, 0), FALSE, col = "grey80")
xsplinelTest(c(0, 1, -1, 0), FALSE, col = "grey80")
xsplinelTest(c(0, 1, 0, 0), FALSE, col = "grey80")
xsplinelTest(c(0, 1, 1, 0), FALSE, col = "grey80")
title("Closed X-splines", outer = TRUE)

x <- sort(stats::rnorm(5))
y <- sort(stats::rnorm(5))
plot(x, y, pch = 19)
res <- xspline(x, y, 1, draw = FALSE)
lines(res)
## the end points may be very close together,
## so use last few for direction
nr <- length(res$x)
arrows(res$x[1], res$y[1], res$x[4], res$y[4], code = 1, length = 0.1)
arrows(res$x[nr-3], res$y[nr-3], res$x[nr], res$y[nr], code = 2, length = 0.1)
Chapter 6

The grid package

---

The Grid Graphics Package

Description

A rewrite of the graphics layout capabilities, plus some support for interaction.

Details

This package contains a graphics system which supplements S-style graphics (see the graphics package).

Further information is available in the following vignettes:

- grid
- displaylist
- frame
- grobs
- interactive
- locndimm
- moveline
- nonfinite
- plotexample
- rotated
- saveload
- sharing
- viewports

For a complete list of functions with individual help pages, use `library(help = "grid")`.

Author(s)

Paul Murrell <paul@stat.auckland.ac.nz>

Maintainer: R Core Team <R-core@r-project.org>
References


---

**absolute.size**

*Absolute Size of a Grob*

**Description**

This function converts a unit object into absolute units. Absolute units are unaffected, but non-absolute units are converted into "null" units.

**Usage**

`absolute.size(unit)`

**Arguments**

- `unit`: An object of class "unit".

**Details**

Absolute units are things like "inches", "cm", and "lines". Non-absolute units are "npc" and "native".

This function is designed to be used in `widthDetails` and `heightDetails` methods.

**Value**

An object of class "unit".

**Author(s)**

Paul Murrell

**See Also**

`widthDetails` and `heightDetails` methods.
arrow

Describe arrows to add to a line.

Description

Produces a description of what arrows to add to a line. The result can be passed to a function that draws a line, e.g., grid.lines.

Usage

arrow(angle = 30, length = unit(0.25, "inches"),
ends = "last", type = "open")

Arguments

angle  The angle of the arrow head in degrees (smaller numbers produce narrower, pointier arrows). Essentially describes the width of the arrow head.
length  A unit specifying the length of the arrow head (from tip to base).
ends  One of "last", "first", or "both", indicating which ends of the line to draw arrow heads.
type  One of "open" or "closed" indicating whether the arrow head should be a closed triangle.

Examples

arrow()

as.mask

Define a Soft Mask

Description

Define either an alpha mask or a luminance mask, based on a grob.

Usage

as.mask(x, type=c("alpha", "luminance"))

Arguments

x  A grob.
type  The type of mask.

Details

A mask may be specified for a viewport either directly as a grob or using this function. In the former case, the result is an alpha mask. This function allows the user to define a luminance mask instead. Not all graphics devices support masks and those that do may only support one type of mask: for example xfig and pictex do not support masks and Cairo-based devices only support alpha masks.
calcStringMetric

Calculate Metric Information for Text

description

This function returns the ascent, descent, and width metric information for a character or expression vector.

Usage

calcStringMetric(text)

Arguments

text A character or expression vector.

Value

A list with three numeric components named ascent, descent, and width. All values are in inches.

WARNING

The metric information from this function is based on the font settings that are in effect when this function is called. It will not necessarily correspond to the metric information of any text that is drawn on the page.
calcStringMetric

Author(s)
Paul Murrell

See Also
stringAscent, stringDescent, grobAscent, and grobDescent.

Examples
grid.newpage()
grid.segments(.01, .5, .99, .5, gp=gpar(col="grey"))
metrics <- calcStringMetric(letters)
grid.rect(x=1:26/27,
  width=unit(metrics$width, "inches"),
  height=unit(metrics$ascent, "inches"),
  just="bottom",
  gp=gpar(col="red"))
grid.rect(x=1:26/27,
  width=unit(metrics$width, "inches"),
  height=unit(metrics$descent, "inches"),
  just="top",
  gp=gpar(col="red"))
grid.text(letters, x=1:26/27, just="bottom")
test <- function(x) {
  grid.text(x, just="bottom")
metric <- calcStringMetric(x)
if (is.character(x)) {
  grid.rect(width=unit(metric$width, "inches"),
    height=unit(metric$ascent, "inches"),
    just="bottom",
    gp=gpar(col=rgb(1,0,0,.5)))
  grid.rect(width=unit(metric$width, "inches"),
    height=unit(metric$descent, "inches"),
    just="top",
    gp=gpar(col=rgb(1,0,0,.5)))
} else {
  grid.rect(width=unit(metric$width, "inches"),
    y=unit(.5, "npc") + unit(metric[2], "inches"),
    height=unit(metric$ascent, "inches"),
    just="bottom",
    gp=gpar(col=rgb(1,0,0,.5)))
  grid.rect(width=unit(metric$width, "inches"),
    height=unit(metric$descent, "inches"),
    just="bottom",
    gp=gpar(col=rgb(1,0,0,.5)))
}
}
tests <- list("t",
  "test",
  "testy",
  "test\ntwo",
  expression(x),
  expression(y),
  expression(x + y),
  expression(x + y + z),
  expression(x + y + z + w))
expression(a + b),
expression(atop(x + y, 2)))

grid.newpage()
nrowcol <- n2mfrow(length(tests))
pushViewport(viewport(layout=grid.layout(nrowcol[1], nrowcol[2]),
gp=gpar(cex=5, lwd=.5)))
for (i in 1:length(tests)) {
  col <- (i - 1) %% nrowcol[2] + 1
  row <- (i - 1) %/% nrowcol[2] + 1
  pushViewport(viewport(layout.pos.row=row, layout.pos.col=col))
test(tests[[i]])
  popViewport()
}

---

**dataViewport**  
Create a Viewport with Scales based on Data

**Description**
This is a convenience function for producing a viewport with x- and/or y-scales based on numeric values passed to the function.

**Usage**

```r
dataViewport(xData = NULL, yData = NULL, xscale = NULL,
  yscale = NULL, extension = 0.05, ...)
```

**Arguments**

- **xData**  
  A numeric vector of data.

- **yData**  
  A numeric vector of data.

- **xscale**  
  A numeric vector (length 2).

- **yscale**  
  A numeric vector (length 2).

- **extension**  
  A numeric. If length greater than 1, then first value is used to extend the xscale and second value is used to extend the yscale.

- **...**  
  All other arguments will be passed to a call to the `viewport()` function.

**Details**

If `xscale` is not specified then the values in `x` are used to generate an x-scale based on the range of `x`, extended by the proportion specified in `extension`. Similarly for the y-scale.

**Value**

A grid viewport object.

**Author(s)**

Paul Murrell
**depth**  

*Determine the number of levels in an object.*

**Description**

Determine the number of levels in a viewport stack or tree, in a viewport path, or in a grob path.

**Usage**

```r
depth(x, ...)  
## S3 method for class 'viewport'
depth(x, ...)  
## S3 method for class 'path'
depth(x, ...)
```

**Arguments**

- `x` Typically a viewport or viewport stack or viewport tree or viewport list, or a viewport path, or a grob path.
- `...` Arguments used by other methods.

**Details**

Depths of paths are pretty straightforward because they contain no branchings. The depth of a viewport stack is the sum of the depths of the components of the stack. The depth of a viewport tree is the depth of the parent plus the depth of the children. The depth of a viewport list is the depth of the last component of the list.

**Value**

An integer value.

**See Also**

- `viewport`, `vpPath`, `gPath`.

**Examples**

```r
vp <- viewport()  
depth(vp)  
depth(vpStack(vp, vp))  
depth(vpList(vpStack(vp, vp), vp))  
depth(vpPath("vp"))  
depth(vpPath("vp1", "vp2"))
```
**deviceLoc**

*Convert Viewport Location to Device Location*

**Description**

These functions take a pair of unit objects and convert them to a pair of device locations (or dimensions) in inches (or native device coordinates).

**Usage**

```r
deviceLoc(x, y, valueOnly = FALSE, device = FALSE)
deviceDim(w, h, valueOnly = FALSE, device = FALSE)
```

**Arguments**

- `x, y, w, h` A unit object.
- `valueOnly` A logical indicating. If `TRUE` then the function does not return a unit object, but rather only the converted numeric values.
- `device` A logical indicating whether the returned values should be in inches or native device units.

**Details**

These functions differ from the functions like `convertX()` because they convert from the coordinate systems within a viewport to inches on the device (i.e., from one viewport to another) and because they only deal with pairs of values (locations or dimensions).

The functions like `convertX()` convert between different units within the same viewport and convert along a single dimension.

**Value**

A list with two components, both of which are unit object in inches (unless `valueOnly` is `TRUE` in which case both components are numeric).

**Warning**

The conversion is only valid for the current device size. If the device is resized then at least some conversions will become invalid.

Furthermore, the returned value only makes sense with respect to the entire device (i.e., within the context of the root viewport).

**Author(s)**

Paul Murrell

**See Also**

`unit`
Examples

```r
## A tautology
grid.newpage()
pushViewport(viewport())
deviceLoc(unit(1, "inches"), unit(1, "inches"))

## Something less obvious
grid.newpage()
pushViewport(viewport(width=.5, height=.5))
grid.rect()
x <- unit(1, "in")
y <- unit(1, "in")
grid.circle(x, y, r=unit(2, "mm"))
loc <- deviceLoc(x, y)
loc
upViewport()
grid.circle(loc$x, loc$y, r=unit(1, "mm"), gp=gpar(fill="black"))

## Something even less obvious
grid.newpage()
pushViewport(viewport(width=.5, height=.5, angle=30))
grid.rect()
x <- unit(.2, "npc")
y <- unit(2, "in")
grid.circle(x, y, r=unit(2, "mm"))
loc <- deviceLoc(x, y)
loc
upViewport()
grid.circle(loc$x, loc$y, r=unit(1, "mm"), gp=gpar(fill="black"))
```

drawDetails

Customising grid Drawing

Description

These generic hook functions are called whenever a grid grob is drawn. They provide an opportunity for customising the drawing of a new class derived from grob (or gTree).

Usage

```r
drawDetails(x, recording)
preDrawDetails(x)
postDrawDetails(x)
```

Arguments

- `x`: A grid grob.
- `recording`: A logical value indicating whether a grob is being added to the display list or redrawn from the display list.
NOTE: these functions have been largely superceded by the `makeContent` and `makeContext` functions, though they are still run and may still be useful in some contexts.

These functions are called by the `grid.draw` methods for grobs and gTrees. `preDrawDetails` is called first during the drawing of a grob. This is where any additional viewports should be pushed. Note that the default behaviour for grobs is to push any viewports in the `vp` slot, and for gTrees is to also push and up any viewports in the `childrenvp` slot so there is typically nothing to do here.

`drawDetails` is called next and is where any additional calculations and graphical output should occur. Note that the default behaviour for gTrees is to draw all grobs in the `children` slot so there is typically nothing to do here.

`postDrawDetails` is called last and should reverse anything done in `preDrawDetails` (i.e., pop or up any viewports that were pushed). Note that the default behaviour for grobs is to pop any viewports that were pushed so there is typically nothing to do here.

Note that `preDrawDetails` and `postDrawDetails` are also called in the calculation of "grobwidth" and "grobheight" units.

**Value**

None of these functions are expected to return a value.

**Author(s)**

Paul Murrell

**References**


**See Also**

`grid.draw` and `makeContent`

---

**editDetails**

**Customising grid Editing**

**Description**

This generic hook function is called whenever a grid grob is edited via `grid.edit` or `editGrob`. This provides an opportunity for customising the editing of a new class derived from grob (or gTree).

**Usage**

`editDetails(x, specs)`

**Arguments**

- `x`  
  A grid grob.

- `specs`  
  A list of named elements. The names indicate the grob slots to modify and the values are the new values for the slots.
Details

This function is called by grid.edit and editGrob. A method should be written for classes derived from grob or gTree if a change in a slot has an effect on other slots in the grob or children of a gTree (e.g., see grid:::editDetails.xaxis).

Note that the slot already has the new value.

Value

The function MUST return the modified grob.

Author(s)

Paul Murrell

See Also

grid.edit

editViewport

Modify a Viewport

Description

This is a convenience function for producing a new viewport from a copy of an existing viewport (by default the current viewport), with specified modifications.

Usage

editViewport(vp=current.viewport(), ...)

Arguments

vp A viewport object.
...
Modification of the viewport (should all be valid arguments to the viewport() function.

Value

A grid viewport object.

Author(s)

Paul Murrell

See Also

viewport.
**explode**  
*Explode a path into its components.*

**Description**

Explode a viewport path or grob path into its components.

**Usage**

```r
explode(x)
## S3 method for class 'character'
explode(x)
## S3 method for class 'path'
explode(x)
```

**Arguments**

- `x`: Typically a viewport path or a grob path, but a character vector containing zero or more path separators may also be given.

**Value**

A character vector.

**See Also**

`vpPath`, `gPath`.

**Examples**

```r
eexplode("vp1::vp2")
eexplode(vpPath("vp1", "vp2"))
```

---

**gEdit**  
*Create and Apply Edit Objects*

**Description**

The functions `gEdit` and `gEditList` create objects representing an edit operation (essentially a list of arguments to `editGrob`).

The functions `applyEdit` and `applyEdits` apply one or more edit operations to a graphical object. These functions are most useful for developers creating new graphical functions and objects.

**Usage**

```r
gEdit(...)  
gEditList(...)  
applyEdit(x, edit)  
applyEdits(x, edits)
```
**getNames**

**Arguments**

... one or more arguments to the `editGrob` function (for `gEdit`) or one or more "gEdit" objects (for `gEditList`).

`x` a grob (grid graphical object).

`edit` a "gEdit" object.

`edits` either a "gEdit" object or a "gEditList" object.

**Value**

`gEdit` returns an object of class "gEdit".

`gEditList` returns an object of class "gEditList".

`applyEdit` and `applyEditList` return the modified grob.

**Author(s)**

Paul Murrell

**See Also**

`grob` `editGrob`

**Examples**

```r
grid.rect(gp=gpar(col="red"))
# same thing, but more verbose
grid.draw(applyEdit(rectGrob(), gEdit(gp=gpar(col="red"))))
```

---

**getNames**

*List the names of grobs on the display list*

**Description**

Returns a character vector containing the names of all top-level grobs on the display list.

**Usage**

`getNames()`

**Value**

A character vector.

**Author(s)**

Paul Murrell

**Examples**

```r
grid.grill()
getNames()
```
Handling Grid Graphical Parameters

gpar() should be used to create a set of graphical parameter settings. It returns an object of class "gpar". This is basically a list of name-value pairs.
gpar() can be used to query the current graphical parameter settings.

Usage

gpar(...)  
get.gpar(names = NULL)

Arguments

... Any number of named arguments.
names A character vector of valid graphical parameter names.

Details

All grid viewports and (predefined) graphical objects have a slot called gp, which contains a "gpar" object. When a viewport is pushed onto the viewport stack and when a graphical object is drawn, the settings in the "gpar" object are enforced. In this way, the graphical output is modified by the gp settings until the graphical object has finished drawing, or until the viewport is popped off the viewport stack, or until some other viewport or graphical object is pushed or begins drawing.

The default parameter settings are defined by the ROOT viewport, which takes its settings from the graphics device. These defaults may differ between devices (e.g., the default fill setting is different for a PNG device compared to a PDF device).

Valid parameter names are:

col Colour for lines and borders.
fill Colour for filling rectangles, polygons, ...
alpha Alpha channel for transparency
lty Line type
lwd Line width
lex Multiplier applied to line width
lineend Line end style (round, butt, square)
linejoin Line join style (round, mitre, bevel)
linemitre Line mitre limit (number greater than 1)
fontsize The size of text (in points)
cex Multiplier applied to fontsize
fontfamily The font family
fontface The font face (bold, italic, ...)
lineheight The height of a line as a multiple of the size of text
font Font face (alias for fontface; for backward compatibility)

For more details of many of these, see the help for the corresponding graphical parameter par in base graphics. (This may have a slightly different name, e.g. lend, ljoin, lmitre, family.)
Colours can be specified in one of the forms returned by `rgb`, as a name (see `colors`) or as a non-negative integer index into the current `palette` (with zero being taken as transparent). (Negative integer values are now an error.)

The `alpha` setting is combined with the alpha channel for individual colours by multiplying (with both alpha settings normalised to the range 0 to 1).

The `fill` setting can also be a linear gradient or a radial gradient or a pattern (see `patterns`).

The size of text is `fontsize*cex`. The size of a line is `fontsize*cex*lineheight`.

The `cex` setting is cumulative; if a viewport is pushed with a `cex` of 0.5 then another viewport is pushed with a `cex` of 0.5, the effective `cex` is 0.25.

The `alpha` and `cex` settings are also cumulative.

Changes to the `fontfamily` may be ignored by some devices, but is supported by PostScript, PDF, X11, Windows, and Quartz. The `fontfamily` may be used to specify one of the Hershey Font families (e.g., `HersheySerif`) and this specification will be honoured on all devices.

The specification of `fontface` can be an integer or a string. If an integer, then it follows the R base graphics standard: 1 = plain, 2 = bold, 3 = italic, 4 = bold italic. If a string, then valid values are: "plain", "bold", "italic", "oblique", and "bold.italic". For the special case of the HersheySerif font family, "cyrillic", "cyrillic.oblique", and "EUC" are also available.

All parameter values can be vectors of multiple values. (This will not always make sense — for example, viewports will only take notice of the first parameter value.)

`get.gpar()` returns all current graphical parameter settings.

Value

An object of class "gpar".

Author(s)

Paul Murrell

See Also

`Hershey`.

Examples

gp <- get.gpar()
utils::str(gp)
#> These *do* nothing but produce a "gpar" object:
gpar(col = "red")
gpar(col = "blue", lty = "solid", lwd = 3, fontsize = 16)
get.gpar(c("col", "lty"))
grid.newpage()

vp <- viewport(width = .8, height = .8, gp = gpar(col="blue"))
grid.draw(gTree(children=gList(rectGrob(gp = gpar(col="red")),
       textGrob(paste("The rect is its own colour (red)
       "but this text is the colour",
       "set by the gTree (green)
       sep = "\n")
       ),
       gp = gpar(col="green"), vp = vp))
grid.text("This text is the colour set by the viewport (blue)",
       y = 1, just = c("center", "bottom"),
       gp = gpar(fontsize=20), vp = vp)
grid.newpage()
## example with multiple values for a parameter
pushViewport(viewport())
grid.points(1:10/11, 1:10/11, gp = gpar(col=1:10))
popViewport()

---

gPath

### Concatenate Grob Names

**Description**

This function can be used to generate a grob path for use in `grid.edit` and friends.
A grob path is a list of nested grob names.

**Usage**

gPath(...)

**Arguments**

... Character values which are grob names.

**Details**

Grob names must only be unique amongst grobs which share the same parent in a gTree.
This function can be used to generate a specification for a grob that includes the grob’s parent’s name (and the name of its parent and so on).
For interactive use, it is possible to directly specify a path, but it is strongly recommended that this function is used otherwise in case the path separator is changed in future versions of grid.

**Value**

A `gPath` object.

**See Also**

grob, editGrob, addGrob, removeGrob, getGrob, setGrob

**Examples**

gPath("g1", "g2")
Description

General information about the grid graphics package.

Details

Grid graphics provides an alternative to the standard R graphics. The user is able to define arbitrary rectangular regions (called viewports) on the graphics device and define a number of coordinate systems for each region. Drawing can be specified to occur in any viewport using any of the available coordinate systems.

Grid graphics and standard R graphics do not mix!

Type `library(help = grid)` to see a list of (public) Grid graphics functions.

Author(s)

Paul Murrell

See Also

`viewport`, `grid.layout`, and `unit`.

Examples

```r
## Diagram of a simple layout
grid.show.layout(grid.layout(4, 2,
    heights=unit(rep(1, 4),
        c("lines", "lines", "lines", "null")),
    widths=unit(c(1, 1), "inches")))
## Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
    width=unit(1, "inches"), height=unit(1, "inches")))
## A flash plotting example
grid.multipanel(vp=viewport(0.5, 0.5, 0.8, 0.8))
```

Grid Viewports

Create a Grid Viewport

Description

These functions create viewports, which describe rectangular regions on a graphics device and define a number of coordinate systems within those regions.
Grid Viewports

Usage

viewport(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
width = unit(1, "npc"), height = unit(1, "npc"),
default.units = "npc", just = "centre",
gp = gpar(), clip = "inherit", mask = "inherit",
yscale = c(0, 1), xscale = c(0, 1),
age = 0,
layout = NULL,
layout.pos.row = NULL, layout.pos.col = NULL,
name = NULL)

vpList(...)
vpStack(...)
vpTree(parent, children)

Arguments

x A numeric vector or unit object specifying x-location.
y A numeric vector or unit object specifying y-location.
width A numeric vector or unit object specifying width.
height A numeric vector or unit object specifying height.
default.units A string indicating the default units to use if x, y, width, or height are only
given as numeric vectors.
just A string or numeric vector specifying the justification of the viewport relative
to its (x, y) location. If there are two values, the first value specifies horizontal
justification and the second value specifies vertical justification. Possible string
values are: "left", "right", "centre", "center", "bottom", and "top". For
numeric values, 0 means left alignment and 1 means right alignment.
gp An object of class "gpar", typically the output from a call to the function gpar.
This is basically a list of graphical parameter settings.
clip One of "on", "inherit", or "off", indicating whether to clip to the extent of
this viewport, inherit the clipping region from the parent viewport, or turn clipping
off altogether. For back-compatibility, a logical value of TRUE corresponds
to "on" and FALSE corresponds to "inherit".
May also be a grob (or a gTree) that describes a clipping path or the result of a
call to as.path.
mask One of "none" (or FALSE) or "inherit" (or TRUE) or a grob (or a gTree) or the
result of call to as.mask. This specifies that the viewport should have no mask,
or it should inherit the mask of its parent, or it should have its own mask, as
described by the grob.
xscale A numeric vector of length two indicating the minimum and maximum on the
x-scale. The limits may not be identical.
yscale A numeric vector of length two indicating the minimum and maximum on the
y-scale. The limits may not be identical.
age A numeric value indicating the angle of rotation of the viewport. Positive values
indicate the amount of rotation, in degrees, anticlockwise from the positive x-
axis.
layout A Grid layout object which splits the viewport into subregions.
layout.pos.row A numeric vector giving the rows occupied by this viewport in its parent’s lay-
out.
Grid Viewports

layout.pos.col A numeric vector giving the columns occupied by this viewport in its parent’s layout.
name A character value to uniquely identify the viewport once it has been pushed onto the viewport tree.
... Any number of grid viewport objects.
parent A grid viewport object.
children A vpList object.

Details

The location and size of a viewport are relative to the coordinate systems defined by the viewport’s parent (either a graphical device or another viewport). The location and size can be specified in a very flexible way by specifying them with unit objects. When specifying the location of a viewport, specifying both layout.pos.row and layout.pos.col as NULL indicates that the viewport ignores its parent’s layout and specifies its own location and size (via its locn). If only one of layout.pos.row and layout.pos.col is NULL, this means occupy ALL of the appropriate row(s)/column(s). For example, layout.pos.row = 1 and layout.pos.col = NULL means occupy all of row 1. Specifying non-NULL values for both layout.pos.row and layout.pos.col means occupy the intersection of the appropriate rows and columns. If a vector of length two is specified for layout.pos.row or layout.pos.col, this indicates a range of rows or columns to occupy. For example, layout.pos.row = c(1, 3) and layout.pos.col = c(2, 4) means occupy cells in the intersection of rows 1, 2, and 3, and columns, 2, 3, and 4.

Clipping obeys only the most recent viewport clip setting. For example, if you clip to viewport1, then clip to viewport2, the clipping region is determined wholly by viewport2, the size and shape of viewport1 is irrelevant (until viewport2 is popped of course).

If a viewport is rotated (because of its own angle setting or because it is within another viewport which is rotated) then the clip flag is ignored.

If clip is a grob, then that grob (which may be more than one shape) defines a clipping path. The function as.path may be used to specify a fill rule for the path.

Viewport names need not be unique. When pushed, viewports sharing the same parent must have unique names, which means that if you push a viewport with the same name as an existing viewport, the existing viewport will be replaced in the viewport tree. A viewport name can be any string, but grid uses the reserved name "ROOT" for the top-level viewport. Also, when specifying a viewport name in downViewport and seekViewport, it is possible to provide a viewport path, which consists of several names concatenated using the separator (currently ::). Consequently, it is not advisable to use this separator in viewport names.

The viewports in a vpList are pushed in parallel. The viewports in a vpStack are pushed in series. When a vpTree is pushed, the parent is pushed first, then the children are pushed in parallel.

Value

An R object of class viewport.

Author(s)

Paul Murrell

See Also

Grid, pushViewport, popViewport, downViewport, seekViewport, upViewport, unit, grid.layout, grid.show.layout.
Examples

# Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
    width=unit(1, "inches"), height=unit(1, "inches")))

# Demonstrate viewport clipping
clip.demo <- function(i, j, clip1, clip2) {
  pushViewport(viewport(layout.pos.col=i,
    layout.pos.row=j))
  pushViewport(viewport(width=0.6, height=0.6, clip=clip1))
  grid.rect(gp=gpar(fill="white"))
  grid.circle(r=0.55, gp=gpar(col="red", fill="pink"))
  popViewport()
  pushViewport(viewport(width=0.6, height=0.6, clip=clip2))
  grid.polygons(x=c(0.5, 1.1, 0.6, 1.1, 0.5, -0.1, 0.4, -0.1),
    y=c(0.6, 1.1, 0.5, -0.1, 0.4, -0.1, 0.5, 1.1),
    gp=gpar(col="blue", fill="light blue"))
  popViewport(2)
}

grid.newpage()
grid.rect(gp=gpar(fill="grey"))
pushViewport(viewport(layout=grid.layout(2, 2)))
clip.demo(1, 1, FALSE, FALSE)
clip.demo(1, 2, TRUE, FALSE)
clip.demo(2, 1, FALSE, TRUE)
clip.demo(2, 2, TRUE, TRUE)
popViewport()

# Demonstrate turning clipping off
grid.newpage()
pushViewport(viewport(width=.5, height=.5, clip="on"))
grid.rect()
grid.circle(r=.6, gp=gpar(lwd=10))
pushViewport(viewport(clip="inherit"))
grid.circle(r=.6, gp=gpar(lwd=5, col="grey"))
pushViewport(viewport(clip="off"))
grid.circle(r=.6)
popViewport(3)

# Demonstrate vpList, vpStack, and vpTree
grid.newpage()
tree <- vpTree(viewport(width=0.8, height=0.8, name="A"),
    vpList(vpStack(viewport(x=0.1, y=0.1, width=0.5, height=0.5,
        just=c("left", "bottom"), name="B"),
        viewport(x=0.1, y=0.1, width=0.5, height=0.5,
        just=c("left", "bottom"), name="C"),
        viewport(x=0.1, y=0.1, width=0.5, height=0.5,
        just=c("left", "bottom"), name="D")),
        viewport(x=0.5, width=0.4, height=0.9,
        just="left", name="E")))

pushViewport(tree)
for (i in LETTERS[1:5]) {
  seekViewport(i)
  grid.rect()
  grid.text(current.vpTree(FALSE),
    x=unit(1, "mm"), y=unit(1, "npc") - unit(1, "mm"),
    just=c("left", "top"),
    gp=gpar(fontsize=8))
grid.add

Add a Grid Graphical Object

Description

Add a grob to a gTree or a descendant of a gTree.

Usage

grid.add(gPath, child, strict = FALSE, grep = FALSE, global = FALSE, allDevices = FALSE, redraw = TRUE)

addGrob(gTree, child, gPath = NULL, strict = FALSE, grep = FALSE, global = FALSE, warn = TRUE)

setChildren(x, children)

Arguments

gTree, x A gTree object.
gPath A gPath object. For grid.add this specifies a gTree on the display list. For addGrob this specifies a descendant of the specified gTree.
child A grob object.
children A gList object.
strict A boolean indicating whether the gPath must be matched exactly.
grep A boolean indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., c(TRUE, FALSE) means that every odd element of the gPath will be treated as a regular expression).
global A boolean indicating whether the function should affect just the first match of the gPath, or whether all matches should be affected.
warn A logical to indicate whether failing to find the specified gPath should trigger an error.
allDevices A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
redraw A logical value to indicate whether to redraw the grob.

Details

addGrob copies the specified grob and returns a modified grob.

grid.add destructively modifies a grob on the display list. If redraw is TRUE it then redraws everything to reflect the change.

setChildren is a basic function for setting all children of a gTree at once (instead of repeated calls to addGrob).
Value

addGrob returns a grob object; grid.add returns NULL.

Author(s)

Paul Murrell

See Also

grob, getGrob, addGrob, removeGrob.

---

grid.bezier  
**Draw a Bezier Curve**

Description

These functions create and draw Bezier Curves (a curve drawn relative to 4 control points).

Usage

```r
grid.bezier(...)  
bezierGrob(x = c(0, 0.5, 1, 0.5), y = c(0.5, 1, 0.5, 0),  
id = NULL, id.lengths = NULL,  
default.units = "npc", arrow = NULL,  
name = NULL, gp = gpar(), vp = NULL)
```

Arguments

- **x**  
  A numeric vector or unit object specifying x-locations of spline control points.
- **y**  
  A numeric vector or unit object specifying y-locations of spline control points.
- **id**  
  A numeric vector used to separate locations in `x` and `y` into multiple beziers. All locations with the same `id` belong to the same bezier.
- **id.lengths**  
  A numeric vector used to separate locations in `x` and `y` into multiple beziers. Specifies consecutive blocks of locations which make up separate beziers.
- **default.units**  
  A string indicating the default units to use if `x` or `y` are only given as numeric vectors.
- **arrow**  
  A list describing arrow heads to place at either end of the bezier, as produced by the `arrow` function.
- **name**  
  A character identifier.
- **gp**  
  An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- **vp**  
  A Grid viewport object (or NULL).
- **...**  
  Arguments to be passed to `bezierGrob`. 
Details

Both functions create a beziergrob (a graphical object describing a Bezier curve), but only grid.bezier draws the Bezier curve.

A Bezier curve is a line drawn relative to 4 control points.

Missing values are not allowed for x and y (i.e., it is not valid for a control point to be missing).

The curve is currently drawn using an approximation based on X-splines.

Value

A grob object.

See Also

Grid, viewport, arrow.
grid.xspline.

Examples

```r
x <- c(0.2, 0.2, 0.4, 0.4)
y <- c(0.2, 0.4, 0.4, 0.2)

grid.newpage()
grid.bezier(x, y)
grid.bezier(c(x, x + .4), c(y + .4, y + .4),
           id=rep(1:2, each=4))
grid.segments(.4, .6, .6, .6)
grid.bezier(x, y,
            gp=gpar(lwd=3, fill="black"),
            arrow=arrow(type="closed"),
            vp=viewport(x=.9))
```

grid.cap

Capture a raster image

Description

Capture the current contents of a graphics device as a raster (bitmap) image.

Usage

grid.cap()

Details

This function is only implemented for on-screen graphics devices.

Value

A matrix of R colour names, or NULL if not available.
grid.circle

Draw a Circle

Description
Functions to create and draw a circle.

Usage
grid.circle(x=0.5, y=0.5, r=0.5, default.units="npc", name=NULL, gp=gpar(), draw=TRUE, vp=NULL)
circleGrob(x=0.5, y=0.5, r=0.5, default.units="npc", name=NULL, gp=gpar(), vp=NULL)

Arguments
x A numeric vector or unit object specifying x-locations.
y A numeric vector or unit object specifying y-locations.
r A numeric vector or unit object specifying radii.
default.units A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
name A character identifier.
gp An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw A logical value indicating whether graphics output should be produced.
vp A Grid viewport object (or NULL).
Both functions create a circle grob (a graphical object describing a circle), but only `grid.circle()` draws the circle (and then only if `draw` is `TRUE`).

The radius may be given in any units; if the units are `relative` (e.g., "npc" or "native") then the radius will be different depending on whether it is interpreted as a width or as a height. In such cases, the smaller of these two values will be the result. To see the effect, type `grid.circle()` and adjust the size of the window.

What happens for very small radii is device-dependent: the circle may become invisible or be shown at a fixed minimum size. Circles of zero radius will not be plotted.

A circle grob. `grid.circle()` returns the value invisibly.

Negative values for the radius are silently converted to their absolute value.

Paul Murrell

These functions set the clipping region within the current viewport without altering the current coordinate system.

`grid.clip(...)`

- `x`: A numeric vector or unit object specifying x-location.
- `y`: A numeric vector or unit object specifying y-location.
- `width`: A numeric vector or unit object specifying width.
- `height`: A numeric vector or unit object specifying height.
The justification of the clip rectangle relative to its (x, y) location. If there are
two values, the first value specifies horizontal justification and the second value
specifies vertical justification. Possible string values are: "left", "right",
"centre", "center", "bottom", and "top". For numeric values, 0 means left
alignment and 1 means right alignment.

A numeric vector specifying horizontal justification. If specified, overrides the
just setting.

A numeric vector specifying vertical justification. If specified, overrides the
just setting.

A string indicating the default units to use if x, y, width, or height are only
given as numeric vectors.

A character identifier.

A Grid viewport object (or NULL).

Arguments passed to clipGrob.

Both functions create a clip rectangle (a graphical object describing a clip rectangle), but only
grid.clip enforces the clipping.

Pushing or popping a viewport always overrides the clip region set by a clip grob, regardless of
whether that viewport explicitly enforces a clipping region.

clipGrob returns a clip grob.

Paul Murrell

Grid, viewport

Examples

# draw across entire viewport, but clipped
grid.clip(x = 0.3, width = 0.1)
grid.lines(gp=gpar(col="green", lwd=5))
# draw across entire viewport, but clipped (in different place)
grid.clip(x = 0.7, width = 0.1)
grid.lines(gp=gpar(col="red", lwd=5))
# Viewport sets new clip region
pushViewport(viewport(width=0.5, height=0.5, clip=TRUE))
grid.lines(gp=gpar(col="grey", lwd=3))
# Return to original viewport; get
# clip region from previous grid.clip()
# (NOT from previous viewport clip region)
popViewport()
grid.lines(gp=gpar(col="black"))
Convert Between Different grid Coordinate Systems

Description

These functions take a unit object and convert it to an equivalent unit object in a different coordinate system.

Usage

convertX(x, unitTo, valueOnly = FALSE)
convertY(x, unitTo, valueOnly = FALSE)
convertWidth(x, unitTo, valueOnly = FALSE)
convertHeight(x, unitTo, valueOnly = FALSE)
convertUnit(x, unitTo, 
    axisFrom = "x", typeFrom = "location",
    axisTo = axisFrom, typeTo = typeFrom,
    valueOnly = FALSE)

Arguments

x A unit object.
unitTo The coordinate system to convert the unit to. See the `unit` function for valid coordinate systems.
axisFrom Either "x" or "y" to indicate whether the unit object represents a value in the x- or y-direction.
typeFrom Either "location" or "dimension" to indicate whether the unit object represents a location or a length.
axisTo Same as `axisFrom`, but applies to the unit object that is to be created.
typeTo Same as `typeFrom`, but applies to the unit object that is to be created.
valueOnly A logical indicating. If TRUE then the function does not return a unit object, but rather only the converted numeric values.

Details

The `convertUnit` function allows for general-purpose conversions. The other four functions are just more convenient front-ends to it for the most common conversions.

The conversions occur within the current viewport.

It is not currently possible to convert to all valid coordinate systems (e.g., "strwidth" or "grob-width"). I'm not sure if all of these are impossible, they just seem implausible at this stage.

In normal usage of grid, these functions should not be necessary. If you want to express a location or dimension in inches rather than user coordinates then you should simply do something like `unit(1, "inches")` rather than something like `unit(0.134, "native").

In some cases, however, it is necessary for the user to perform calculations on a unit value and this function becomes necessary. In such cases, please take note of the warning below.
Value
A unit object in the specified coordinate system (unless valueOnly is TRUE in which case the returned value is a numeric).

Warning
The conversion is only valid for the current device size. If the device is resized then at least some conversions will become invalid. For example, suppose that I create a unit object as follows: oneinch <- convertUnit(unit(1, "inches"), "native"). Now if I resize the device, the unit object in oneinch no longer corresponds to a physical length of 1 inch.

Author(s)
Paul Murrell

See Also
unit

Examples
## A tautology
convertX(unit(1, "inches"), "inches")
## The physical units
convertX(unit(2.54, "cm"), "inches")
convertX(unit(25.4, "mm"), "inches")
convertX(unit(72.27, "points"), "inches")
convertX(unit(1/12*72.27, "picas"), "inches")
convertX(unit(72, "bigpts"), "inches")
convertX(unit(1157/1238*72.27, "dida"), "inches")
convertX(unit(1157/1238*72.27, "cicero"), "inches")
convertX(unit(65536*72.27, "scaledpts"), "inches")
convertX(unit(1/2.54, "inches"), "cm")
convertX(unit(1/25.4, "inches"), "mm")
convertX(unit(1/72.27, "inches"), "points")
convertX(unit(1/(1/12*72.27), "inches"), "picas")
convertX(unit(1/72, "inches"), "bigpts")
convertX(unit(1/(1157/1238*72.27), "dida"), "inches")
convertX(unit(1/(1157/1238*72.27), "cicero"), "inches")
convertX(unit(1/(65536*72.27), "scaledpts"), "inches")

pushViewport(viewport(width=unit(1, "inches"),
                     height=unit(2, "inches"),
                     xscale=c(0, 1),
                     yscale=c(1, 3)))
## Location versus dimension
convertY(unit(2, "native"), "inches")
convertHeight(unit(2, "native"), "inches")
## From "x" to "y" (the conversion is via "inches")
convertUnit(unit(1, "native"), "native",
            axisFrom="x", axisTo="y")
## Convert several values at once
convertX(unit(c(0.5, 2.54), c("npc", "cm")),
         c("inches", "native"))
popViewport()
## Convert a complex unit
grid.copy

Make a Copy of a Grid Graphical Object

Description

This function is redundant and will disappear in future versions.

Usage

grid.copy(grob)

Arguments

grob  A grob object.

Value

A copy of the grob object.

Author(s)

Paul Murrell

See Also

grid.grob.

grid.curve  Draw a Curve Between Locations

Description

These functions create and draw a curve from one location to another.

Usage

grid.curve(...)  
curveGrob(x1, y1, x2, y2, default.units = "npc",  
  curvature = 1, angle = 90, ncp = 1, shape = 0.5,  
  square = TRUE, squareShape = 1,  
  inflect = FALSE, arrow = NULL, open = TRUE,  
  debug = FALSE,  
  name = NULL, gp = gpar(), vp = NULL)  
arcCurvature(theta)
Arguments

- **x1**: A numeric vector or unit object specifying the x-location of the start point.
- **y1**: A numeric vector or unit object specifying the y-location of the start point.
- **x2**: A numeric vector or unit object specifying the x-location of the end point.
- **y2**: A numeric vector or unit object specifying the y-location of the end point.
- **default.units**: A string indicating the default units to use if x1, y1, x2 or y2 are only given as numeric values.
- **curvature**: A numeric value giving the amount of curvature. Negative values produce left-hand curves, positive values produce right-hand curves, and zero produces a straight line.
- **angle**: A numeric value between 0 and 180, giving an amount to skew the control points of the curve. Values less than 90 skew the curve towards the start point and values greater than 90 skew the curve towards the end point.
- **ncp**: The number of control points used to draw the curve. More control points creates a smoother curve.
- **shape**: A numeric vector of values between -1 and 1, which control the shape of the curve relative to its control points. See `grid.xspline` for more details.
- **square**: A logical value that controls whether control points for the curve are created city-block fashion or obliquely. When ncp is 1 and angle is 90, this is typically TRUE, otherwise this should probably be set to FALSE (see Examples below).
- **squareShape**: A shape value to control the behaviour of the curve relative to any additional control point that is inserted if square is TRUE.
- **inflect**: A logical value specifying whether the curve should be cut in half and inverted (see Examples below).
- **arrow**: A list describing arrow heads to place at either end of the curve, as produced by the arrow function.
- **open**: A logical value indicating whether to close the curve (connect the start and end points).
- **debug**: A logical value indicating whether debugging information should be drawn.
- **name**: A character identifier.
- **gp**: An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- **vp**: A Grid viewport object (or NULL).
- **...**: Arguments to be passed to `curveGrob`.
- **theta**: An angle (in degrees).

Details

Both functions create a curve grob (a graphical object describing an curve), but only `grid.curve` draws the curve.

The `arcCurvature` function can be used to calculate a curvature such that control points are generated on an arc corresponding to angle theta. This is typically used in conjunction with a large ncp to produce a curve corresponding to the desired arc.

Value

A grob object.
grid.delay

See Also
Grid, viewport, grid.xspline, arrow

Examples

```r
curveTest <- function(i, j, ...) {
  pushViewport(viewport(layout.pos.col=j, layout.pos.row=i))
  do.call("grid.curve", c(list(x1=.25, y1=.25, x2=.75, y2=.75), list(...)))
  grid.text(sub("list\((.*)\)", \1",
              deparse(substitute(list(...))),
              y=unit(1, "npc"))
  popViewport()
}
# grid.newpage()
pushViewport(plotViewport(c(0, 0, 1, 0),
                         layout=grid.layout(2, 1, heights=c(2, 1))))
pushViewport(viewport(layout.pos.row=1,
                         layout=grid.layout(3, 3, respect=TRUE)))
  curveTest(1, 1)
curveTest(1, 2, inflect=TRUE)
curveTest(1, 3, angle=135)
curveTest(2, 1, arrow=arrow())
curveTest(2, 2, ncp=8)
curveTest(2, 3, shape=0)
curveTest(3, 1, curvature=-1)
curveTest(3, 2, square=FALSE)
curveTest(3, 3, debug=TRUE)
  popViewport()
pushViewport(viewport(layout.pos.row=2,
                         layout=grid.layout(3, 3)))
  curveTest(1, 1)
curveTest(1, 2, inflect=TRUE)
curveTest(1, 3, angle=135)
curveTest(2, 1, arrow=arrow())
curveTest(2, 2, ncp=8)
curveTest(2, 3, shape=0)
curveTest(3, 1, curvature=-1)
curveTest(3, 2, square=FALSE)
curveTest(3, 3, debug=TRUE)
  popViewport(2)
```

grid.delay

Encapsulate calculations and generating a grob

Description

Evaluates an expression that includes both calculations and generating a grob that depends on the calculations so that both the calculations and the grob generation will be rerun when the scene is redrawn (e.g., device resize or editing).

Intended only for expert use.

Usage

delayGrob(expr, list, name=NULL, gp=NULL, vp=NULL)
grid.delay(expr, list, name=NULL, gp=NULL, vp=NULL)
grid.display.list

Control the Grid Display List

Description

Turn the Grid display list on or off.

Usage

grid.display.list(on=TRUE)
engine.display.list(on=TRUE)
Arguments

on
A logical value to indicate whether the display list should be on or off.

Details

All drawing and viewport-setting operations are (by default) recorded in the Grid display list. This allows redrawing to occur following an editing operation.

This display list could get very large so it may be useful to turn it off in some cases; this will of course disable redrawing.

All graphics output is also recorded on the main display list of the R graphics engine (by default). This supports redrawing following a device resize and allows copying between devices.

Turning off this display list means that grid will redraw from its own display list for device resizes and copies. This will be slower than using the graphics engine display list.

Value

None.

WARNING

Turning the display list on causes the display list to be erased!

Turning off both the grid display list and the graphics engine display list will result in no redrawing whatsoever.

Author(s)

Paul Murrell

grid.DLapply

Modify the Grid Display List

Description

Call a function on each element of the current display list.

Usage

grid.DLapply(FUN, ...)

Arguments

FUN
A function; the first argument to this function is passed each element of the display list.

... Further arguments to pass to FUN.
This function is insanely dangerous for the grid display list. Two token efforts are made to try to avoid ending up with complete garbage on the display list:

1. The display list is only replaced once all new elements have been generated (so an error during generation does not result in a half-finished display list).
2. All new elements must be either NULL or inherit from the class of the element that they are replacing.

The side effect of these functions is usually to modify the grid display list.

grid.newpage()
grid.rect(width=.4, height=.4, x=.25, y=.75, gp=gpar(fill="black"), name="r1")
grid.rect(width=.4, height=.4, x=.5, y=.5, gp=gpar(fill="grey"), name="r2")
grid.rect(width=.4, height=.4, x=.75, y=.25, gp=gpar(fill="white"), name="r3")
grid.DLapply(function(x) { if (is.grob(x)) x$gp <- gpar(); x })
grid.refresh()
**Value**

None.

**Author(s)**

Paul Murrell

**See Also**

grob.

**Examples**

grid.newpage()
## Create a graphical object, but don’t draw it
l <- linesGrob()
## Draw it
grid.draw(l)

---

**grid.edit**

*Edit the Description of a Grid Graphical Object*

**Description**

Changes the value of one of the slots of a grob and redraws the grob.

**Usage**

```r
grid.edit(gPath, ..., strict = FALSE, grep = FALSE,
          global = FALSE, allDevices = FALSE, redraw = TRUE)
```

```r
grid.gedit(..., grep = TRUE, global = TRUE)
```

```r
editGrob(grob, gPath = NULL, ..., strict = FALSE, grep = FALSE,
         global = FALSE, warn = TRUE)
```

**Arguments**

- `grob` A grob object.
- `...` Zero or more named arguments specifying new slot values.
- `gPath` A gPath object. For `grid.edit` this specifies a grob on the display list. For `editGrob` this specifies a descendant of the specified grob.
- `strict` A boolean indicating whether the `gPath` must be matched exactly.
- `grep` A boolean indicating whether the `gPath` should be treated as a regular expression. Values are recycled across elements of the `gPath` (e.g., `c(TRUE, FALSE)` means that every odd element of the `gPath` will be treated as a regular expression).
- `global` A boolean indicating whether the function should affect just the first match of the `gPath`, or whether all matches should be affected.
### grid.force

**Description**

Some grobs only generate their content to draw at drawing time; this function replaces such grobs with their at-drawing-time content.

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>warn</td>
<td>A logical to indicate whether failing to find the specified gPath should trigger an error.</td>
</tr>
<tr>
<td>allDevices</td>
<td>A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.</td>
</tr>
<tr>
<td>redraw</td>
<td>A logical value to indicate whether to redraw the grob.</td>
</tr>
</tbody>
</table>

### Details

- `editGrob` copies the specified grob and returns a modified grob.
- `grid.edit` destructively modifies a grob on the display list. If `redraw` is `TRUE` it then redraws everything to reflect the change.

Both functions call `editDetails` to allow a grob to perform custom actions and `validDetails` to check that the modified grob is still coherent.

`grid.gedit (g for global)` is just a convenience wrapper for `grid.edit` with different defaults.

### Value

- `editGrob` returns a grob object; `grid.edit` returns `NULL`.

### Author(s)

Paul Murrell

### See Also

`grob`, `getGrob`, `addGrob`, `removeGrob`.

### Examples

```r
grid.newpage()
grid.xaxis(name = "xa", vp = viewport(width=.5, height=.5))
grid.edit("xa", gp = gpar(col="red"))
# won't work because no ticks (at is NULL)
try(grid.edit(gPath("xa", "ticks"), gp = gpar(col="green")))
grid.edit("xa", at = 1:4/5)
# Now it should work
try(grid.edit(gPath("xa", "ticks"), gp = gpar(col="green")))
```
grid.force

Usage

grid.force(x, ...)  
## Default S3 method: 
grid.force(x, redraw = FALSE, ...)  
## S3 method for class 'gPath' 
grid.force(x, strict = FALSE, grep = FALSE, global = FALSE, 
redraw = FALSE, ...)  
## S3 method for class 'grob' 
grid.force(x, draw = FALSE, ...)  
forceGrob(x)  
grid.revert(x, ...)  
## S3 method for class 'gPath' 
grid.revert(x, strict = FALSE, grep = FALSE, global = FALSE, 
redraw = FALSE, ...)  
## S3 method for class 'grob' 
grid.revert(x, draw = FALSE, ...)

Arguments

x For the default method, x should not be specified. Otherwise, x should be a grob or a gPath. If x is character, it is assumed to be a gPath.
strict A boolean indicating whether the path must be matched exactly.
grep Whether the path should be treated as a regular expression.
global A boolean indicating whether the function should affect just the first match of the path, or whether all matches should be affected.
draw logical value indicating whether a grob should be drawn after it is forced.
redraw logical value indicating whether to redraw the grid scene after the forcing operation.
... Further arguments for use by methods.

Details

Some grobs wait until drawing time to generate what content will actually be drawn (an axis, as produced by grid.xaxis(), with an at or NULL is a good example because it has to see what viewport it is going to be drawn in before it can decide what tick marks to draw).

The content of such grobs (e.g., the tick marks) are not usually visible to grid.ls() or accessible to grid.edit().

The grid.force() function replaces a grob with its at-drawing-time contents. For example, an axis will be replaced by a vanilla gTree with lines and text representing the axis tick marks that were actually drawn. This makes the tick marks visible to grid.ls() and accessible to grid.edit().

The forceGrob() function is the internal work horse for grid.force(), so will not normally be called directly by the user. It is exported so that methods can be written for custom grob classes if necessary.

The grid.revert() function reverses the effect of grid.force(), replacing forced content with the original grob.

Warning

Forcing an explicit grob produces a result as if the grob were drawn in the current drawing context. It may not make sense to draw the result in a different drawing context.
grid.frame

Create a Frame for Packing Objects

Description

These functions, together with grid.pack, grid.place, packGrob, and placeGrob are part of a GUI-builder-like interface to constructing graphical images. The idea is that you create a frame with this function then use grid.pack or whatever to pack/place objects into the frame.

Usage

grid.frame(layout=NULL, name=NULL, gp=gpar(), vp=NULL, draw=TRUE)
frameGrob(layout=NULL, name=NULL, gp=gpar(), vp=NULL)
**grid.function**

**Draw a curve representing a function**

**Description**

Draw a curve representing a function.

**Usage**

```r
grid.function(...) functionGrob(f, n = 101, range = "x", units = "native", name = NULL, gp=gpar(), vp = NULL)
grid.abline(intercept, slope, ...)```

**Arguments**

- **layout**: A Grid layout, or NULL. This can be used to initialise the frame with a number of rows and columns, with initial widths and heights, etc.
- **name**: A character identifier.
- **vp**: An object of class `viewport`, or NULL.
- **gp**: An object of class "gpar"; typically the output from a call to the function `gpar`.
- **draw**: Should the frame be drawn.

**Details**

Both functions create a frame grob (a graphical object describing a frame), but only `grid.frame()` draws the frame (and then only if `draw` is TRUE). Nothing will actually be drawn, but it will put the frame on the display list, which means that the output will be dynamically updated as objects are packed into the frame. Possibly useful for debugging.

**Value**

A frame grob. `grid.frame()` returns the value invisibly.

**Author(s)**

Paul Murrell

**See Also**

`grid.pack`

**Examples**

```r
grid.newpage()
grid.frame(name="gf", draw=TRUE)
grid.pack("gf", rectGrob(gp=gpar(fill="grey")), width=unit(1, "null"))
grid.pack("gf", textGrob("hi there"), side="right")
```
grid.function

Arguments

- **f**: A function that must take a single argument and return a list with two numeric components named `x` and `y`.
- **n**: The number values that will be generated as input to the function `f`.
- **range**: Either "x", "y", or a numeric vector. See the 'Details' section.
- **units**: A string indicating the units to use for the `x` and `y` values generated by the function.
- **intercept**: Numeric.
- **slope**: Numeric.
- **...**: Arguments passed to `grid.function()`.
- **name**: A character identifier.
- **gp**: An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- **vp**: A Grid viewport object (or NULL).

Details

`n` values are generated and passed to the function `f` and a series of lines are drawn through the resulting `x` and `y` values.

The generation of the `n` values depends on the value of `range`. In the default case, `dim` is "x", which means that a set of `x` values are generated covering the range of the current viewport scale in the `x`-dimension. If `dim` is "y" then values are generated from the current `y`-scale instead. If `range` is a numeric vector, then values are generated from that range.

`grid.abline()` provides a simple front-end for a straight line parameterized by `intercept` and `slope`.

Value

A function grob.

Author(s)

Paul Murrell

See Also

Grid, viewport

Examples

```r
# abline
# NOTE: in ROOT viewport on screen, (0, 0) at top-left
# and "native" is pixels!
grid.function(function(x) list(x=x, y=0 + 1*x))
# a more "normal" viewport with default normalized "native" coords
grid.newpage()
pushViewport(viewport())
grid.function(function(x) list(x=x, y=0 + 1*x))
# slightly simpler
grid.newpage()
```
pushViewport(viewport())
g.grid.abline()
# sine curve
g.grid.newpage()
pushViewport(viewport(xscale=c(0, 2*pi), yscale=c(-1, 1)))
g.grid.function(function(x) list(x=x, y=sin(x)))
# constrained sine curve
g.grid.newpage()
pushViewport(viewport(xscale=c(0, 2*pi), yscale=c(-1, 1)))
g.grid.function(function(x) list(x=x, y=sin(x)), range=0:1)
# inverse sine curve
g.grid.newpage()
pushViewport(viewport(xscale=c(-1, 1), yscale=c(0, 2*pi)))
g.grid.function(function(y) list(x=sin(y), y=y), range="y")
# parametric function
g.grid.newpage()
pushViewport(viewport(xscale=c(-1, 1), yscale=c(-1, 1)))
g.grid.function(function(t) list(x=cos(t), y=sin(t)), range=c(0, 9*pi/5))
# physical abline
g.grid.newpage()
g.grid.function(function(x) list(x=x, y=0 + 1*x), units="in")

---

**grid.get**

*Get a Grid Graphical Object*

**Description**

Retrieve a grob or a descendant of a grob.

**Usage**

```r
g.grid.get(gPath, strict = FALSE, grep = FALSE, global = FALSE, allDevices = FALSE)
g.grid.gget(..., grep = TRUE, global = TRUE)
getGrob(gTree, gPath, strict = FALSE, grep = FALSE, global = FALSE)
```

**Arguments**

- **gTree**: A gTree object.
- **gPath**: A gPath object. For `grid.get` this specifies a grob on the display list. For `getGrob` this specifies a descendant of the specified gTree.
- **strict**: A boolean indicating whether the gPath must be matched exactly.
- **grep**: A boolean indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., `c(TRUE, FALSE)` means that every odd element of the gPath will be treated as a regular expression).
grid.glyph

grid.glyph(...)
glyphGrob(glyphInfo,
    x=.5, y=.5, default.units="npc",
    hjust="centre", vjust="centre",
    gp=gpar(), vp=NULL, name=NULL)

Description

These functions create and draw a set of typeset glyphs.

Usage

grid.glyph(...)
glyphGrob(glyphInfo,
    x=.5, y=.5, default.units="npc",
    hjust="centre", vjust="centre",
    gp=gpar(), vp=NULL, name=NULL)
grid.grab

Arguments

glyphInfo An "RGlyphInfo" object from a call to `glyphInfo`.

x A numeric vector or unit object specifying x-location.

y A numeric vector or unit object specifying y-location.

default.units A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.

hjust, vjust The justification of the glyphs relative to the (x, y) location. Can be character (e.g., "left"), numeric (e.g., 0), or the result of a call to `glyphJust`.

name A character identifier.

gp An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.

vp A Grid viewport object (or NULL).

... Arguments passed to `glyphGrob()`.

Details

Both functions create a glyph grob (a graphical object describing glyphs), but only `grid.glyph` draws the glyphs.

Value

A glyph grob.

Author(s)

Paul Murrell

See Also

Grid, `glyphInfo`

Description

`grid.grab` Grab the current grid output

Creates a gTree object from the current grid display list or from a scene generated by user-specified code.

Usage

`grid.grab(warn = 2, wrap = wrap.grobs, wrap.grobs = FALSE, ...)`

`grid.grabExpr(expr, warn = 2, wrap = wrap.grobs, wrap.grobs = FALSE, width = 7, height = 7, device = offscreen, ...)`
Arguments

expr  
An expression to be evaluated. Typically, some calls to grid drawing functions.

warn  
An integer specifying the amount of warnings to emit. 0 means no warnings, 1 means warn when it is certain that the grab will not faithfully represent the original scene. 2 means warn if there’s any possibility that the grab will not faithfully represent the original scene.

wrap  
A logical indicating how the output should be captured. If TRUE, each non-grob element on the display list is captured by wrapping it in a grob.

wrap.grobs  
A logical indicating whether, if we are wrapping elements (wrap=TRUE), we should wrap grobs (or just wrap viewports).

width, height  
Size of the device used for temporary rendering.

device  
A function that opens a graphics device for temporary rendering. By default this is an off-screen, in-memory device based on the pdf device, but this default device may not be satisfactory when using custom fonts.

...  
arguments passed to gTree, for example, a name and/or class for the gTree that is created.

Details

There are four ways to capture grid output as a gTree.

There are two functions for capturing output: use grid.grab to capture an existing drawing and grid.grabExpr to capture the output from an expression (without drawing anything).

For each of these functions, the output can be captured in two ways. One way tries to be clever and make a gTree with a childrenvp slot containing all viewports on the display list (including those that are popped) and every grob on the display list as a child of the new gTree; each child has a vpPath in the vp slot so that it is drawn in the appropriate viewport. In other words, the gTree contains all elements on the display list, but in a slightly altered form.

The other way, wrap=TRUE, is to create a grob for every element on the display list (and make all of those grobs children of the gTree). Only viewports are wrapped unless wrap.grobs is also TRUE.

The first approach creates a more compact and elegant gTree, which is more flexible to work with, but is not guaranteed to faithfully replicate all possible grid output. The second approach is more brute force, and harder to work with, but is more likely to replicate the original output.

An example of a case that will NOT be replicated by wrapping, with wrap.grobs=TRUE, is a scene where the placement of one grob is dependent on another grob (e.g., via grobX or grobWidth).

Value

A gTree object.

See Also

gTree

Examples

pushViewport(viewport(width=.5, height=.5))
grid.rect()
grid.points(stats::runif(10), stats::runif(10))
popViewport()
grab <- grid.grab()
grid.grep

Search for Grobs and/or Viewports

Description
Given a path, find all matching grobs and/or viewports on the display list or within a given grob.

Usage
grid.grep(path, x = NULL, grobs = TRUE, viewports = FALSE,
strict = FALSE, grep = FALSE, global = FALSE,
no.match = character(), vpPath = viewports)

Arguments
path  
a gPath or a vpPath or a character value that could be interpreted as either.

x  
a grob or NULL. If NULL, the display list is searched.

grobs  
A logical value indicating whether to search for grobs.

viewports  
A logical value indicating whether to search for viewports.

strict  
A boolean indicating whether the path must be matched exactly.

grep  
Whether the path should be treated as a regular expression.

global  
A boolean indicating whether the function should affect just the first match of the path, or whether all matches should be affected.

no.match  
The value to return if no matches are found.

vpPath  
A logical value indicating whether to return the vpPath for each grob as an attribute of the result.

Value
Either a gPath or a vpPath or, if global is TRUE a list of gPaths and/or vpPaths.

If vpPath is TRUE, each gPath result will have an attribute "vpPath".

If there are no matches, no.match is returned.

See Also
grid.ls()

Examples
# A gTree, called "grandparent", with child gTree,
# called "parent", with childrenvp vpStack (vp2 within vp1)
# and child grob, called "child", with vp vpPath (down to vp2)
sampleGTree <- gTree(name="grandparent",
children=gList(gTree(name="parent",
children=gList(grob(name="child", vp="vp1::vp2")),
childrenvp=vpStack(viewport(name="vp1")),

grid.newpage()
grid.draw(grab)
grid.grill  

**Draw a Grill**

This function draws a grill within a Grid viewport.

### Arguments

- **h**
  A numeric vector or unit object indicating the horizontal location of the vertical grill lines.

- **v**
  A numeric vector or unit object indicating the vertical location of the horizontal grill lines.

- **default.units**
  A string indicating the default units to use if **h** or **v** are only given as numeric vectors.

- **gp**
  An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.

- **vp**
  A Grid viewport object.

### Value

None.

### Author(s)

Paul Murrell
grid.grob

Create Grid Graphical Objects, aka "Grob"s

Description

Creating grid graphical objects, short ("grob"s).

`grob()` and `gTree()` are the basic creators, `grobTree()` and `gList()` take several grobs to build a new one.

Usage

```r
## Grob Creation:

grob (...,
     name = NULL,
     gp = NULL,
     vp = NULL,
     cl = NULL)

gTree (...,
     name = NULL,
     gp = NULL,
     vp = NULL,
     children = NULL,
     childrenvp = NULL,
     cl = NULL)

grobTree(...,
     name = NULL,
     gp = NULL,
     vp = NULL,
     childrenvp = NULL,
     cl = NULL)

gList(...)
```

## Grob Properties:

```r
childNames(gTree)
is.grob(x)
```

Arguments

```r
...
name
children
childrenvp
gp
vp
cl
gTree
x
```

For `grob` and `gTree`, the named slots describing important features of the graphical object. For `gList` and `grobTree`, a series of grob objects.

- `name` a character identifier for the grob. Used to find the grob on the display list and/or as a child of another grob.
- `children` a "gList" object.
- `childrenvp` a `viewport` object (or NULL).
- `gp` A "gpar" object, typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- `vp` a `viewport` object (or NULL).
- `cl` string giving the class attribute for the new class.
- `gTree` a "gTree" object.
- `x` An R object.

See Also

`Grid`, `viewport`.
Details

These functions can be used to create a basic "grob", "gTree", or "gList" object, or a new class derived from one of these.

A grid graphical object ("grob") is a description of a graphical item. These basic classes provide default behaviour for validating, drawing, and modifying graphical objects. Both grob() and gTree() call the function validDetails to check that the object returned is internally coherent.

A "gTree" can have other grobs as children: when a gTree is drawn, it draws all of its children. Before drawing its children, a gTree pushes its childrenvp slot and then navigates back up (calls upViewport) so that the children can specify their location within the childrenvp via a vpPath.

Grob names need not be unique in general, but all children of a gTree must have different names. A grob name can be any string, though it is not advisable to use the gPath separator (currently :) in grob names.

The function childNames returns the names of the grobs which are children of a gTree.

All grid primitives (grid.lines, grid.rect, ...) and some higher-level grid components (e.g., grid.xaxis and grid.yaxis) are derived from these classes.

grobTree is just a convenient wrapper for gTree when the only components of the gTree are grobs (so all unnamed arguments become children of the gTree).

The grid.grob function is defunct.

Value

An R object of class "grob", a graphical object.

Author(s)

Paul Murrell

See Also

grid.draw, grid.edit, grid.get.
grid.group

grid.define(src, op = "over", dst = NULL, coords = TRUE,
   name = NULL, gp=gpar(), vp=NULL)

useGrob(group, transform=viewportTransform,
   name=NULL, gp=gpar(), vp=NULL)

grid.use(group, transform=viewportTransform,
   name=NULL, gp=gpar(), vp=NULL)

Arguments

src  A grob.
op  The name of a compositing operator (see Details).
dst  A grob.
coords  A logical indicating whether grob coordinates should be calculated for the
   group.

group  A character identified referring to the name of a defined group.
transform  A function that returns an affine transformation matrix; see
   viewportTransform.
name  A character identifier.
gp  An object of class "gpar", typically the output from a call to the function gpar.
   This is basically a list of graphical parameter settings.
vp  A Grid viewport object (or NULL).

Details

In the simplest usage, we can use grid.group() to specify a grob to be drawn in isolation before
being combined with the main image. This can be different from normal drawing if, for example,
the grob draws more than one shape and there is a mask currently in effect.

Another possible use of grid.group() is to specify both src and dst and combine them us-
ing a compositing operator other than the default "over", before combining the result with the
main image. For example, if we use the "dest.out" operator then dst is only drawn where it is
NOT overlapped by src. The following (extended) Porter-Duff operators are available: "clear",
"source", "over", "in", "out", "atop", "dest", "dest.over", "dest.in", "dest.out",
"dest.atop", "xor", "add", and "saturate". In addition, there are operators corresponding to
PDF blend modes: "multiply", "screen", "overlay", "darken", "lighten", "color.dodge",
"color.burn", "hard.light", "soft.light", "difference", and "exclusion". However,
even if a graphics device supports groups, it may not support all compositing operators; see
dev.capabilities.

It is also possible to break the process into two steps by first using grid.define() to define a group
and then grid.use() to draw the group. This allows for reuse of a group (define the group once
and use it several times).

If a group is defined in one viewport and used in a different viewport, an implicit transformation is
applied. This could be a simple transformation (if the viewports are in different locations, but are
the same size), or it could be more complex if the viewports are also different sizes or at different
orientations.

NOTE: transformations occur on the graphics device so affect all aspects of drawing. For example,
text and line widths are transformed as well as locations.

See viewportTransform for more information about transformations and how to customise them.
Not all graphics devices support these functions: for example xfig and pictex do not. For devices that do provide support, that support may only be partial (e.g., the Cairo-based devices support more compositing operators than the pdf() device).

### Value

A grob object.

### Author(s)

Paul Murrell

### See Also

Grid

### Examples

```r
## NOTE: on devices without support for groups (or masks or patterns),
## there will only be two overlapping opaque circles
grid.newpage()
pat <- pattern(rasterGrob(matrix(c(.5, 1, 1, .5), nrow=2),
           width=unit(1, "cm"),
           height=unit(1, "cm"),
           interpolate=FALSE),
           width=unit(1, "cm"), height=unit(1, "cm"),
           extend="repeat")
grid.rect(gp=gpar(col=NA, fill=pat))
masks <- dev.capabilities()$masks
if (is.character(masks) && "luminance" %in% masks) {
  mask <- as.mask(rectGrob(gp=gpar(col=NA, fill="grey50")), type="luminance")
} else {
  mask <- rectGrob(gp=gpar(col=NA, fill=rgb(0,0,0,.5)))
}
pushViewport(viewport(mask=mask))
pushViewport(viewport(y=.5, height=.5, just="bottom"))
grid.circle(1:2/3, r=.45, gp=gpar(fill=2:3))
popViewport()
pushViewport(viewport(y=0, height=.5, just="bottom"))
grid.group(circleGrob(1:2/3, r=.45, gp=gpar(fill=2:3)))
popViewport()
```

---

**grid.layout Create a Grid Layout**

### Description

This function returns a Grid layout, which describes a subdivision of a rectangular region.
grid.layout

Usage

grid.layout(nrow = 1, ncol = 1,
    widths = unit(rep_len(1, ncol), "null"),
    heights = unit(rep_len(1, nrow), "null"),
    default.units = "null", respect = FALSE,
    just="centre")

Arguments

nrow An integer describing the number of rows in the layout.
ncol An integer describing the number of columns in the layout.
widths A numeric vector or unit object describing the widths of the columns in the layout.
heights A numeric vector or unit object describing the heights of the rows in the layout.
default.units A string indicating the default units to use if widths or heights are only given as numeric vectors.
respect A logical value or a numeric matrix. If a logical, this indicates whether row heights and column widths should respect each other. If a matrix, non-zero values indicate that the corresponding row and column should be respected (see examples below).
just A string or numeric vector specifying how the layout should be justified if it is not the same size as its parent viewport. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment. NOTE that in this context, "left", for example, means align the left edge of the left-most layout column with the left edge of the parent viewport.

Details

The unit objects given for the widths and heights of a layout may use a special units that only has meaning for layouts. This is the "null" unit, which indicates what relative fraction of the available width/height the column/row occupies. See the reference for a better description of relative widths and heights in layouts.

Value

A Grid layout object.

WARNING

This function must NOT be confused with the base R graphics function layout. In particular, do not use layout in combination with Grid graphics. The documentation for layout may provide some useful information and this function should behave identically in comparable situations. The grid.layout function has added the ability to specify a broader range of units for row heights and column widths, and allows for nested layouts (see viewport).

Author(s)

Paul Murrell
References


See Also

*Grid, grid.show.layout, viewport, layout*

Examples

```r
## A variety of layouts (some a bit mid-bending ...)
layout.torture()
## Demonstration of layout justification
grid.newpage()
testlay <- function(just="centre") {
  pushViewport(viewport(layout=grid.layout(1, 1, widths=unit(1, "inches"),
                             heights=unit(0.25, "npc"),
                             just=just)))
  pushViewport(viewport(layout.pos.col=1, layout.pos.row=1))
  grid.rect()
  grid.text(paste(just, collapse="-"))
  popViewport(2)
}
testlay()
testlay(c("left", "top"))
testlay(c("right", "top"))
testlay(c("right", "bottom"))
testlay(c("left", "bottom"))
testlay(c("left"))
testlay(c("right"))
testlay(c("bottom"))
testlay(c("top"))
```

grid.lines

*Draw Lines in a Grid Viewport*

Description

These functions create and draw a series of lines.

Usage

```r
grid.lines(x = unit(c(0, 1), "npc"),
           y = unit(c(0, 1), "npc"),
           default.units = "npc",
           arrow = NULL, name = NULL,
           gp=gpar(), draw = TRUE, vp = NULL)
linesGrob(x = unit(c(0, 1), "npc"),
          y = unit(c(0, 1), "npc"),
          default.units = "npc",
          arrow = NULL, name = NULL,
          gp=gpar(), vp = NULL)
ggrid.polyline(...)
```
polylineGrob(x = unit(c(0, 1), "npc"),
         y = unit(c(0, 1), "npc"),
         id=NULL, id.lengths=NULL,
         default.units = "npc",
         arrow = NULL, name = NULL,
         gp=gpar(), vp = NULL)

Arguments

  x        A numeric vector or unit object specifying x-values.
  y        A numeric vector or unit object specifying y-values.
  default.units A string indicating the default units to use if x or y are only given as numeric vectors.
  arrow    A list describing arrow heads to place at either end of the line, as produced by the arrow function.
  name     A character identifier.
  gp        An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
  draw     A logical value indicating whether graphics output should be produced.
  vp        A Grid viewport object (or NULL).
  id        A numeric vector used to separate locations in x and y into multiple lines. All locations with the same id belong to the same line.
  id.lengths A numeric vector used to separate locations in x and y into multiple lines. Specifies consecutive blocks of locations which make up separate lines.
  ...    Arguments passed to polylineGrob.

Details

The first two functions create a lines grob (a graphical object describing lines), and grid.lines draws the lines (if draw is TRUE).

The second two functions create or draw a polyline grob, which is just like a lines grob, except that there can be multiple distinct lines drawn.

Value

A lines grob or a polyline grob. grid.lines returns a lines grob invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport, arrow
Examples

grid.locator()
# Using id (NOTE: locations are not in consecutive blocks)
grid.newpage()
grid.polyline(x=c((0:4)/10, rep(.5, 5), (10:6)/10, rep(.5, 5)),
    y=c(rep(.5, 5), (10:6/10), rep(.5, 5), (0:4)/10),
    id=rep(1:5, 4),
    gp=gpar(col=1:5, lwd=3))
# Using id.lengths
grid.newpage()
grid.polyline(x=outer(c(0, .5, 1, .5), 5:1/5),
    y=outer(c(.5, 1, .5, 0), 5:1/5),
    id.lengths=rep(4, 5),
    gp=gpar(col=1:5, lwd=3))

Description

Allows the user to click the mouse once within the current graphics device and returns the location of the mouse click within the current viewport, in the specified coordinate system.

Usage

grid.locator(unit = "native")

Arguments

unit The coordinate system in which to return the location of the mouse click. See the unit function for valid coordinate systems.

Details

This function is modal (like the graphics package function locator) so the command line and graphics drawing is blocked until the use has clicked the mouse in the current device.

Value

A unit object representing the location of the mouse click within the current viewport, in the specified coordinate system.

If the user did not click mouse button 1, the function (invisibly) returns NULL.

Author(s)

Paul Murrell

See Also

viewport, unit, locator in package graphics, and for an application see trellis.focus and panel.identify in package lattice.
grid.ls

List the names of grobs or viewports

Description

Return a listing of the names of grobs or viewports.

This is a generic function with methods for grobs (including gTrees) and viewports (including vpTrees).

Usage

grid.ls(x=NULL, grobs=TRUE, viewports=FALSE, fullNames=FALSE, recursive=TRUE, print=TRUE, flatten=TRUE, ...)

nestedListing(x, gindent=“”, vpindent=gindent)
pathListing(x, gvpSep=“|”, gAlign=TRUE)
grobPathListing(x, ...)

Examples

if (dev.interactive()) {
  ## Need to write a more sophisticated unit as.character method
  unittrim <- function(unit) {
    sub("^[0-9]+\[0-9]+[.][0-9]*", "\\\", as.character(unit))
  }
  do.click <- function(unit) {
    click.locn <- grid.locator(unit)
    grid.segments(unit.c(click.locn$x, unit(0, "npc")),
                   unit.c(unit(0, "npc"), click.locn$y),
                   click.locn$x, click.locn$y,
                   gp=gpar(lty="dashed", col="grey"))
    grid.points(click.locn$x, click.locn$y, pch=16, size=unit(1, "mm"))
    clickx <- unittrim(click.locn$x)
    clicky <- unittrim(click.locn$y)
    grid.text(paste0("(", clickx, ",", clicky, ")"),
              click.locn$x + unit(2, "mm"), click.locn$y,
              just="left")
  }
  grid.newpage() # (empty slate)
  ## device
  do.click("inches")
  Sys.sleep(1)
  pushViewport(viewport(width=0.5, height=0.5,
                        xscale=c(0, 100),yscale=c(0, 10)))
  grid.rect()
  grid.xaxis()
  grid.yaxis()
  do.click("native")
  popViewport()
}
Arguments

x  A grob or viewport or NULL. If NULL, the current grid display list is listed. For print functions, this should be the result of a call to grid.ls.
grobs  A logical value indicating whether to list grobs.
viewports  A logical value indicating whether to list viewports.
fullNames  A logical value indicating whether to embellish object names with information about the object type.
recursive  A logical value indicating whether recursive structures should also list their children.
print  A logical indicating whether to print the listing or a function that will print the listing.
flatten  A logical value indicating whether to flatten the listing. Otherwise a more complex hierarchical object is produced.
gindent  The indent used to show nesting in the output for grobs.
vpindent  The indent used to show nesting in the output for viewports.
gvpSep  The string used to separate viewport paths from grob paths.
gAlign  Logical indicating whether to align the left hand edge of all grob paths.
...  Arguments passed to the print function.

Details

If the argument x is NULL, the current contents of the grid display list are listed (both viewports and grobs). In other words, all objects representing the current scene are listed.

Otherwise, x should be a grob or a viewport.

The default behaviour of this function is to print information about the grobs in the current scene. It is also possible to add information about the viewports in the scene. By default, the listing is recursive, so all children of gTrees and all nested viewports are reported.

The format of the information can be controlled via the print argument, which can be given a function to perform the formatting. The nestedListing function produces a line per grob or viewport, with indenting used to show nesting. The pathListing function produces a line per grob or viewport, with viewport paths and grob paths used to show nesting. The grobPathListing is a simple derivation that only shows lines for grobs. The user can define new functions.

Value

The result of this function is either a "gridFlatListing" object (if flatten is TRUE) or a "gridListing" object.

The former is a simple (flat) list of vectors. This is convenient, for example, for working programmatically with the list of grob and viewport names, or for writing a new display function for the listing.

The latter is a more complex hierarchical object (list of lists), but it does contain more detailed information so may be of use for more advanced customisations.

Author(s)

Paul Murrell
grid.move.to

Move or Draw to a Specified Position

Description

Grid has the notion of a current location. These functions sets that location.

Usage

grid.move.to(x = 0, y = 0, default.units = "npc", name = NULL, draw = TRUE, vp = NULL)
moveToGrob(x = 0, y = 0, default.units = "npc", name = NULL, vp = NULL)

grid.line.to(x = 1, y = 1, default.units = "npc", arrow = NULL, name = NULL, gp = gpar(), draw = TRUE, vp = NULL)
lineToGrob(x = 1, y = 1, default.units = "npc", arrow = NULL, name = NULL, gp = gpar(), vp = NULL)

Examples

# A gTree, called "parent", with childrenvp vpTree (vp2 within vp1)
# and child grob, called "child", with vp vpPath (down to vp2)
sampleGTree <- gTree(name="parent",
  children=gList(grob(name="child", vp="vp1::vp2")),
  childrenvp=vpTree(parent=viewport(name="vp1"),
    children=vpList(viewport(name="vp2"))))

grid.ls(sampleGTree)
# Show viewports too
grid.ls(sampleGTree, viewports=TRUE)
# Only show viewports
grid.ls(sampleGTree, viewports=TRUE, grobs=FALSE)
# Alternate displays
# nested listing, custom indent
grid.ls(sampleGTree, viewports=TRUE, print=nestedListing, gindent="--")
# path listing
grid.ls(sampleGTree, viewports=TRUE, print=pathListing)
# path listing, without grobs aligned
grid.ls(sampleGTree, viewports=TRUE, print=pathListing, gAlign=FALSE)
# grob path listing
grid.ls(sampleGTree, viewports=TRUE, print=grobPathListing)
# path listing, grobs only
grid.ls(sampleGTree, print=pathListing)
# path listing, viewports only
grid.ls(sampleGTree, viewports=TRUE, grobs=FALSE, print=pathListing)
# raw flat listing
str(grid.ls(sampleGTree, viewports=TRUE, print=FALSE))
Arguments

- **x**: A numeric value or a unit object specifying an x-value.
- **y**: A numeric value or a unit object specifying a y-value.
- **default.units**: A string indicating the default units to use if x or y are only given as numeric values.
- **arrow**: A list describing arrow heads to place at either end of the line, as produced by the `arrow` function.
- **name**: A character identifier.
- **draw**: A logical value indicating whether graphics output should be produced.
- **gp**: An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- **vp**: A Grid viewport object (or NULL).

Details

Both functions create a move.to/line.to grob (a graphical object describing a move-to/line-to), but only `grid.move.to/line.to()` draws the move.to/line.to (and then only if `draw` is TRUE).

Value

A move.to/line.to grob. `grid.move.to/line.to()` returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport, arrow

Examples

```r
grid.newpage()
grid.move.to(0.5, 0.5)
grid.line.to(1, 1)
grid.line.to(0.5, 0)
pushViewport(viewport(x=0, y=0, width=0.25, height=0.25, just=c("left", "bottom")))
grid.rect()
grid.grill()
grid.line.to(0.5, 0.5)
popViewport()
```
grid.newpage  
*Move to a New Page on a Grid Device*

**Description**

This function erases the current device or moves to a new page.

**Usage**

```r
grid.newpage(recording = TRUE, clearGroups = TRUE)
```

**Arguments**

- `recording`: A logical value to indicate whether the new-page operation should be saved onto the Grid display list.
- `clearGroups`: A logical value indicating whether any groups that have been defined on the current page should be released (see `grid.group`).

**Details**

The new page is painted with the fill colour (`gpar("fill")`), which is often transparent. For devices with a *canvas* colour (the on-screen devices `X11`, `windows` and `quartz`), the page is first painted with the canvas colour and then the background colour.

There are two hooks called "before.grid.newpage" and "grid.newpage" (see `setHook`). The latter is used in the testing code to annotate the new page. The hook function(s) are called with no argument. (If the value is a character string, `get` is called on it from within the `grid` namespace.)

**Value**

None.

**Author(s)**

Paul Murrell

**See Also**

- `Grid`

---

grid.null  
*Null Graphical Object*

**Description**

These functions create a NULL graphical object, which has zero width, zero height, and draw nothing. It can be used as a place-holder or as an invisible reference point for other drawing.
Usage

```
nullGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
    default.units = "npc",
    name = NULL, vp = NULL)
grid.null(...)
```

Arguments

- **x**: A numeric vector or unit object specifying x-location.
- **y**: A numeric vector or unit object specifying y-location.
- **default.units**: A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
- **name**: A character identifier.
- **vp**: A Grid viewport object (or NULL).
- **...**: Arguments passed to `nullGrob()`.

Value

A null grob.

Author(s)

Paul Murrell

See Also

`Grid`, `viewport`

Examples

```
grid.newpage()
grid.null(name="ref")
grid.rect(height=grobHeight("ref"))
grid.segments(0, 0, grobX("ref", 0), grobY("ref", 0))
```

Description

These functions, together with `grid.frame` and `frameGrob` are part of a GUI-builder-like interface to constructing graphical images. The idea is that you create a frame with `grid.frame` or `frameGrob` then use these functions to pack objects into the frame.
grid.pack

Usage

grid.pack(gPath, grob, redraw = TRUE, side = NULL,
    row = NULL, row.before = NULL, row.after = NULL,
    col = NULL, col.before = NULL, col.after = NULL,
    width = NULL, height = NULL,
    force.width = FALSE, force.height = FALSE, border = NULL,
    dynamic = FALSE)

packGrob(frame, grob, side = NULL,
    row = NULL, row.before = NULL, row.after = NULL,
    col = NULL, col.before = NULL, col.after = NULL,
    width = NULL, height = NULL,
    force.width = FALSE, force.height = FALSE, border = NULL,
    dynamic = FALSE)

Arguments

gPath A gPath object, which specifies a frame on the display list.
frame An object of class frame, typically the output from a call to grid.frame.
grob An object of class grob. The object to be packed.
redraw A boolean indicating whether the output should be updated.
side One of "left", "top", "right", "bottom" to indicate which side to pack the
go...b on.
row Which row to add the object to. Must be between 1 and the-number-of-rows-
currently-in-the-frame + 1, or NULL in which case the object occupies all rows.
row.before Add the object to a new row just before this row.
row.after Add the object to a new row just after this row.
col Which col to add the object to. Must be between 1 and the-number-of-cols-
currently-in-the-frame + 1, or NULL in which case the object occupies all cols.
col.before Add the object to a new col just before this col.
col.after Add the object to a new col just after this col.
width Specifies the width of the column that the object is added to (rather than allowing
the width to be taken from the object).
height Specifies the height of the row that the object is added to (rather than allowing
the height to be taken from the object).
force.width A logical value indicating whether the width of the column that the grob is being
packed into should be EITHER the width specified in the call to grid.pack OR
the maximum of that width and the pre-existing width.
force.height A logical value indicating whether the height of the column that the grob is being
packed into should be EITHER the height specified in the call to grid.pack OR
the maximum of that height and the pre-existing height.
border A unit object of length 4 indicating the borders around the object.
dynamic If the width/height is taken from the grob being packed, this boolean flag indi-
cates whether the grobwidth/height unit refers directly to the grob, or uses a
gPath to the grob. In the latter case, changes to the grob will trigger a recalcula-
tion of the width/height.
Details

packGrob modifies the given frame grob and returns the modified frame grob.
grid.pack destructively modifies a frame grob on the display list (and redraws the display list if
redraw is TRUE).

These are (meant to be) very flexible functions. There are many different ways to specify where the
new object is to be added relative to the objects already in the frame. The function checks that the
specification is not self-contradictory.

NOTE that the width/height of the row,col that the object is added to is taken from the object itself
unless the width/height is specified.

Value

packGrob returns a frame grob, but grid.pack returns NULL.

Author(s)

Paul Murrell

See Also

grid.frame, grid.place, grid.edit, and gPath.

grid.path  
Draw a Path

Description

These functions create and draw one or more paths. The final point of a path will automatically be
connected to the initial point.

Usage

pathGrob(x, y,
    id=NULL, id.lengths=NULL,
    pathId=NULL, pathId.lengths=NULL,
    rule="winding",
    default.units="npc",
    name=NULL, gp=gpar(), vp=NULL)
grid.path(...)

Arguments

x  A numeric vector or unit object specifying x-locations.
y  A numeric vector or unit object specifying y-locations.
id  A numeric vector used to separate locations in x and y into sub-paths. All loca-
tions with the same id belong to the same sub-path.
id.lengths  A numeric vector used to separate locations in x and y into sub-paths. Specifies
consecutive blocks of locations which make up separate sub-paths.
grid.path

A numeric vector used to separate locations in x and y into distinct paths. All locations with the same pathId belong to the same path.

A numeric vector used to separate locations in x and y into paths. Specifies consecutive blocks of locations which make up separate paths.

A character value specifying the fill rule: either "winding" or "evenodd".

A string indicating the default units to use if x or y are only given as numeric vectors.

A character identifier.

An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.

A Grid viewport object (or NULL).

Arguments passed to pathGrob().

Both functions create a path grob (a graphical object describing a path), but only grid.path draws the path (and then only if draw is TRUE).

A path is like a polygon except that the former can contain holes, as interpreted by the fill rule; these fill a region if the path border encircles it an odd or non-zero number of times, respectively.

Not all graphics devices support this function: for example xfig and pictex do not.

A grob object.

Paul Murrell

Grid, viewport

Examples

pathSample <- function(x, y, rule, gp = gpar()) {
  if (is.na(rule))
    grid.path(x, y, id = rep(1:2, each = 4), gp = gp)
  else
    grid.path(x, y, id = rep(1:2, each = 4), rule = rule, gp = gp)
  if (!is.na(rule))
    grid.text(paste("Rule:", rule), y = 0, just = "bottom")
}

pathTriplet <- function(x, y, title) {
  pushViewport(viewport(height = 0.9, layout = grid.layout(1, 3),
                     gp = gpar(cex = .7)))
  grid.rect(y = 1, height = unit(1, "char"), just = "top",
            gp = gpar(col = NA, fill = "grey"))
  grid.text(title, y = 1, just = "top")
  pushViewport(viewport(layout.pos.col = 1))
  pathSample(x, y, rule = "winding", ...)
pathTest <- function() {
  grid.newpage()
  pushViewport(viewport(layout = grid.layout(5, 1)))
  pushViewport(viewport(layout.pos.row = 1))
  pathTriplet(c(.1, .1, .9, .9, .2, .2, .8, .8),
              c(.1, .9, .9, .1, .2, .8, .8, .2),
              "Nested rectangles, both clockwise")
  popViewport()
  pushViewport(viewport(layout.pos.row = 2))
  pathTriplet(c(.1, .1, .9, .9, .2, .8, .8, .2),
              c(.1, .9, .9, .1, .2, .2, .8, .8),
              "Nested rectangles, outer clockwise, inner anti-clockwise")
  popViewport()
  pushViewport(viewport(layout.pos.row = 3))
  pathTriplet(c(.1, .1, .4, .4, .6, .9, .9, .6),
              c(.1, .4, .4, .1, .6, .6, .9, .9),
              "Disjoint rectangles")
  popViewport()
  pushViewport(viewport(layout.pos.row = 4))
  pathTriplet(c(.1, .1, .6, .6, .4, .4, .9, .9),
              c(.1, .6, .6, .1, .4, .9, .9, .4),
              "Overlapping rectangles, both clockwise")
  popViewport()
  pushViewport(viewport(layout.pos.row = 5))
  pathTriplet(c(.1, .1, .6, .6, .4, .9, .9, .4),
              c(.1, .6, .6, .1, .4, .4, .9, .9),
              "Overlapping rectangles, one clockwise, other anti-clockwise")
  popViewport()
}

pathTest()
place = 'evenodd')

# Not specifying pathId will treat all points as part of the same path, thus
# having same fill
grid.newpage()
grid.path(x = holed_rects[, 1], y = holed_rects[, 2],
  id = rep(1:6, each = 4),
  gp = gpar(fill = c('red', 'blue', 'green')),
  rule = 'evenodd')

---

grid.place

**Place an Object within a Frame**

**Description**

These functions provide a simpler (and faster) alternative to the `grid.pack()` and `packGrob()` functions. They can be used to place objects within the existing rows and columns of a frame layout. They do not provide the ability to add new rows and columns nor do they affect the heights and widths of the rows and columns.

**Usage**

```r
grid.place(gPath, grob, row = 1, col = 1, redraw = TRUE)
placeGrob(frame, grob, row = NULL, col = NULL)
```

**Arguments**

- **gPath**
  A gPath object, which specifies a frame on the display list.
- **frame**
  An object of class `frame`, typically the output from a call to `grid.frame`. 
- **grob**
  An object of class `grob`. The object to be placed.
- **row**
  Which row to add the object to. Must be between 1 and the-number-of-rows-currently-in-the-frame.
- **col**
  Which col to add the object to. Must be between 1 and the-number-of-cols-currently-in-the-frame.
- **redraw**
  A boolean indicating whether the output should be updated.

**Details**

`placeGrob` modifies the given frame grob and returns the modified frame grob. 
`grid.place` destructively modifies a frame grob on the display list (and redraws the display list if `redraw` is `TRUE`).

**Value**

`placeGrob` returns a frame grob, but `grid.place` returns `NULL`.

**Author(s)**

Paul Murrell

**See Also**

`grid.frame`, `grid.pack`, `grid.edit`, and `gPath`.
grid.plot.and.legend  A Simple Plot and Legend Demo

Description

This function is just a wrapper for a simple demonstration of how a basic plot and legend can be drawn from scratch using grid.

Usage

grid.plot.and.legend()

Author(s)

Paul Murrell

Examples

grid.plot.and.legend()

grid.points  Draw Data Symbols

Description

These functions create and draw data symbols.

Usage

grid.points(x = stats::runif(10),
           y = stats::runif(10),
           pch = 1, size = unit(1, "char"),
           default.units = "native", name = NULL,
           gp = gpar(), draw = TRUE, vp = NULL)
pointsGrob(x = stats::runif(10),
           y = stats::runif(10),
           pch = 1, size = unit(1, "char"),
           default.units = "native", name = NULL,
           gp = gpar(), vp = NULL)

Arguments

x  numeric vector or unit object specifying x-values.
y  numeric vector or unit object specifying y-values.
pch  numeric or character vector indicating what sort of plotting symbol to use. See points for the interpretation of these values, and note fill below.
size  unit object specifying the size of the plotting symbols.
default.units  string indicating the default units to use if x or y are only given as numeric vectors.
grid.polygon

name  character identifier.

gp    an R object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings; note that fill (and not bg as in package graphics points) is used to “fill”, i.e., color the background of symbols with pch = 21:25.

draw  logical indicating whether graphics output should be produced.

vp    A Grid viewport object (or NULL).

Details

Both functions create a points grob (a graphical object describing points), but only grid.points draws the points (and then only if draw is TRUE).

Value

A points grob. grid.points returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport

grid.polygon  Draw a Polygon

Description

These functions create and draw a polygon. The final point will automatically be connected to the initial point.

Usage

grid.polygon(x=c(0, 0.5, 1, 0.5), y=c(0.5, 1, 0.5, 0), id=NULL, id.lengths=NULL, default.units="npc", name=NULL, gp=gpar(), draw=TRUE, vp=NULL)
polygonGrob(x=c(0, 0.5, 1, 0.5), y=c(0.5, 1, 0.5, 0), id=NULL, id.lengths=NULL, default.units="npc", name=NULL, gp=gpar(), vp=NULL)
Arguments

`x`  A numeric vector or unit object specifying x-locations.

`y`  A numeric vector or unit object specifying y-locations.

`id`  A numeric vector used to separate locations in `x` and `y` into multiple polygons. All locations with the same `id` belong to the same polygon.

`id.lengths`  A numeric vector used to separate locations in `x` and `y` into multiple polygons. Specifies consecutive blocks of locations which make up separate polygons.

`default.units`  A string indicating the default units to use if `x`, `y`, `width`, or `height` are only given as numeric vectors.

`name`  A character identifier.

`gp`  An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.

`draw`  A logical value indicating whether graphics output should be produced.

`vp`  A Grid viewport object (or NULL).

Details

Both functions create a polygon grob (a graphical object describing a polygon), but only `grid.polygon` draws the polygon (and then only if `draw` is `TRUE`).

Value

A grob object.

Author(s)

Paul Murrell

See Also

Grid, viewport

Examples

```r
grid.polygon()
# Using id (NOTE: locations are not in consecutive blocks)
grid.newpage()
grid.polygon(x=c((0:4)/10, rep(.5, 5), (10:6)/10, rep(.5, 5)),
    y=c(rep(.5, 5), (10:6)/10, rep(.5, 5), (0:4)/10),
    id=rep(1:5, 4),
    gp=gpar(fill=1:5))
# Using id.lengths
grid.newpage()
grid.polygon(x=outer(c(0, .5, 1, .5), 5:1/5),
    y=outer(c(.5, 1, .5, 0), 5:1/5),
    id.lengths=rep(4, 5),
    gp=gpar(fill=1:5))
```
grid.pretty

Generate a Sensible ("Pretty") Set of Breakpoints

Description

Produces a pretty set of approximately n breakpoints within the range given.
This is a direct interface to R’s graphical engine GEpretty() function, which also underlies base
graphics’ package axis(), axTicks(), etc.

Usage

grid.pretty(range, n = 5)

Arguments

range a numeric vector of length at least two, as e.g., returned by range().
n a non-negative integer specifying the approximate number of breakpoints to be
produced.

Value

A numeric vector of “pretty” breakpoints.

Author(s)

Paul Murrell

grid.raster

Render a raster object

Description

Render a raster object (bitmap image) at the given location, size, and orientation.

Usage

grid.raster(image,
    x = unit(0.5, "npc"), y = unit(0.5, "npc"),
    width = NULL, height = NULL,
    just = "centre", hjust = NULL, vjust = NULL,
    interpolate = TRUE, default.units = "npc",
    name = NULL, gp = gpar(), vp = NULL)

rasterGrob(image,
    x = unit(0.5, "npc"), y = unit(0.5, "npc"),
    width = NULL, height = NULL,
    just = "centre", hjust = NULL, vjust = NULL,
    interpolate = TRUE, default.units = "npc",
    name = NULL, gp = gpar(), vp = NULL)
Arguments

image Any R object that can be coerced to a raster object.
x A numeric vector or unit object specifying x-location.
y A numeric vector or unit object specifying y-location.
width A numeric vector or unit object specifying width.
height A numeric vector or unit object specifying height.
just The justification of the rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.
hjust A numeric vector specifying horizontal justification. If specified, overrides the just setting.
vjust A numeric vector specifying vertical justification. If specified, overrides the just setting.
default.units A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.
name A character identifier.
gp An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
vp A Grid viewport object (or NULL).
interpolate A logical value indicating whether to linearly interpolate the image (the alternative is to use nearest-neighbour interpolation, which gives a more blocky result).

Details

Neither width nor height needs to be specified, in which case, the aspect ratio of the image is preserved. If both width and height are specified, it is likely that the image will be distorted.

Not all graphics devices are capable of rendering raster images and some may not be able to produce rotated images (i.e., if a raster object is rendered within a rotated viewport). See also the comments under rasterImage.

All graphical parameter settings in gp will be ignored, including alpha.

Value

A rastergrob grob.

Author(s)

Paul Murrell

See Also

as.raster.
dev.capabilities to see if it is supported.
Examples

```r
redGradient <- matrix(hcl(0, 80, seq(50, 80, 10)),
    nrow=4, ncol=5)
# interpolated
grid.newpage()
grid.raster(redGradient)
# blocky
grid.newpage()
grid.raster(redGradient, interpolate=FALSE)
# blocky and stretched
grid.newpage()
grid.raster(redGradient, interpolate=FALSE, height=unit(1, "npc"))

# The same raster drawn several times
grid.newpage()
grid.raster(0, x=1:3/4, y=1:3/4, width=.1, interpolate=FALSE)
```

grid.record

Encapsulate calculations and drawing

Description

Evaluates an expression that includes both calculations and drawing that depends on the calculations so that both the calculations and the drawing will be rerun when the scene is redrawn (e.g., device resize or editing).

Intended only for expert use.

Usage

```r
recordGrob(expr, list, name=NULL, gp=NULL, vp=NULL)
grid.record(expr, list, name=NULL, gp=NULL, vp=NULL)
```

Arguments

- `expr`: object of mode `expression` or call or an unevaluated expression.
- `list`: a list defining the environment in which `expr` is to be evaluated.
- `name`: A character identifier.
- `gp`: An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- `vp`: A Grid viewport object (or NULL).

Details

A grob is created of special class "recordedGrob" (and drawn, in the case of `grid.record`). The `drawDetails` method for this class evaluates the expression with the list as the evaluation environment (and the grid Namespace as the parent of that environment).

Note

This function must be used instead of the function `recordGraphics`; all of the dire warnings about using `recordGraphics` responsibly also apply here.
grid.rect

Author(s)
Paul Murrell

See Also
recordGraphics

Examples
grid.record({
  w <- convertWidth(unit(1, "inches"). "npc")
  grid.rect(width=w)
},
list())

grid.rect
Draw rectangles

Description
These functions create and draw rectangles.

Usage
grid.rect(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
  width = unit(1, "npc"), height = unit(1, "npc"),
  just = "centre", hjust = NULL, vjust = NULL,
  default.units = "npc", name = NULL,
  gp=gpar(), draw = TRUE, vp = NULL)
rectGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
  width = unit(1, "npc"), height = unit(1, "npc"),
  just = "centre", hjust = NULL, vjust = NULL,
  default.units = "npc", name = NULL,
  gp=gpar(), vp = NULL)

Arguments
x A numeric vector or unit object specifying x-location.
y A numeric vector or unit object specifying y-location.
width A numeric vector or unit object specifying width.
height A numeric vector or unit object specifying height.
just The justification of the rectangle relative to its (x, y) location. If there are two
values, the first value specifies horizontal justification and the second value
specifies vertical justification. Possible string values are: "left", "right",
"centre", "center", "bottom", and "top". For numeric values, 0 means left
alignment and 1 means right alignment.
hjust A numeric vector specifying horizontal justification. If specified, overrides the
just setting.
vjust A numeric vector specifying vertical justification. If specified, overrides the
just setting.
default.units A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.

name A character identifier.

gp An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.

draw A logical value indicating whether graphics output should be produced.

vp A Grid viewport object (or NULL).

Details

Both functions create a rect grob (a graphical object describing rectangles), but only grid.rect draws the rectangles (and then only if draw is TRUE).

Value

A rect grob. grid.rect returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport

grid.refresh Refresh the current grid scene

Description

Replays the current grid display list.

Usage

grid.refresh()

Author(s)

Paul Murrell
grid.remove  Remove a Grid Graphical Object

Description

Remove a grob from a gTree or a descendant of a gTree.

Usage

grid.remove(gPath, warn = TRUE, strict = FALSE, grep = FALSE, 
global = FALSE, allDevices = FALSE, redraw = TRUE)

grid.gremove(..., grep = TRUE, global = TRUE)

removeGrob(gTree, gPath, strict = FALSE, grep = FALSE, 
global = FALSE, warn = TRUE)

Arguments

gTree  A gTree object.
gPath  a gPath object. For grid.remove this specifies a gTree on the display list. For 
removeGrob this specifies a descendant of the specified gTree.
strict  a logical indicating whether the gPath must be matched exactly.
grep  a logical indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., c(TRUE, FALSE) means that every odd element of the gPath will be treated as a regular expression).
global  a logical indicating whether the function should affect just the first match of the gPath, or whether all matches should be affected.
allDevices  a logical indicating whether all open devices should be searched for matches, 
or just the current device. NOT YET IMPLEMENTED.
warn  A logical to indicate whether failing to find the specified grob should trigger an 
error.
redraw  A logical value to indicate whether to redraw the grob.
...  arguments passed to grid.get.

Details

removeGrob copies the specified grob and returns a modified grob.

grid.remove destructively modifies a grob on the display list. If redraw is TRUE it then redraws 
everything to reflect the change.

grid.gremove (g for global) is just a convenience wrapper for grid.remove with different defaults.

Value

removeGrob returns a grob object; grid.remove returns NULL.
grid.reorder

Description
Change the order in which the children of a gTree get drawn.

Usage
grid.reorder(gPath, order, back=TRUE, grep=FALSE, redraw=TRUE)
reorderGrob(x, order, back=TRUE)

Arguments
gPath A gPath object specifying a gTree within the current scene.
x A gTree object to be modified.
order A character vector or a numeric vector that specifies the new drawing order for the children of the gTree. May not refer to all children of the gTree (see Details).
back Controls what happens when the order does not specify all children of the gTree (see Details).
grep Should the gPath be treated as a regular expression?
redraw Should the modified scene be redrawn?

Details
In the simplest case, order specifies a new ordering for all of the children of the gTree. The children may be specified either by name or by existing numerical order.

If the order does not specify all children of the gTree then, by default, the children specified by order are drawn first and then all remaining children are drawn. If back=FALSE then the children not specified in order are drawn first, followed by the specified children. This makes it easy to specify a send-to-back or bring-to-front reordering. The order argument is always in back-to-front order.

It is not possible to reorder the grid display list (the top-level grobs in the current scene) because the display list is a mixture of grobs and viewports (so it is not clear what reordering even means and it would be too easy to end up with a scene that would not draw). If you want to reorder the grid display list, try grid.grab() to create a gTree and then reorder (and redraw) that gTree.

Value
grid.reorder() is called for its side-effect of modifying the current scene. reorderGrob() returns the modified gTree.
**Warning**

This function may return a gTree that will not draw. For example, a gTree has two children, A and B (in that order), and the width of child B depends on the width of child A (e.g., a box around a piece of text). Switching the order so that B is drawn before A will not allow B to be drawn. If this happens with `grid.reorder()`, the modification will not be performed. If this happens with `reorderGrob()` it should be possible simply to restore the original order.

**Author(s)**

Paul Murrell

**Examples**

```r
# gTree with two children, "red-rect" and "blue-rect" (in that order)
gt <- gTree(children=gList(
  rectGrob(gp=gpar(col=NA, fill="red"),
  width=.8, height=.2, name="red-rect"),
  rectGrob(gp=gpar(col=NA, fill="blue"),
  width=.2, height=.8, name="blue-rect")),
  name="gt")
grid.newpage()
grid.draw(gt)
# Spec entire order as numeric (blue-rect, red-rect)
grid.reorder("gt", 2:1)
# Spec entire order as character
grid.reorder("gt", c("red-rect", "blue-rect"))
# Only spec the one I want behind as character
grid.reorder("gt", "blue-rect")
# Only spec the one I want in front as character
grid.reorder("gt", "blue-rect", back=FALSE)
```

---

**grid.segments**  
**Draw Line Segments**

**Description**

These functions create and draw line segments.

**Usage**

```r
grid.segments(x0 = unit(0, "npc"), y0 = unit(0, "npc"),
  x1 = unit(1, "npc"), y1 = unit(1, "npc"),
  default.units = "npc",
  arrow = NULL,
  name = NULL, gp = gpar(), draw = TRUE, vp = NULL)
segmentsGrob(x0 = unit(0, "npc"), y0 = unit(0, "npc"),
  x1 = unit(1, "npc"), y1 = unit(1, "npc"),
  default.units = "npc",
  arrow = NULL, name = NULL, gp = gpar(), vp = NULL)
```
Arguments

x0  Numeric indicating the starting x-values of the line segments.
y0  Numeric indicating the starting y-values of the line segments.
x1  Numeric indicating the stopping x-values of the line segments.
y1  Numeric indicating the stopping y-values of the line segments.
default.units  A string.
arrow  A list describing arrow heads to place at either end of the line segments, as produced by the arrow function.
name  A character identifier.
gp  An object of class "gpar", typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw  A logical value indicating whether graphics output should be produced.
vp  A Grid viewport object (or NULL).

Details

Both functions create a segments grob (a graphical object describing segments), but only grid.segments draws the segments (and then only if draw is TRUE).

Value

A segments grob. grid.segments returns the value invisibly.

Author(s)

Paul Murrell

See Also

Grid, viewport, arrow

grid.set  Set a Grid Graphical Object

Description

Replace a grob or a descendant of a grob.

Usage

grid.set(gPath, newGrob, strict = FALSE, grep = FALSE, redraw = TRUE)

setGrob(gTree, gPath, newGrob, strict = FALSE, grep = FALSE)
Arguments

- **gTree**: A gTree object.
- **gPath**: A gPath object. For `grid.set` this specifies a grob on the display list. For `setGrob` this specifies a descendant of the specified gTree.
- **newGrob**: A grob object.
- **strict**: A boolean indicating whether the gPath must be matched exactly.
- **grep**: A boolean indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., `c(TRUE, FALSE)` means that every odd element of the gPath will be treated as a regular expression).
- **redraw**: A logical value to indicate whether to redraw the grob.

Details

- `setGrob` copies the specified grob and returns a modified grob.
- `grid.set` destructively replaces a grob on the display list. If `redraw` is `TRUE` it then redraws everything to reflect the change.

These functions should not normally be called by the user.

Value

- `setGrob` returns a grob object; `grid.set` returns `NULL`.

Author(s)

Paul Murrell

See Also

- `grid.grob`

grid.show.layout  
**Draw a Diagram of a Grid Layout**

Description

This function uses Grid graphics to draw a diagram of a Grid layout.

Usage

```r
grid.show.layout(l, newpage=TRUE, vp.ex = 0.8, bg = "light grey", cell.border = "blue", cell.fill = "light blue", cell.label = TRUE, label.col = "blue", unit.col = "red", vp = NULL, ...)
```
Arguments

l             A Grid layout object.
newpage       A logical value indicating whether to move on to a new page before drawing the diagram.
vp.ex          positive number, typically in (0, 1], specifying the scaling of the layout.
bg             The colour used for the background.
cell.border   The colour used to draw the borders of the cells in the layout.
cell.fill     The colour used to fill the cells in the layout.
cell.label    A logical indicating whether the layout cells should be labelled.
label.col     The colour used for layout cell labels.
unit.col      The colour used for labelling the widths/heights of columns/rows.
vp             A Grid viewport object (or NULL).
...           Arguments passed to format for formatting the layout width and height annotations.

Details

A viewport is created within vp to provide a margin for annotation, and the layout is drawn within that new viewport. The margin is filled with light grey, the new viewport is filled with white and framed with a black border, and the layout regions are filled with light blue and framed with a blue border. The diagram is annotated with the widths and heights (including units) of the columns and rows of the layout using red text. (All colours are defaults and may be customised via function arguments.)

Value

None.

Author(s)

Paul Murrell

See Also

Grid, viewport, grid.layout

Examples

## Diagram of a simple layout
grid.show.layout(grid.layout(4,2,
    heights=unit(rep(1, 4),
    c("lines", "lines", "lines", "null")),
    widths=unit(c(1, 1), "inches")))
grid.show.viewport  

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Description

This function uses Grid graphics to draw a diagram of a Grid viewport.

Usage

```r
grid.show.viewport(v, parent.layout = NULL, newpage = TRUE,
                   vp.ex = 0.8, border.fill="light grey",
                   vp.col="blue", vp.fill="light blue",
                   scale.col="red",
                   vp = NULL)
```

Arguments

- **v**: A Grid viewport object.
- **parent.layout**: A grid layout object. If this is not NULL and the viewport given in `v` has its location specified relative to the layout, then the diagram shows the layout and which cells `v` occupies within the layout.
- **newpage**: A logical value to indicate whether to move to a new page before drawing the diagram.
- **vp.ex**: positive number, typically in (0, 1], specifying the scaling of the layout.
- **border.fill**: Colour to fill the border margin.
- **vp.col**: Colour for the border of the viewport region.
- **vp.fill**: Colour to fill the viewport region.
- **scale.col**: Colour to draw the viewport axes.
- **vp**: A Grid viewport object (or NULL).

Details

A viewport is created within `vp` to provide a margin for annotation, and the diagram is drawn within that new viewport. By default, the margin is filled with light grey, the new viewport is filled with white and framed with a black border, and the viewport region is filled with light blue and framed with a blue border. The diagram is annotated with the width and height (including units) of the viewport, the (x, y) location of the viewport, and the x- and y-scales of the viewport, using red lines and text.

Value

None.

Author(s)

Paul Murrell

See Also

Grid, viewport
Examples

```r
## Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
    width=unit(1, "inches"), height=unit(1, "inches")))
grid.show.viewport(viewport(layout.pos.row=2, layout.pos.col=2:3),
    grid.layout(3, 4))
```

Description

These functions stroke (draw a line along the border) or fill (or both) a path, where the path is defined by a grob.

Usage

```r
strokeGrob(x, ...)  
# S3 method for class 'grob'
strokeGrob(x, name=NULL, gp=gpar(), vp=NULL, ...)
# S3 method for class 'GridPath'
strokeGrob(x, name=NULL, vp=NULL, ...)
grid.stroke(...)
fillGrob(x, ...)  
# S3 method for class 'grob'
fillGrob(x, rule=c("winding", "evenodd"),
    name=NULL, gp=gpar(), vp=NULL, ...)
# S3 method for class 'GridPath'
fillGrob(x, name=NULL, vp=NULL, ...)
grid.fill(...)
fillStrokeGrob(x, ...)  
# S3 method for class 'grob'
fillStrokeGrob(x, rule=c("winding", "evenodd"),
    name=NULL, gp=gpar(), vp=NULL, ...)
# S3 method for class 'GridPath'
fillStrokeGrob(x, name=NULL, vp=NULL, ...)
grid.fillStroke(...)
as.path(x, gp=gpar(), rule=c("winding", "evenodd"))
```

Arguments

- **x**: A grob or the result of a call to `as.path()`.
- **rule**: A fill rule.
- **name**: A character identifier.
- **gp**: An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- **vp**: A Grid viewport object (or NULL).
- **...**: Arguments to `grid.*()` passed on to *Grob(), or additional arguments passed on to methods.
grid.text

Details
A path is defined by the shapes that the grob given in x would draw. The grob only contributes to the outline of the path; graphical parameter settings such as line colour and fill are ignored. grid.stroke() will only ever draw the border (even when a fill is specified). grid.fill() will only ever fill the path (even when a line colour is specified). A stroke will only ever happen if a non-transparent line colour is specified and a fill will only ever happen if a non-transparent fill is specified.
as.path() allows graphical parameter settings and a fill rule to be associated with a grob. This can be useful when specifying a clipping path for a viewport (see viewport). Not all graphics devices support these functions: for example xfig and pictex do not.

Value
A grob object.

Author(s)
Paul Murrell

See Also
Grid

Examples
## NOTE: on devices without support for stroking and filling
## nothing will be drawn
grid.newpage()
grid.stroke(textGrob("hello", gp=gpar(cex=10)))
grid.fill(circleGrob(1:2/3, r=.3), gp=gpar(fill=rgb(1,0,0,.5)))

grid.text

Draw Text

Description
These functions create and draw text and plotmath expressions.

Usage
grid.text(label, x = unit(0.5, "npc"), y = unit(0.5, "npc"),
just = "centre", hjust = NULL, vjust = NULL, rot = 0,
check.overlap = FALSE, default.units = "npc",
name = NULL, gp = gpar(), draw = TRUE, vp = NULL)
textGrob(label, x = unit(0.5, "npc"), y = unit(0.5, "npc"),
just = "centre", hjust = NULL, vjust = NULL, rot = 0,
check.overlap = FALSE, default.units = "npc",
name = NULL, gp = gpar(), vp = NULL)
Arguments

label
A character or expression vector. Other objects are coerced by \texttt{as.graphicsAnnot}.

\textbf{x}
A numeric vector or unit object specifying x-values.

\textbf{y}
A numeric vector or unit object specifying y-values.

\textbf{just}
The justification of the text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left (bottom) alignment and 1 means right (top) alignment.

\textbf{hjust}
A numeric vector specifying horizontal justification. If specified, overrides the \texttt{just} setting.

\textbf{vjust}
A numeric vector specifying vertical justification. If specified, overrides the \texttt{just} setting.

\textbf{rot}
The angle to rotate the text.

\textbf{check.overlap}
A logical value to indicate whether to check for and omit overlapping text (within that grob).

\textbf{default.units}
A string indicating the default units to use if \texttt{x} or \texttt{y} are only given as numeric vectors.

\textbf{name}
A character identifier.

\textbf{gp}
An object of class "gp\texttt{ar}". typically the output from a call to the function \texttt{gp\texttt{ar}}. This is basically a list of graphical parameter settings.

\textbf{draw}
A logical value indicating whether graphics output should be produced.

\textbf{vp}
A Grid viewport object (or NULL).

Details

Both functions create a text grob (a graphical object describing text), but only \texttt{grid.text} draws the text (and then only if \texttt{draw} is \texttt{TRUE}).

If the \texttt{label} argument is an expression, the output is formatted as a mathematical annotation, as for base graphics text.

Value

A text grob. \texttt{grid.text()} returns the value invisibly.

Author(s)

Paul Murrell

See Also

\texttt{Grid, viewport}
Examples

grid.newpage()
x <- stats::runif(20)
y <- stats::runif(20)
rot <- stats::runif(20, 0, 360)
grid.text("SOMETHING NICE AND BIG", x=x, y=y, rot=rot,
gp=gpar(fontsize=20, col="grey"))
grid.text("SOMETHING NICE AND BIG", x=x, y=y, rot=rot,
gp=gpar(fontsize=20), check.overlap=TRUE)

grid.newpage() ## plotmath example
grid.text(quote(frac(e^{-x^2/2}, sqrt(2*pi))), x=x, y=y, rot=stats::runif(20, -45,45),
gp=gpar(fontsize=17, col=4), check.overlap=TRUE)

grid.newpage()
draw.text <- function(just, i, j) {
  grid.text("ABCD", x=x[j], y=y[i], just=just)
  grid.text(deparse(substitute(just)), x=x[j], y=y[i] + unit(2, "lines"),
gp=gpar(col="grey", fontsize=8))
}
x <- unit(1:4/5, "npc")
y <- unit(1:4/5, "npc")
grid.grill(h=y, v=x, gp=gpar(col="grey"))
draw.text(c("bottom"), 1, 1)
draw.text(c("left", "bottom"), 2, 1)
draw.text(c("right", "bottom"), 3, 1)
draw.text(c("centre", "bottom"), 4, 1)
draw.text(c("centre"), 1, 2)
draw.text(c("left", "centre"), 2, 2)
draw.text(c("right", "centre"), 3, 2)
draw.text(c("centre", "centre"), 4, 2)
draw.text(c("top"), 1, 3)
draw.text(c("left", "top"), 2, 3)
draw.text(c("right", "top"), 3, 3)
draw.text(c("centre", "top"), 4, 3)
draw.text(c(), 1, 4)
draw.text(c("left"), 2, 4)
draw.text(c("right"), 3, 4)
draw.text(c("centre"), 4, 4)

draw.text(c("bottom"), 1, 1)
draw.text(c("left", "bottom"), 2, 1)
draw.text(c("right", "bottom"), 3, 1)
draw.text(c("centre", "bottom"), 4, 1)
draw.text(c("centre"), 1, 2)
draw.text(c("left", "centre"), 2, 2)
draw.text(c("right", "centre"), 3, 2)
draw.text(c("centre", "centre"), 4, 2)
draw.text(c("top"), 1, 3)
draw.text(c("left", "top"), 2, 3)
draw.text(c("right", "top"), 3, 3)
draw.text(c("centre", "top"), 4, 3)
draw.text(c(), 1, 4)
draw.text(c("left"), 2, 4)
draw.text(c("right"), 3, 4)
draw.text(c("centre"), 4, 4)

grid.xaxis

Draw an X-Axis

Description

These functions create and draw an x-axis.

Usage

grid.xaxis(at = NULL, label = TRUE, main = TRUE, edits = NULL, name = NULL,
gp = gpar(), draw = TRUE, vp = NULL)

xaxisGrob(at = NULL, label = TRUE, main = TRUE,
edits = NULL, name = NULL, 
 gp = gpar(), vp = NULL)

Arguments

 at A numeric vector of x-value locations for the tick marks.
 label A logical value indicating whether to draw the labels on the tick marks, or an 
 expression or character vector which specify the labels to use. If not logical, 
 must be the same length as the at argument.
 main A logical value indicating whether to draw the axis at the bottom (TRUE) or at 
 the top (FALSE) of the viewport.
 edits A gEdit or gEditList containing edit operations to apply (to the children of the 
 axis) when the axis is first created and during redrawing whenever at is NULL.
 name A character identifier.
 gp An object of class "gpar", typically the output from a call to the function gpar. 
 This is basically a list of graphical parameter settings.
 draw A logical value indicating whether graphics output should be produced.
 vp A Grid viewport object (or NULL).

Details

Both functions create an xaxis grob (a graphical object describing an xaxis), but only grid.xaxis 
draws the xaxis (and then only if draw is TRUE).

Value

An xaxis grob. grid.xaxis returns the value invisibly.

Children

If the at slot of an xaxis grob is not NULL then the xaxis will have the following children:

 major representing the line at the base of the tick marks.
 ticks representing the tick marks.
 labels representing the tick labels.

If the at slot is NULL then there are no children and ticks are drawn based on the current viewport 

scale.

Author(s)

Paul Murrell

See Also

Grid, viewport, grid.yaxis
grid.xspline

**Draw an Xspline**

**Description**

These functions create and draw an xspline, a curve drawn relative to control points.

**Usage**

```r
grid.xspline(...)
xsplineGrob(x = c(0, 0.5, 1, 0.5), y = c(0.5, 1, 0.5, 0),
           id = NULL, id.lengths = NULL,
           default.units = "npc",
           shape = 0, open = TRUE, arrow = NULL, repEnds = TRUE,
           name = NULL, gp = gpar(), vp = NULL)
```

**Arguments**

- `x` A numeric vector or unit object specifying x-locations of spline control points.
- `y` A numeric vector or unit object specifying y-locations of spline control points.
- `id` A numeric vector used to separate locations in `x` and `y` into multiple xsplines. All locations with the same `id` belong to the same xspline.
- `id.lengths` A numeric vector used to separate locations in `x` and `y` into multiple xsplines. Specifies consecutive blocks of locations which make up separate xsplines.
- `default.units` A string indicating the default units to use if `x` or `y` are only given as numeric vectors.
- `shape` A numeric vector of values between -1 and 1, which control the shape of the spline relative to the control points.
- `open` A logical value indicating whether the spline is a line or a closed shape.
- `arrow` A list describing arrow heads to place at either end of the xspline, as produced by the `arrow` function.
- `repEnds` A logical value indicating whether the first and last control points should be replicated for drawing the curve (see Details below).
- `name` A character identifier.
- `gp` An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.
- `vp` A Grid viewport object (or NULL).
- `...` Arguments to be passed to `xsplineGrob`.

**Details**

Both functions create an xspline grob (a graphical object describing an xspline), but only `grid.xspline` draws the xspline.

An xspline is a line drawn relative to control points. For each control point, the line may pass through (interpolate) the control point or it may only approach (approximate) the control point; the behaviour is determined by a shape parameter for each control point.
If the shape parameter is greater than zero, the spline approximates the control points (and is very similar to a cubic B-spline when the shape is 1). If the shape parameter is less than zero, the spline interpolates the control points (and is very similar to a Catmull-Rom spline when the shape is -1). If the shape parameter is 0, the spline forms a sharp corner at that control point.

For open xsplines, the start and end control points must have a shape of 0 (and non-zero values are silently converted to zero without warning).

For open xsplines, by default the start and end control points are actually replicated before the curve is drawn. A curve is drawn between (interpolating or approximating) the second and third of each set of four control points, so this default behaviour ensures that the resulting curve starts at the first control point you have specified and ends at the last control point. The default behaviour can be turned off via the repEnds argument, in which case the curve that is drawn starts (approximately) at the second control point and ends (approximately) at the first and second-to-last control point.

The repEnds argument is ignored for closed xsplines.

Missing values are not allowed for x and y (i.e., it is not valid for a control point to be missing).

For closed xsplines, a curve is automatically drawn between the final control point and the initial control point.

**Value**

A grob object.

**References**


**See Also**

Grid, viewport, arrow.

xspline.

**Examples**

```r
x <- c(0.25, 0.25, 0.75, 0.75)
y <- c(0.25, 0.75, 0.75, 0.25)
xsplineTest <- function(s, i, j, open) {
pushViewport(viewport(layout.pos.col=j, layout.pos.row=i))
grid.points(x, y, default.units="npc", pch=16, size=unit(2, "mm"))
g xspline(x, y, shape=s, open=open, gp=gpar(fill="grey"))
g text(x, gp=gpar(col="grey"),
  x=unit(x, "npc") + unit(c(-1, -1, 1, 1), "mm"),
y=unit(y, "npc") + unit(c(-1, 1, 1, -1), "mm"),
hjust=c(1, 1, 0, 0),
vjust=c(1, 0, 0, 1))
popViewport()
}
pushViewport(viewport(width=.5, x=0, just="left",
  layout=grid.layout(3, 3, respect=TRUE)))
pushViewport(viewport(layout.pos.row=1))
g text("Open Splines", y=1, just="bottom")
```
grid.yaxis

**Description**

These functions create and draw a y-axis.

**Usage**

```r
grid.yaxis(at = NULL, label = TRUE, main = TRUE,
            edits = NULL, name = NULL,
            gp = gpar(), draw = TRUE, vp = NULL)
yaxisGrob(at = NULL, label = TRUE, main = TRUE,
          edits = NULL, name = NULL,
          gp = gpar(), vp = NULL)
```

**Arguments**

- `at`  
  A numeric vector of y-value locations for the tick marks.

- `label`  
  A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the `at` argument.

- `main`  
  A logical value indicating whether to draw the axis at the left (TRUE) or at the right (FALSE) of the viewport.
edits A `gEdit` or `gEditList` containing edit operations to apply (to the children of the axis) when the axis is first created and during redrawing whenever `at` is `NULL`.

name A character identifier.

gp An object of class "gpar", typically the output from a call to the function `gpar`. This is basically a list of graphical parameter settings.

draw A logical value indicating whether graphics output should be produced.

vp A Grid viewport object (or `NULL`).

Details
Both functions create a yaxis grob (a graphical object describing a yaxis), but only `grid.yaxis` draws the yaxis (and then only if `draw` is `TRUE`).

Value
A yaxis grob. `grid.yaxis` returns the value invisibly.

Children
If the `at` slot of an xaxis grob is not `NULL` then the xaxis will have the following children:

- **major** representing the line at the base of the tick marks.
- **ticks** representing the tick marks.
- **labels** representing the tick labels.

If the `at` slot is `NULL` then there are no children and ticks are drawn based on the current viewport scale.

Author(s)
Paul Murrell

See Also
`Grid`, `viewport`, `grid.xaxis`

---

### Create Sets of Coordinates for Grid Grobs

**gridCoords**

These functions support the development of `grobPoints` methods for custom grobs.

#### Usage

```r
gridCoords(x, y)
ggridGrobs(x, name, rule = NULL)
ggridGTreeCoords(x, name)
empty_coords
emptyGrobCoords(name)
emptyGTreeCoords(name)
isEmptyGCoords(coords)
```
Arguments

x For gridCoords a numeric vector. For gridGrobCoords a list of "GridCoords" objects. For gridGTreeCoords a list of either "GridGrobCoords" or "GridGTreeCoords" objects.
y A numeric vector.
nname A character value.
rule A fill rule, either "winding" or "evenodd", or NULL.
coords A set of grob coordinates (as generated by grobCoords).

Details

These functions help the developer of a grobPoints method to generate the coordinates from a custom grob.
The emptyCoords object can be used to return a "null" result (e.g., when asking for closed coordinates on an open line) and the isEmptyCoords function can be used to check for "null" results.

Value

For gridCoords a "GridCoords" object. For gridGrobCoords a "GridGrobCoords" object. For gridGTreeCoords a "GridGTreeCoords" object.

Author(s)

Paul Murrell

grobCoords Calculate Points on the Perimeter of a Grob

Description

These functions calculate points along the perimeter (or length) of a grob.

Usage

grobCoords(x, closed, ...)
grobPoints(x, closed, ...)
isClosed(x, ...)

Arguments

x A grob object.
closed Whether we are asking for points along the perimeter of a closed object or points along the length of an open object. Some grobs (e.g., X-splines) can do both. This defaults to TRUE except for known cases that are not closed (e.g., lines and segments).
... Arguments to be used by methods.
Details

The difference between grobCoords and grobPoints is that grobCoords performs all pre- and post-drawing operations on the grob that would normally occur if the grob was being drawn, then calls grobPoints. So the former takes into account any vp and gp settings on the grob. This means that users should usually only want to call grobCoords; only (expert) developers may have a need to call grobPoints.

Custom grobs can write their own methods for grobPoints (see gridCoords).

The isClosed function returns TRUE or FALSE to indicate whether a grob is a closed shape. The default response is TRUE, unless a method has been defined otherwise (e.g., for lines and line segments).

Value

Either a "GridGrobCoords" object (a list of lists with components x and y) or a "GridGTreeCoords" object (a list of "GridGrobCoords" and/or "GridGTreeCoords" objects).

All locations are in inches relative to the current grid viewport.

Author(s)

Paul Murrell
grobWidth

Create a Unit Describing the Width of a Grob

Description
These functions create a unit object describing the width or height of a grob. They are generic.

Usage
- grobWidth(x)
- grobHeight(x)
- grobAscent(x)
- grobDescent(x)

Arguments
- x: A grob object.

Value
A unit object.

Author(s)
Paul Murrell

See Also
- unit and stringWidth

---

grobX

Create a Unit Describing a Grob Boundary Location

Description
These functions create a unit object describing a location somewhere on the boundary of a grob. They are generic.

Usage
- grobX(x, theta)
- grobY(x, theta)

Arguments
- x: A grob, or gList, or gTree, or gPath.
- theta: An angle indicating where the location is on the grob boundary. Can be one of "east", "north", "west", or "south", which correspond to angles 0, 90, 180, and 270, respectively.
Details

The angle is anti-clockwise with zero corresponding to a line with an origin centred between the extreme points of the shape, and pointing at 3 o’clock.

If the grob describes a single shape, the boundary value should correspond to the exact edge of the shape.

If the grob describes multiple shapes, the boundary value will either correspond to the edge of a bounding box around all of the shapes described by the grob (for multiple rectangles, circles, xsplines, or text), or to a convex hull around all vertices of all shapes described by the grob (for multiple polygons, points, lines, polylines, and segments).

Points grobs are currently a special case because the convex hull is based on the data symbol locations and does not take into account the extent of the data symbols themselves.

The extents of any arrow heads are currently not taken into account.

Value

A unit object.

Author(s)

Paul Murrell

See Also

unit and grobWidth

Description

Constructing a legend grob (in progress)

Usage

legendGrob(labels, nrow, ncol, byrow = FALSE, 
do.lines = has.lty || has.lwd, lines.first = TRUE, 
hgap = unit(1, "lines"), vgap = unit(1, "lines"), 
default.units = "lines", pch, gp = gpar(), vp = NULL)

grid.legend(..., draw=TRUE)

Arguments

labels legend labels (expressions)
nrow, ncol integer; the number of rows or columns, respectively of the legend “layout”. 
ncol is optional and typically computed from the number of labels and ncol.
byrow logical indicating whether rows of the legend are filled first.
do.lines logical indicating whether legend lines are drawn.
legendGrob

lines.first logical indicating whether legend lines are drawn first and hence in a plain “below” legend symbols.
hgap horizontal space between the legend entries
vgap vertical space between the legend entries
default.units default units, see unit.
pch legend symbol, numeric or character, passed to pointsGrob(); see also points for interpretation of the numeric codes.
gp an R object of class “gpar”, typically the output from a call to the function gpar, is basically a list of graphical parameter settings.
vp a Grid viewport object (or NULL).
... for grid.legend(): all the arguments above are passed to legendGrob().
draw logical indicating whether graphics output should be produced.

Value

Both functions create a legend grob (a graphical object describing a plot legend), but only grid.legend draws it (only if draw is TRUE).

See Also

Grid, viewport; pointsGrob, linesGrob.
grid.plot.and.legend contains a simple example.

Examples

## Data:
n <- 10
x <- stats::runif(n) ; y1 <- stats::runif(n) ; y2 <- stats::runif(n)
## Construct the grobs:
plot <- gTree(children=gList(rectGrob(),
             pointsGrob(x, y1, pch=21, gp=gpar(col=2, fill="gray")),
             pointsGrob(x, y2, pch=22, gp=gpar(col=3, fill="gray")),
             xaxisGrob(),
             yaxisGrob()))
legd <- legendGrob(c("Girls", "Boys", "Other"), pch=21:23, gp=gpar(col = 2:4, fill = "gray"))

## Now draw it on a new device page:
grid.newpage()
pushViewport(viewport(width=0.8, height=0.8))
grid.draw(gg)
## makeContent

### Customised grid Grobs

#### Description

These generic hook functions are called whenever a grid grob is drawn. They provide an opportunity for customising the drawing context and drawing content of a new class derived from grob (or gTree).

#### Usage

```
makeContext(x)
makeContent(x)
```

#### Arguments

- **x**: A grid grob.

#### Details

These functions are called by the `grid.draw` methods for grobs and gTrees.

- `makeContext` is called first during the drawing of a grob. This function should be used to modify the `vp` slot of `x` (and/or the `childrenvp` slot if `x` is a gTree). The function must return the modified `x`. Note that the default behaviour for grobs is to push any viewports in the `vp` slot, and for gTrees is to also push up any viewports in the `childrenvp` slot, so this function is used to customise the drawing context for a grob or gTree.

- `makeContent` is called next and is where any additional calculations should occur and graphical content should be generated (see, for example, `grid:::makeContent.xaxis`). This function should be used to modify the children of a gTree. The function must return the modified `x`. Note that the default behaviour for gTrees is to draw all grobs in the `children` slot, so this function is used to customise the drawing content for a gTree. It is also possible to customise the drawing content for a simple grob, but more care needs to be taken; for example, the function should return a standard grid primitive with a `drawDetails()` method in this case.

Note that these functions should be **cumulative** in their effects, so that the `x` returned by `makeContent()` includes any changes made by `makeContext()`.

Note that `makeContext` is also called in the calculation of "grobwidth" and "grobheight" units.

#### Value

Both functions are expected to return a grob or gTree (a modified version of `x`).

#### Author(s)

- Paul Murrell

#### References

See Also
grid.draw

patterns Define Gradient and Pattern Fills

Description

Functions to define gradient fills and pattern fills.

Usage

linearGradient(colours = c("black", "white"),
    stops = seq(0, 1, length.out = length(colours)),
    x1 = unit(0, "npc"), y1 = unit(0, "npc"),
    x2 = unit(1, "npc"), y2 = unit(1, "npc"),
    default.units = "npc",
    extend = c("pad", "repeat", "reflect", "none"),
    group = TRUE)
radiGradient(colours = c("black", "white"),
    stops = seq(0, 1, length.out = length(colours)),
    cx1 = unit(.5, "npc"), cy1 = unit(.5, "npc"),
    r1 = unit(0, "npc"),
    cx2 = unit(.5, "npc"), cy2 = unit(.5, "npc"),
    r2 = unit(.5, "npc"),
    default.units = "npc",
    extend = c("pad", "repeat", "reflect", "none"),
    group = TRUE)

pattern(grob,
    x = 0.5, y = 0.5, width = 1, height = 1,
    default.units = "npc",
    just="centre", hjust=NULL, vjust=NULL,
    extend = c("pad", "repeat", "reflect", "none"),
    gp = gpar(fill="transparent"),
    group = TRUE)

Arguments

colours Two or more colours for the gradient to transition between.

stars Locations of the gradient colours between the start and end points of the gradient
(as a proportion of the distance from the start point to the end point).

x1, y1, x2, y2 The start and end points for a linear gradient.

default.units The coordinate system to use if any location or dimension is specified as just a
numeric value.

extend What happens outside the start and end of the gradient (see Details).

cx1, cy1, r1, cx2, cy2, r2 The centre and radius of the start and end circles for a radial gradient.

grob A grob (or a gTree) that will be drawn as the tile in a pattern fill.
patterns

\[ x, y, \text{width}, \text{height} \]

The size of the tile for a pattern fill.

\[ \text{just, hjust, vjust} \]

The justification of the tile relative to its location.

\[ \text{gp} \]

Default graphical parameter settings for the tile.

\[ \text{group} \]

A logical indicating whether the gradient or pattern is relative to the bounding box of the grob or whether it is relative to individual shapes within the grob.

Details

Use these functions to define a gradient fill or pattern fill and then use the resulting object as the value for fill in a call to the \text{gpar()}\ function.

The possible values of extend, and their meanings, are:

- \text{[pad:]} propagate the value of the gradient at its boundary.
- \text{[none:]} produce no fill beyond the limits of the gradient.
- \text{[repeat:]} repeat the fill.
- \text{[reflect:]} repeat the fill in reverse.

To create a tiling pattern, provide a simple grob (like a circle), specify the location and size of the pattern to include the simple grob, and specify extend="repeat".

On viewports, gradients and patterns are relative to the entire viewport, unless group = FALSE, in which case they are relative to individual grobs as they are drawn. On gTrees, gradients and patterns are relative to a bounding box around all of the children of the gTree, unless group = FALSE, in which case they are relative to individual children as they are drawn. On grobs, gradients and patterns are relative to a bounding box around all of the shapes that are drawn by the grob, unless group = FALSE, in which case they are relative to individual shapes.

Value

A linear gradient or radial gradient or pattern object.

Warning

Gradient fills and pattern fills are not supported on all graphics devices. Where they are not supported, closed shapes will be rendered with a transparent fill. Where they are supported, not all values of extend are supported.

Author(s)

Paul Murrell

See Also

\text{gpar}
plotViewport  

Create a Viewport with a Standard Plot Layout

Description

This is a convenience function for producing a viewport with the common S-style plot layout – i.e., a central plot region surrounded by margins given in terms of a number of lines of text.

Usage

plotViewport(margins=c(5.1, 4.1, 4.1, 2.1), ...)

Arguments

margins  A numeric vector interpreted in the same way as par(mar) in base graphics.

...  All other arguments will be passed to a call to the viewport() function.

Value

A grid viewport object.

Author(s)

Paul Murrell

See Also

viewport and dataViewport.

Querying the Viewport Tree

Get the Current Grid Viewport (Tree)

Description

current.viewport() returns the viewport that Grid is going to draw into.
current.parent returns the parent of the current viewport.
current.vpTree returns the entire Grid viewport tree.
current.vpPath returns the viewport path to the current viewport.
current.transform returns the transformation matrix for the current viewport.
current.rotation returns the (total) rotation for the current viewport.

Usage

current.viewport()
current.parent(n=1)
current.vpTree(all=TRUE)
current.vpPath()
current.transform()
Querying the Viewport Tree

Arguments

- **n**: The number of generations to go up.
- **all**: A logical value indicating whether the entire viewport tree should be returned.

Details

It is possible to get the grandparent of the current viewport (or higher) using the `n` argument to `current.parent()`.

The parent of the ROOT viewport is `NULL`. It is an error to request the grandparent of the ROOT viewport.

If `all` is `FALSE` then `current.vpTree` only returns the subtree below the current viewport.

Value

- A Grid viewport object from `current.viewport` or `current.vpTree`.
- `current.transform` returns a 4x4 transformation matrix.

The viewport path returned by `current.vpPath` is `NULL` if the current viewport is the ROOT viewport.

Author(s)

- Paul Murrell

See Also

- `viewport`

Examples

```r
grid.newpage()
pushViewport(viewport(width=0.8, height=0.8, name="A"))
pushViewport(viewport(x=0.1, width=0.3, height=0.6,
    just="left", name="B"))
upViewport(1)
pushViewport(viewport(x=0.5, width=0.4, height=0.8,
    just="left", name="C"))
pushViewport(viewport(width=0.8, height=0.8, name="D"))
current.vpPath()
upViewport(1)
current.vpPath()
current.vpTree()
current.viewport()
current.vpTree(all=FALSE)
popViewport(0)
```
**resolveRasterSize**  
Utility function to resolve the size of a raster grob

**Description**

Determine the width and height of a raster grob when one or both are not given explicitly.

The result depends on both the aspect ratio of the raster image and the aspect ratio of the physical drawing context, so the result is only valid for the drawing context in which this function is called.

**Usage**

resolveRasterSize(x)

**Arguments**

x  
A raster grob

**Details**

A raster grob can be specified with width and/or height of NULL, which means that the size at which the raster is drawn will be decided at drawing time.

**Value**

A raster grob, with explicit width and height.

**See Also**

grid.raster

**Examples**

# Square raster  
rg <- rasterGrob(matrix(0))  
# Fill the complete page (if page is square)  
grid.newpage()  
resolveRasterSize(rg)$height  
grid.draw(rg)  
# Forced to fit tall thin region  
grid.newpage()  
pushViewport(viewport(width=.1))  
resolveRasterSize(rg)$height  
grid.draw(rg)


**roundrect**  

*Draw a rectangle with rounded corners*

---

**Description**

Draw a *single* rectangle with rounded corners.

**Usage**

```r
roundrectGrob(x=0.5, y=0.5, width=1, height=1,  
  default.units="npc",  
  r=unit(0.1, "snpc"),  
  just="centre",  
  name=NULL, gp=NULL, vp=NULL)
```

**grid.roundrect(...)**

**Arguments**

- `x, y, width, height`: The location and size of the rectangle.
- `default.units`: A string indicating the default units to use if `x`, `y`, `width`, or `height` are only given as numeric vectors.
- `r`: The radius of the rounded corners.
- `just`: The justification of the rectangle relative to its location.
- `name`: A name to identify the grob.
- `gp`: Graphical parameters to apply to the grob.
- `vp`: A viewport object or `NULL`.
- `...`: Arguments to be passed to `roundrectGrob()`.

**Details**

At present, this function can only be used to draw *one* rounded rectangle.

**Examples**

```r
grid.roundrect(width=.5, height=.5, name="rr")
theta <- seq(0, 360, length.out=50)
for (i in 1:50)
  grid.circle(x=grobX("rr", theta[i]),  
              y=grobY("rr", theta[i]),  
              r=unit(1, "mm"),  
              gp=gpar(fill="black"))
```
showGrob

Label grid grobs.

Description

Produces a graphical display of (by default) the current grid scene, with labels showing the names of each grob in the scene. It is also possible to label only specific grobs in the scene.

Usage

showGrob(x = NULL, 
        gPath = NULL, strict = FALSE, grep = FALSE, 
        recurse = TRUE, depth = NULL, 
        labelfun = grobLabel, ...)

Arguments

x
If NULL, the current grid scene is labelled. Otherwise, a grob (or gTree) to draw and then label.

gPath
A path identifying a subset of the current scene or grob to be labelled.

strict
Logical indicating whether the gPath is strict.

grep
Logical indicating whether the gPath is a regular expression.

recurse
Should the children of gTrees also be labelled?

depth
Only display grobs at the specified depth (may be a vector of depths).

labelfun
Function used to generate a label from each grob.

...  Arguments passed to labelfun to control fine details of the generated label.

Details

None of the labelling is recorded on the grid display list so the original scene can be reproduced by calling grid.refresh.

See Also

grob and gTree

Examples

grid.newpage()
gt <- gTree(children=vpStack(
    viewport(x=0, width=.5, just="left", name="vp"),
    viewport(y=.5, height=.5, just="bottom", name="vp2")),
children=gList(rectGrob(vp="vp::vp2", name="child")),
    name="parent")
grid.draw(gt)
showGrob()
showGrob(gPath="child")
showGrob(recurse=FALSE)
showGrob(depth=1)
showGrob(depth=2)
showViewport

Display grid viewports.

Description

Produces a graphical display of (by default) the current grid viewport tree. It is also possible to display only specific viewports. Each viewport is drawn as a rectangle and the leaf viewports are labelled with the viewport name.

Usage

showViewport(vp = NULL, recurse = TRUE, depth = NULL, newpage = FALSE, leaves = FALSE, col = rgb(0, 0, 1, 0.2), fill = rgb(0, 0, 1, 0.1), label = TRUE, nrow = 3, ncol = nrow)
stringWidth

Create a Unit Describing the Width and Height of a String or Math Expression

Description

These functions create a unit object describing the width or height of a string.

Usage

stringWidth(string)
stringHeight(string)
stringAscent(string)
stringDescent(string)
Arguments

string A character vector or a language object (as used for ‘plotmath’ calls).

Value

A unit object.

Author(s)

Paul Murrell

See Also

unit and grobWidth
strwidth in the graphics package for more details of the typographic concepts behind the computations.

unit Function to Create a Unit Object

Description

This function creates a unit object — a vector of unit values. A unit value is typically just a single numeric value with an associated unit.

Usage

unit(x, units, data=NULL)
is.unit(x)

Arguments

x A numeric vector.
For is.unit, any R object.
units A character vector specifying the units for the corresponding numeric values.
data This argument is used to supply extra information for special unit types.

Details

Unit objects allow the user to specify locations and dimensions in a large number of different coordinate systems. All drawing occurs relative to a viewport and the units specifies what coordinate system to use within that viewport.

Possible units (coordinate systems) are:

"npc" Normalised Parent Coordinates (the default). The origin of the viewport is (0, 0) and the viewport has a width and height of 1 unit. For example, (0.5, 0.5) is the centre of the viewport.
"cm" Centimetres.
"inches" Inches. 1 in = 2.54 cm.
"mm" Millimetres. 10 mm = 1 cm.
"points"  Points. 72.27 pt = 1 in.
"picas"  Picas. 1 pc = 12 pt.
"bigpts"  Big Points. 72 bp = 1 in.
"dida"  Dida. 1157 dd = 1238 pt.
"cicero"  Cicero. 1 cc = 12 dd.
"scaledpts"  Scaled Points. 65536 sp = 1 pt.
"lines"  Lines of text. Locations and dimensions are in terms of multiples of the default text size of the viewport (as specified by the viewport's fontsize and lineheight).
"char"  Multiples of nominal font height of the viewport (as specified by the viewport's fontsize).
"native"  Locations and dimensions are relative to the viewport's xscale and yscale.
"snpc"  Square Normalised Parent Coordinates. Same as Normalised Parent Coordinates, except gives the same answer for horizontal and vertical locations/dimensions. It uses the lesser of npc-width and npc-height. This is useful for making things which are a proportion of the viewport, but have to be square (or have a fixed aspect ratio).
"strwidth"  Multiples of the width of the string specified in the data argument. The font size is determined by the pointsize of the viewport.
"strheight"  Multiples of the height of the string specified in the data argument. The font size is determined by the pointsize of the viewport.
"grobwidth"  Multiples of the width of the grob specified in the data argument.
"grobheight"  Multiples of the height of the grob specified in the data argument.

A number of variations are also allowed for the most common units. For example, it is possible to use "in" or "inch" instead of "inches" and "centimetre" or "centimeter" instead of "cm".

A special units value of "null" is also allowed, but only makes sense when used in specifying widths of columns or heights of rows in grid layouts (see grid.layout).

The data argument must be a list when the unit.length() is greater than 1. For example,

unit(rep(1, 3), c("npc", "strwidth", "inches"), data = list(NULL, "my string", NULL))

It is possible to subset unit objects in the normal way and to perform subassignment (see the examples), but a special function unit.c is provided for combining unit objects.

Certain arithmetic and summary operations are defined for unit objects. In particular, it is possible to add and subtract unit objects (e.g., unit(1, "npc") - unit(1, "inches")), and to specify the minimum or maximum of a list of unit objects (e.g., min(unit(0.5, "npc"), unit(1, "inches"))).

There is a format method for units, which should respond to the arguments for the default format method, e.g., digits to control the number of significant digits printed for numeric values.

The is.unit() function is a convenience for checking whether x inherits from the "unit" class.

Value

An object of class "unit".

WARNING

There is a special function unit.c for concatenating several unit objects.

The c function will not give the right answer.

There used to be "mylines", "mychar", "mystrwidth", "mystrheight" units. These will still be accepted, but work exactly the same as "lines", "char", "strwidth", "strheight".
unit.c

Author(s)
Paul Murrell

See Also
unit.c

Examples

unit(1, "npc")
unit(1:3/4, "npc")
unit(1:3/4, "npc") + unit(1, "inches")
min(unit(0.5, "npc"), unit(1, "inches"))
unit.c(unit(0.5, "npc"), unit(2, "inches") + unit(1:3/4, "npc"),
unit(1, "strwidth", "hi there"))

x <- unit(1:5, "npc")
x[2:4]
x[2:4] <- unit(1, "mm")
x

unit.c Combine Unit Objects

Description
This function produces a new unit object by combining the unit objects specified as arguments.

Usage
unit.c(..., check = TRUE)

Arguments

... An arbitrary number of unit objects.
check Should input be checked? If you are certain all arguments are unit objects this can be set to FALSE

Value
An object of class unit.

Author(s)
Paul Murrell

See Also
unit.
unit.length | Length of a Unit Object

**Description**

The length of a unit object is defined as the number of unit values in the unit object.

This function has been deprecated in favour of a unit method for the generic length function.

**Usage**

```r
unit.length(unit)
```

**Arguments**

- `unit` A unit object.

**Value**

An integer value.

**Author(s)**

Paul Murrell

**See Also**

`unit`

**Examples**

```r
code
length(unit(1:3, "npc"))
length(unit(1:3, "npc") + unit(1, "inches"))
length(max(unit(1:3, "npc") + unit(1, "inches")))
length(max(unit(1:3, "npc") + unit(1, "strwidth", "a")*4))
length(unit(1:3, "npc") + unit(1, "strwidth", "a")*4)
```

unit.pmin | Parallel Unit Minima and Maxima

**Description**

Returns a unit object whose i’th value is the minimum (or maximum) of the i’th values of the arguments.

**Usage**

```r
unit.pmin(...)  
unit.pmax(...)  
unit.psum(...) 
```
Arguments

... One or more unit objects.

Details

The length of the result is the maximum of the lengths of the arguments; shorter arguments are recycled in the usual manner.

Value

A unit object.

Author(s)

Paul Murrell

Examples

max(unit(1:3, "cm"), unit(0.5, "npc"))
unit.pmax(unit(1:3, "cm"), unit(0.5, "npc"))

unit.rep Replicate Elements of Unit Objects

Description

Replicates the units according to the values given in times and length.out.

This function has been deprecated in favour of a unit method for the generic rep function.

Usage

unit.rep(x, ...)

Arguments

x An object of class "unit".

... arguments to be passed to rep such as times and length.out.

Value

An object of class "unit".

Author(s)

Paul Murrell

See Also

rep
Examples

```r
rep(unit(1:3, "npc"), 3)
rep(unit(1:3, "npc"), 1:3)
rep(unit(1:3, "npc") + unit(1, "inches"), 3)
rep(max(unit(1:3, "npc") + unit(1, "inches")), 3)
rep(max(unit(1:3, "npc") + unit(1, "strwidth", "a")*4), 3)
rep(unit(1:3, "npc") + unit(1, "strwidth", "a")*4, 3)
```

**Description**

This function returns the units of a unit object.

**Usage**

```r
unitType(x, recurse = FALSE)
```

**Arguments**

- `x` A unit object.
- `recurse` Whether to recurse into complex units.

**Value**

For simple units, this will be just a vector of coordinate systems, like "inches" or "npc".

More complex units that involve an operation on units return an operator, like "sum", "min", or "max".

When `recurse = TRUE`, the result is always a list and more complex units generate sublists (see the Examples below).

**Author(s)**

Thomas Lin Pedersen and Paul Murrell

**See Also**

`unit`

**Examples**

```r
u <- unit(1:5, c("cm", "mm", "in", "pt", "null"))

unitType(u)
unitType(unit(1, "npc"))
unitType(unit(1:3/4, "npc"))
unitType(unit(1:3/4, "npc") + unit(1, "inches"))
unitType(min(unit(0.5, "npc"), unit(1, "inches")))
unitType(unit.c(unit(0.5, "npc"), unit(2, "inches") + unit(1:3/4, "npc"),
unit(1, "strwidth", "hi there")))
unitType(min(unit(1, "in"), unit(1, "npc") + unit(1, "mm")))
```
valid.just

Validate a Justification

Description
Utility functions for determining whether a justification specification is valid and for resolving a single justification value from a combination of character and numeric values.

Usage
valid.just(just)
resolveHJust(just, hjust)
resolveVJust(just, vjust)

Arguments
just A justification either as a character value, e.g., "left", or as a numeric value, e.g., 0.
hjust A numeric horizontal justification
vjust A numeric vertical justification

Details
These functions may be useful within a validDetails method when writing a new grob class.

Value
A numeric representation of the justification (e.g., "left" becomes 0, "right" becomes 1, etc, ...). An error is given if the justification is not valid.

Author(s)
Paul Murrell
validDetails  

**Customising grid grob Validation**

**Description**

This generic hook function is called whenever a grid grob is created or edited via `grob`, `gTree`, `grid.edit` or `editGrob`. This provides an opportunity for customising the validation of a new class derived from grob (or gTree).

**Usage**

validDetails(x)

**Arguments**

- `x`: A grid grob.

**Details**

This function is called by `grob`, `gTree`, `grid.edit` and `editGrob`. A method should be written for classes derived from grob or gTree to validate the values of slots specific to the new class. (e.g., see `grid:::validDetails.axis`).

Note that the standard slots for grobs and gTrees are automatically validated (e.g., `vp`, `gp` slots for grobs and, in addition, `children`, and `childrenvp` slots for gTrees) so only slots specific to a new class need to be addressed.

**Value**

The function MUST return the validated grob.

**Author(s)**

Paul Murrell

**See Also**

- `grid.edit`

---

**viewportTransform**  

**Define a Group Transformation**

**Description**

These functions define the transformation that will be applied when a `grid.define()`d group is `grid.use()`d.
viewportTransform

Usage

viewportTransform(group, shear=groupShear(), flip=groupFlip(), device=TRUE)
viewportScale(group, device=TRUE)
viewportRotate(group, device=TRUE)
defnTranslate(group, inverse=FALSE, device=TRUE)
defnScale(group, inverse=FALSE)
defnRotate(group, inverse=FALSE, device=TRUE)
useTranslate(inverse=FALSE, device=TRUE)
useScale(inverse=FALSE, device=TRUE)
useRotate(inverse=FALSE, device=TRUE)
groupTranslate(dx=0, dy=0)
groupRotate(r=0, device=TRUE)
groupScale(sx=1, sy=1)
groupShear(sx=0, sy=0)
groupFlip(flipX=FALSE, flipY=FALSE)

Arguments

group The group that is being transformed.
inverse A logical indicating whether we want the forward or backward transformation.
shear An affine transformation matrix that describes a shear transformation.
flip A affine transformation matrix that describes a scaling inversion.
dx, dy The translation to apply.
r The rotation to apply.
sx, sy The scaling (or shear) to apply.
flipX, flipY Whether to negate the x-scaling or y-scaling (logical).
device A logical indicating whether transformation should be relative to the device or relative to the current viewport.

Details

The viewport*() functions are not called directly. They are passed as the transform argument to grid.use.

The defn*() and use*() functions are also not called directly, but can be useful to create custom transformation functions. For example, see the source code for viewportTransform.

The group*() functions generate basic affine transformation matrices and may also be useful to create custom transformation functions. For example, the groupShear() function can be used to specify a shear transform to viewportTransform().

It is also possible to define any function that returns a 3x3 matrix (as long as the last column contains 0, 0, and 1) and use it as the transform argument to grid.use, but the results will probably be device-dependent, and may be very difficult to predict. The function will be called with two arguments: group and device.

Value

An affine transformation matrix.
vpPath

Author(s)

Paul Murrell

See Also

Grid

Examples

## NOTE: on devices without support for groups nothing will be drawn
grid.newpage()
## Define and use group in same viewport
pushViewport(viewport(width=.2, height=.2))
grid.define(circleGrob(gp=gpar(lwd=5)), name="circle")
grid.use("circle")
popViewport()
## Use group in viewport that is translated and scaled
pushViewport(viewport(x=.2, y=.2, width=.1, height=.1))
grid.use("circle")
popViewport()
## Use group in viewport that is translated and scaled
## BUT only make use of the translation
pushViewport(viewport(x=.2, y=.8, width=.1, height=.1))
grid.use("circle", transform=viewportTranslate)
popViewport()
## Use group in viewport that is translated and scaled
## unevenly (distorted)
pushViewport(viewport(x=.8, y=.7, width=.2, height=.4))
grid.use("circle")
popViewport()

---

vpPath

Concatenate Viewport Names

Description

This function can be used to generate a viewport path for use in downViewport or seekViewport.
A viewport path is a list of nested viewport names.

Usage

vpPath(...)

Arguments

... Character values which are viewport names.
Details

Viewport names must only be unique amongst viewports which share the same parent in the viewport tree.

This function can be used to generate a specification for a viewport that includes the viewport’s parent’s name (and the name of its parent and so on).

For interactive use, it is possible to directly specify a path, but it is strongly recommended that this function is used otherwise in case the path separator is changed in future versions of grid.

Value

A `vpPath` object.

See Also

`viewport`, `pushViewport`, `popViewport`, `downViewport`, `seekViewport`, `upViewport`

Examples

```r
vpPath("vp1", "vp2")
```

widthDetails

Width and Height of a grid grob

Description

These generic functions are used to determine the size of grid grobs.

Usage

```r
widthDetails(x)
heightDetails(x)
ascentDetails(x)
descentDetails(x)
```

Arguments

x

A grid grob.

Details

These functions are called in the calculation of "grobwidth" and "grobheight" units. Methods should be written for classes derived from grob or gTree where the size of the grob can be determined (see, for example `grid::widthDetails.frame`).

The ascent of a grob is the height of the grob by default and the descent of a grob is zero by default, except for text grobs where the label is a single character value or expression.

Value

A unit object.
Working with Viewports

Description

Grid maintains a tree of viewports — nested drawing contexts. These functions provide ways to add or remove viewports and to navigate amongst viewports in the tree.

Usage

pushViewport(..., recording=TRUE)
popViewport(n = 1, recording=TRUE)
downViewport(name, strict=FALSE, recording=TRUE)
seekViewport(name, recording=TRUE)
upViewport(n = 1, recording=TRUE)

Arguments

... One or more objects of class "viewport".

n An integer value indicating how many viewports to pop or navigate up. The special value 0 indicates to pop or navigate viewports right up to the root viewport.

name A character value to identify a viewport in the tree.

strict A boolean indicating whether the vpPath must be matched exactly.

recording A logical value to indicate whether the viewport operation should be recorded on the Grid display list.

Details

Objects created by the viewport() function are only descriptions of a drawing context. A viewport object must be pushed onto the viewport tree before it has any effect on drawing.

The viewport tree always has a single root viewport (created by the system) which corresponds to the entire device (and default graphical parameter settings). Viewports may be added to the tree using pushViewport() and removed from the tree using popViewport().

There is only ever one current viewport, which is the current position within the viewport tree. All drawing and viewport operations are relative to the current viewport. When a viewport is pushed it becomes the current viewport. When a viewport is popped, the parent viewport becomes the current viewport. Use upViewport to navigate to the parent of the current viewport, without removing the current viewport from the viewploot tree. Use downViewport to navigate to a viewport further down the viewport tree and seekViewport to navigate to a viewport anywhere else in the tree.

If a viewport is pushed and it has the same name as a viewport at the same level in the tree, then it replaces the existing viewport in the tree.
Value

downViewport returns the number of viewports it went down.

This can be useful for returning to your starting point by doing something like depth <-
downViewport() then upViewport(depth).

Author(s)

Paul Murrell

See Also

`viewport` and `vpPath`.

Examples

```r
# push the same viewport several times
grid.newpage()
vp <- viewport(width=0.5, height=0.5)
pushViewport(vp)
grid.rect(gp=gpar(col="blue"))
grid.text("Quarter of the device",
y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="blue"))
pushViewport(vp)
grid.rect(gp=gpar(col="red"))
grid.text("Quarter of the parent viewport",
y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="red"))
popViewport(2)

# push several viewports then navigate amongst them
grid.newpage()
grid.rect(gp=gpar(col="grey"))
grid.text("Top-level viewport",
y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="grey"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(width=0.8, height=0.7, name="A"))
grid.rect(gp=gpar(col="blue"))
grid.text("1. Push Viewport A",
y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(x=0.1, width=0.3, height=0.6,
just="left", name="B"))
grid.rect(gp=gpar(col="red"))
grid.text("2. Push Viewport B (in A)",
y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="red"))
if (interactive()) Sys.sleep(1.0)
upViewport(1)
grid.text("3. Up from B to A",
y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(x=0.5, width=0.4, height=0.8,
just="left", name="C"))
grid.rect(gp=gpar(col="green"))
grid.text("4. Push Viewport C (in A)",
y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="green"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(width=0.8, height=0.6, name="D"))
grid.rect()
```
grid.text("5. Push Viewport D (in C)",
y=unit(1, "npc") - unit(1, "lines"))
if (interactive()) Sys.sleep(1.0)
upViewport(0)
grid.text("6. Up from D to top-level",
y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="grey"))
if (interactive()) Sys.sleep(1.0)
downViewport("D")
grid.text("7. Down from top-level to D",
y=unit(1, "npc") - unit(2, "lines"))
if (interactive()) Sys.sleep(1.0)
seekViewport("D")
grid.text("8. Seek from D to B",
y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="red"))
pushViewport(viewport(width=0.9, height=0.5, name="A"))
grid.rect()
grid.text("9. Push Viewport A (in B)",
y=unit(1, "npc") - unit(1, "lines"))
if (interactive()) Sys.sleep(1.0)
seekViewport("A")
grid.text("10. Seek from B to A (in ROOT)",
y=unit(1, "npc") - unit(3, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
seekViewport(vpPath("B", "A"))
grid.text("11. Seek from A (in ROOT) into A (in B)"
popViewport(0)

xDetails

Boundary of a grid grob

Description

These generic functions are used to determine a location on the boundary of a grid grob.

Usage

xDetails(x, theta)
yDetails(x, theta)

Arguments

x A grid grob.
theta A numeric angle, in degrees, measured anti-clockwise from the 3 o’clock or one of the following character strings: "north", "east", "west", "south".

Details

The location on the grob boundary is determined by taking a line from the centre of the grob at the angle theta and intersecting it with the convex hull of the grob (for the basic grob primitives, the centre is determined as half way between the minimum and maximum values in x and y directions). These functions are called in the calculation of "grobx" and "groby" units as produced by the grobx and groby functions. Methods should be written for classes derived from grob or gTree where the boundary of the grob can be determined.
Value
A unit object.

Author(s)
Paul Murrell

See Also
grobX, grobY.

xsplinePoints
Return the points that would be used to draw an Xspline (or a Bezier curve).

Description
Rather than drawing an Xspline (or Bezier curve), this function returns the points that would be used to draw the series of line segments for the Xspline. This may be useful to post-process the Xspline curve, for example, to clip the curve.

Usage
xsplinePoints(x)
bezierPoints(x)

Arguments
x An Xspline grob, as produced by the xsplineGrob() function (or a beziergrob, as produced by the bezierGrob() function).

Details
The points returned by this function will only be relevant for the drawing context in force when this function was called.

Value
Depends on how many Xsplines would be drawn. If only one, then a list with two components, named x and y, both of which are unit objects (in inches). If several Xsplines would be drawn then the result of this function is a list of lists.

Author(s)
Paul Murrell

See Also
xsplineGrob and bezierGrob
Examples

```r
grid.newpage()
xsg <- xsplineGrob(c(.1, .1, .9, .9), c(.1, .9, .9, .1), shape=1)
grid.draw(xsg)
trace <- xsplinePoints(xsg)
grid.circle(trace$x, trace$y, default.units="inches", r=unit(.5, "mm"))

grid.newpage()
vp <- viewport(width=.5)
xg <- xsplineGrob(x=c(0, .2, .4, .2, .5, .7, .9, .7),
y=c(.5, 1, .5, .5, 1, .5, 0, 0),
id=rep(1:2, each=4),
    shape=1,
    vp=vp)
grid.draw(xg)
trace <- xsplinePoints(xg)
pushViewport(vp)
invisible(lapply(trace, function(t) grid.lines(t$x, t$y, gp=gpar(col="red"))))
popViewport()

grid.newpage()
bg <- bezierGrob(c(.2, .2, .8, .8), c(.2, .8, .8, .2))
grid.draw(bg)
trace <- bezierPoints(bg)
grid.circle(trace$x, trace$y, default.units="inches", r=unit(.5, "mm"))
```
Chapter 7

The methods package

---

**methods-package**  *Formal Methods and Classes*

**Description**

Formally defined methods and classes for R objects, plus other programming tools, as described in the references.

**Details**

This package provides the “S4” or “S version 4” approach to methods and classes in a functional language.

For basic use of the techniques, start with Introduction and follow the links there to the key functions for programming, notably `setClass` and `setMethod`.

Some specific topics:

**Classes:** Creating one, see `setClass`; examining definitions, see `getClassDef` and `classRepresentation`; inheritance and coercing, see `is` and `as`

**Generic functions:** Basic programming, see `setGeneric`; the class of objects, see `genericFunction`; other functions to examine or manipulate them, see `GenericFunctions`.

**S3:** Using classes, see `setOldClass`; methods, see `Methods_for_S3`.

**Reference classes:** See `ReferenceClasses`.

**Class unions; virtual classes** See `setClassUnion`.

These pages will have additional links to related topics.

For a complete list of functions and classes, use `library(help="methods")`.

**Author(s)**

R Core Team

Maintainer: R Core Team <R-core@r-project.org>
References


Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Chapter 10 has some additional details.)

---

**BasicFunsList**

*List of Built-in and Special Functions*

**Description**

A named list providing instructions for turning built-in and special functions into generic functions.

Functions in R that are defined as `.Primitive(<name>)` are not suitable for formal methods, because they lack the basic reflectance property. You can’t find the argument list for these functions by examining the function object itself.

Future versions of R may fix this by attaching a formal argument list to the corresponding function. While generally the names of arguments are not checked by the internal code implementing the function, the number of arguments frequently is.

In any case, some definition of a formal argument list is needed if users are to define methods for these functions. In particular, if methods are to be merged from multiple packages, the different sets of methods need to agree on the formal arguments.

In the absence of reflectance, this list provides the relevant information via a dummy function associated with each of the known specials for which methods are allowed.

At the same, the list flags those specials for which methods are meaningless (e.g., `for`) or just a very bad idea (e.g., `.Primitive`).

A generic function created via `setMethod`, for example, for one of these special functions will have the argument list from `BasicFunsList`. If no entry exists, the argument list `(x, ...)` is assumed.

---

**as**

*Force an Object to Belong to a Class*

**Description**

Coerce an object to a given class.

**Usage**

```r
as(object, Class, strict=TRUE, ext)

as(object, Class) <- value
```
**Arguments**

- `object`: any R object.
- `Class`: the name of the class to which `object` should be coerced.
- `strict`: logical flag. If `TRUE`, the returned object must be strictly from the target class (unless that class is a virtual class, in which case the object will be from the closest actual class, in particular the original object, if that class extends the virtual class directly).
  
  If `strict = FALSE`, any simple extension of the target class will be returned, without further change. A simple extension is, roughly, one that just adds slots to an existing class.
- `value`: The value to use to modify `object` (see the discussion below). You should supply an object with class `Class`; some coercion is done, but you're unwise to rely on it.
- `ext`: an optional object defining how `Class` is extended by the class of the object (as returned by `possibleExtends`). This argument is used internally; do not use it directly.

**Description**

`as(object)` returns the version of this object coerced to be the given `Class`. When used in the replacement form on the left of an assignment, the portion of the object corresponding to `Class` is replaced by `value`.

The operation of `as()` in either form depends on the definition of coerce methods. Methods are defined automatically when the two classes are related by inheritance; that is, when one of the classes is a subclass of the other.

Coerce methods are also predefined for basic classes (including all the types of vectors, functions and a few others).

Beyond these two sources of methods, further methods are defined by calls to the `setAs` function. See that documentation also for details of how coerce methods work. Use `showMethods(coerce)` for a list of all currently defined methods, as in the example below.

**Basic Coercion Methods**

Methods are pre-defined for coercing any object to one of the basic datatypes. For example, `as(x, "numeric")` uses the existing `as.numeric` function. These and all other existing methods can be listed as shown in the example.

**References**


**See Also**

If you think of using `try(as(x, cl))`, consider `canCoerce(x, cl)` instead.

**Examples**

```r
## Show all the existing methods for as()
showMethods("coerce")```
BasicClasses

Classes Corresponding to Basic Data Types

Description

Formal classes exist corresponding to the basic R object types, allowing these types to be used in method signatures, as slots in class definitions, and to be extended by new classes.

Usage

### The following are all basic vector classes.

### They can appear as class names in method signatures,

### in calls to as(), is(), and new().

"character"
"complex"
"double"
"expression"
"integer"
"list"
"logical"
"numeric"
"single"
"raw"

### the class

"vector"

### is a virtual class, extended by all the above

### the class

"S4"

### is an object type for S4 objects that do not extend

### any of the basic vector classes. It is a virtual class.

### The following are additional basic classes

"NULL" # NULL objects
"Function" # function objects, including primitives
"externalPtr" # raw external pointers for use in C code

"ANY" # virtual classes used by the methods package itself
"VIRTUAL"
"missing"

"namedList" # the alternative to "list" that preserves

# the names attribute

Objects from the Classes

If a class is not virtual (see section in Classes_Details), objects can be created by calls of the form new(Class, ...), where Class is the quoted class name, and the remaining arguments if any are objects to be interpreted as vectors of this class. Multiple arguments will be concatenated.
The class "expression" is slightly odd, in that the arguments will not be evaluated; therefore, don't enclose them in a call to `quote()`.

Note that class "list" is a pure vector. Although lists with names go back to the earliest versions of S, they are an extension of the vector concept in that they have an attribute (which can now be a slot) and which is either `NULL` or a character vector of the same length as the vector. If you want to guarantee that list names are preserved, use class "namedList", rather than "list". Objects from this class must have a names attribute, corresponding to slot "names", of type "character". Internally, R treats names for lists specially, which makes it impractical to have the corresponding slot in class "namedList" be a union of character names and `NULL`.

### Classes and Types

The basic classes include classes for the basic R types. Note that objects of these types will not usually be S4 objects (`isS4` will return `FALSE`), although objects from classes that contain the basic class will be S4 objects, still with the same type. The type as returned by `typeof` will sometimes differ from the class, either just from a choice of terminology (type "symbol" and class "name", for example) or because there is not a one-to-one correspondence between class and type (most of the classes that inherit from class "language" have type "language", for example).

### Extends

The vector classes extend "vector", directly.

### Methods

- **coerce** Methods are defined to coerce arbitrary objects to the vector classes, by calling the corresponding basic function, for example, `as(x, "numeric")` calls `as.numeric(x)`.

---

### callGeneric

**Call the Current Generic Function from a Method**

### Description

A call to `callGeneric` can only appear inside a method definition. It then results in a call to the current generic function. The value of that call is the value of `callGeneric`. While it can be called from any method, it is useful and typically used in methods for group generic functions.

### Usage

`callGeneric(...)`

### Arguments

- `...` Optionally, the arguments to the function in its next call.
  If no arguments are included in the call to `callGeneric`, the effect is to call the function with the current arguments. See the detailed description for what this really means.
Details

The name and package of the current generic function is stored in the environment of the method definition object. This name is looked up and the corresponding function called.

The statement that passing no arguments to callGeneric causes the generic function to be called with the current arguments is more precisely as follows. Arguments that were missing in the current call are still missing (remember that "missing" is a valid class in a method signature). For a formal argument, say x, that appears in the original call, there is a corresponding argument in the generated call equivalent to x = x. In effect, this means that the generic function sees the same actual arguments, but arguments are evaluated only once.

Using callGeneric with no arguments is prone to creating infinite recursion, unless one of the arguments in the signature has been modified in the current method so that a different method is selected.

Value

The value returned by the new call.

References


See Also

GroupGenericFunctions for other information about group generic functions; Methods_Details for the general behavior of method dispatch

Examples

```r
## the method for group generic function Ops
## for signature( e1="structure", e2="vector")
function (e1, e2)
{
  value <- callGeneric(e1@.Data, e2)
  if (length(value) == length(e1)) {
    e1@.Data <- value
    e1
  } else value
}

## For more examples
## Not run:
showMethods("Ops", includeDefs = TRUE)

## End(Not run)
```
**Description**

A call to `callNextMethod` can only appear inside a method definition. It then results in a call to the first inherited method after the current method, with the arguments to the current method passed down to the next method. The value of that method call is the value of `callNextMethod`.

**Usage**

`callNextMethod(...)`

**Arguments**

Optionally, the arguments to the function in its next call (but note that the dispatch is as in the detailed description below; the arguments have no effect on selecting the next method.)

If no arguments are included in the call to `callNextMethod`, the effect is to call the method with the current arguments. See the detailed description for what this really means.

Calling with no arguments is often the natural way to use `callNextMethod`; see the examples.

**Details**

The ‘next’ method (i.e., the first inherited method) is defined to be that method which *would* have been called if the current method did not exist. This is more-or-less literally what happens: The current method (to be precise, the method with signature given by the defined slot of the method from which `callNextMethod` is called) is deleted from a copy of the methods for the current generic, and `selectMethod` is called to find the next method (the result is cached in the method object where the call occurred, so the search typically happens only once per session per combination of argument classes).

The next method is defined from the signature of the current method, not from the actual classes of the arguments. In particular, modifying any of the arguments has no effect on the selection. As a result, the selected next method can be called with invalid arguments if the calling function assigns objects of a different class before the `callNextMethod()` call. Be careful of any assignments to such arguments.

It is possible for the selection of the next method to be ambiguous, even though the original set of methods was consistent. See the section “Ambiguous Selection”.

The statement that the method is called with the current arguments is more precisely as follows. Arguments that were missing in the current call are still missing (remember that “missing” is a valid class in a method signature). For a formal argument, say `x`, that appears in the original call, there is a corresponding argument in the next method call equivalent to `x = x`. In effect, this means that the next method sees the same actual arguments, but arguments are evaluated only once.

**Value**

The value returned by the selected method.
Ambiguous Selection

There are two fairly common situations in which the choice of a next method is ambiguous, even when the original set of methods uniquely defines all method selection unambiguously. In these situations, \texttt{callNextMethod()} should be replaced, either by a call to a specific function or by recalling the generic with different arguments.

The most likely situation arises with methods for binary operators, typically through one of the group generic functions. See the example for class "rnum" below. Examples of this sort usually require three methods: two for the case that the first or the second argument comes from the class, and a third for the case that both arguments come from the class. If that last method uses \texttt{callNextMethod}, the other two methods are equally valid. The ambiguity is exactly the same that required defining the two-argument method in the first place.

In fact, the two possibilities are equally valid conceptually as well as formally. As in the example below, the logic of the application usually requires selecting a computation explicitly or else calling the generic function with modified arguments to select an appropriate method.

The other likely source of ambiguity arises from a class that inherits directly from more than one other class (a “mixin” in standard terminology). If the generic has methods corresponding to both superclasses, a method for the current class is again needed to resolve ambiguity. Using \texttt{callNextMethod} will again reimpose the ambiguity. Again, some explicit choice has to be made in the calling method instead.

These ambiguities are not the result of bad design, but they do require workarounds. Other ambiguities usually reflect inconsistencies in the tree of inheritances, such as a class appearing in more than one place among the superclasses. Such cases should be rare, but with the independent definition of classes in multiple packages, they can’t be ruled out.

References

Chambers, John M. (2016) \textit{Extending R}, Chapman & Hall. (Chapters 9 and 10.)

See Also

\texttt{callGeneric} to call the generic function with the current dispatch rules (typically for a group generic function); \texttt{Methods_Details} for the general behavior of method dispatch.

Examples

## callNextMethod() used for the Math, Math2 group generic functions

## A class to automatically round numeric results to "d" digits

```
rnum <- setClass("rnum", slots = c(d = "integer"), contains = "numeric")
```

## Math functions operate on the rounded numbers, return a plain vector. The next method will always be the default, usually a primitive.

```
setMethod("Math", "rnum",
  function(x)
    callNextMethod(round(as.numeric(x), x@d)))
setMethod("Math2", "rnum",
  function(x, digits)
    callNextMethod(round(as.numeric(x), x@d), digits))
```

## Examples of callNextMethod with two arguments in the signature.

## For arithmetic and one rnum with anything, callNextMethod with no arguments
callNextMethod

```r
## round the full accuracy result, and return as plain vector
setMethod("Arith", c(e1 = "rnum"),
          function(e1, e2)
            as.numeric(round(callNextMethod(), e1@d)))
setMethod("Arith", c(e2 = "rnum"),
          function(e1, e2)
            as.numeric(round(callNextMethod(), e2@d)))

## A method for BOTH arguments from "rnum" would be ambiguous
## for callNextMethod(): the two methods above are equally valid.
## The method chooses the smaller number of digits,
## and then calls the generic function, postponing the method selection
## until it's not ambiguous.
setMethod("Arith", c(e1 = "rnum", e2 = "rnum"),
          function(e1, e2) {
            if(e1@d <= e2@d)
              callGeneric(e1, as.numeric(e2))
            else
              callGeneric(as.numeric(e1), e2)
          })

## For comparisons, callNextMethod with the rounded arguments
setMethod("Compare", c(e1 = "rnum"),
          function(e1, e2)
            callNextMethod(round(e1, e1@d), round(e2, e1@d)))
setMethod("Compare", c(e2 = "rnum"),
          function(e1, e2)
            callNextMethod(round(e1, e2@d), round(e2, e2@d)))

## similarly to the Arith case, the method for two "rnum" objects
## can not unambiguously use callNextMethod(). Instead, we rely on
## The rnum() method inherited from Math2 to return plain vectors.
setMethod("Compare", c(e1 = "rnum", e2 = "rnum"),
          function(e1, e2) {
            d <- min(e1@d, e2@d)
            callGeneric(round(e1, d), round(e2, d))
          })

set.seed(867)

x1 <- rnum(10*runif(5), d=1L)
x2 <- rnum(10*runif(5), d=2L)
x1+1
x2*2
x1-x2

## Simple examples to illustrate callNextMethod with and without arguments
B0 <- setClass("B0", slots = c(s0 = "numeric"))

## and a function to illustrate callNextMethod
f <- function(x, text = "default") {
  str(x) # print a summary
```
```r
callNextMethod

setGeneric("f")
setMethod("f", "B0", function(x, text = "B0") {
    cat("B0 method called with s0 =", as.character(x@s0), ", s1 ="
    callNextMethod()
})

b0 <- B0(s0 = 1)

## call f() with 2 arguments: callNextMethod passes both to the default method
## f(b0, "first test")

## call f() with 1 argument: the default "B0" is not passed by callNextMethod
## f(b0)

## Now, a class that extends B0, with no methods for f()
B1 <- setClass("B1", slots = c(s1 = "character"), contains = "B0")
b1 <- B1(s0 = 2, s1 = "Testing B1")

## the two cases work as before, by inheriting the "B0" method
f(b1, b1@s1)
f(b1)

B2 <- setClass("B2", contains = "B1")

## And, a method for "B2" that calls with explicit arguments.
## Note that the method selection in callNextMethod
## uses the class of the *argument* to consistently select the "B0" method
setMethod("f", "B2", function(x, text = "B1 method") {
    y <- B1(s0 = -x@s0, s1 = "Modified x")
    callNextMethod(y, text)
})
b2 <- B2(s1 = "Testing B2", s0 = 10)
f(b2, b2@s1)
f(b2)

## Be careful: the argument passed must be legal for the method selected
## Although the argument here is numeric, it's still the "B0" method that's called
setMethod("f", "B2", function(x, text = "B1 method") {
    callNextMethod(x@s0, text)
})

## Now the call will cause an error:
tryCatch(f(b2), error = function(e) cat(e$message,"\n"))
```
canCoerce

Description

Test if an object can be coerced to a given S4 class. Maybe useful inside if() to ensure that calling as(object, Class) will find a method.

Usage

canCoerce(object, Class)

Arguments

object any R object, typically of a formal S4 class.
Class an S4 class (see isClass).

Value

a scalar logical, TRUE if there is a coerce method (as defined by e.g. setAs) for the signature (from = class(object), to = Class).

See Also

as, setAs, selectMethod, setClass.

Examples

m <- matrix(pi, 2,3)
cancoerce(m, "numeric") # TRUE
cancoerce(m, "array")  # TRUE

cbind2

Combine two Objects by Columns or Rows

Description

Combine two matrix-like R objects by columns (cbind2) or rows (rbind2). These are (S4) generic functions with default methods.

Usage

cbind2(x, y, ...)
rbind2(x, y, ...)
Arguments

- **x**: any R object, typically matrix-like.
- **y**: any R object, typically similar to `x`, or missing completely.
- **...**: optional arguments for methods.

Details

The main use of `cbind2` (or `rbind2`) is to be called recursively by `cbind()` (or `rbind()`) when both of these requirements are met:

- There is at least one argument that is an S4 object, and
- S3 dispatch fails (see the Dispatch section under `cbind`).

The methods on `cbind2` and `rbind2` effectively define the type promotion policy when combining a heterogeneous set of arguments. The homogeneous case, where all objects derive from some S4 class, can be handled via S4 dispatch on the ... argument via an externally defined S4 `cbind` (or `rbind`) generic.

Since (for legacy reasons) S3 dispatch is attempted first, it is generally a good idea to additionally define an S3 method on `cbind` (or `rbind`) for the S4 class. The S3 method will be invoked when the arguments include objects of the S4 class, along with arguments of classes for which no S3 method exists. Also, in case there is an argument that selects a different S3 method (like the one for `data.frame`), this S3 method serves to introduce an ambiguity in dispatch that triggers the recursive fallback to `cbind2` (or `rbind2`). Otherwise, the other S3 method would be called, which may not be appropriate.

Value

A matrix (or matrix-like object) combining the columns (or rows) of `x` and `y`. Note that methods must construct `colnames` and `rownames` from the corresponding column and row names of `x` and `y` (but not from deparsing argument names such as in `cbind(..., deparse.level = d)` for `d ≥ 1`).

Methods

- `signature(x = "ANY", y = "ANY")`: the default method using R’s internal code.
- `signature(x = "ANY", y = "missing")`: the default method for one argument using R’s internal code.

See Also

`cbind`, `rbind`; further, `cBind`, `rBind` in the `Matrix` package.

Examples

```r
cbind2(1:3, 4)
m <- matrix(3:8, 2,3, dimnames=list(c("a","b"), LETTERS[1:3]))
cbind2(1:2, m) # keeps dimnames from m

## rbind() and cbind() now make use of rbind2()/cbind2() methods
setClass("Num", contains="numeric")
setMethod("cbind2", c("Num", "missing"),
  function(x,y, ...){ cat("Num-miss--meth\n"); as.matrix(x)})
setMethod("cbind2", c("Num","ANY"), function(x,y,...) {
  cat("Num-A.--method\n") ; cbind(getDataPart(x), y, ...) })
```
setMethod("cbind2", c("ANY","Num"), function(x,y, ...) {
    cat("A.-Num--method\n") ; cbind(x, getDataPart(y), ...) })

a <- new("Num", 1:3)
trace("cbind2")
cbind(a)
cbind(a, four=4, 7:9)# calling cbind2() twice

cbind(m,a, ch=c("D","E"), a*3)
cbind(1,a, m) # ok with a warning
untrace("cbind2")

---

Classes

S4 Class Documentation

Description

You have navigated to an old link to documentation of S4 classes.

For basic use of classes and methods, see Introduction; to create new class definitions, see setClass; for technical details on S4 classes, see Classes_Details.

References


---

classesToAM

Compute an Adjacency Matrix for Superclasses of Class Definitions

Description

Given a vector of class names or a list of class definitions, the function returns an adjacency matrix of the superclasses of these classes; that is, a matrix with class names as the row and column names and with element [i, j] being 1 if the class in column j is a direct superclass of the class in row i, and 0 otherwise.

The matrix has the information implied by the contains slot of the class definitions, but in a form that is often more convenient for further analysis; for example, an adjacency matrix is used in packages and other software to construct graph representations of relationships.

Usage

classesToAM(classes, includeSubclasses = FALSE, abbreviate = 2)
classesToAM

Arguments

classes  Either a character vector of class names or a list, whose elements can be either class names or class definitions. The list is convenient, for example, to include the package slot for the class name. See the examples.

includeSubclasses  A logical flag: if TRUE, then the matrix will include all the known subclasses of the specified classes as well as the superclasses. The argument can also be a logical vector of the same length as classes, to include subclasses for some but not all the classes.

abbreviate  Control of the abbreviation of the row and/or column labels of the matrix returned: values 0, 1, 2, or 3 abbreviate neither, rows, columns or both. The default, 2, is useful for printing the matrix, since class names tend to be more than one character long, making for spread-out printing. Values of 0 or 3 would be appropriate for making a graph (3 avoids the tendency of some graph plotting software to produce labels in minuscule font size).

Details

For each of the classes, the calculation gets all the superclass names from the class definition, and finds the edges in those classes’ definitions; that is, all the superclasses at distance 1. The corresponding elements of the adjacency matrix are set to 1. The adjacency matrices for the individual class definitions are merged. Note two possible kinds of inconsistency, neither of which should cause problems except possibly with identically named classes from different packages. Edges are computed from each superclass definition, so that information overrides a possible inference from extension elements with distance > 1 (and it should). When matrices from successive classes in the argument are merged, the computations do not currently check for inconsistencies—this is the area where possible multiple classes with the same name could cause confusion. A later revision may include consistency checks.

Value

As described, a matrix with entries 0 or 1, non-zero values indicating that the class corresponding to the column is a direct superclass of the class corresponding to the row. The row and column names are the class names (without package slot).

See Also

extends and classRepresentation for the underlying information from the class definition.

Examples

## the super- and subclasses of "standardGeneric"
## and "derivedDefaultValue"
am <- classesToAM(list(class(show), class(getMethod(show))), TRUE)
am

## Not run:
## the following function depends on the Bioconductor package Rgraphviz
plotInheritance <- function(classes, subclasses = FALSE, ...) {
  if(!require("Rgraphviz", quietly=TRUE))
    stop("Only implemented if Rgraphviz is available")
  mm <- classesToAM(classes, subclasses)
  classes <- rownames(mm); rownames(mm) <- colnames(mm)
Classes_Details

Class Definitions

Description

Class definitions are objects that contain the formal definition of a class of \(R\) objects, usually referred to as an S4 class, to distinguish them from the informal S3 classes. This document gives an overview of S4 classes; for details of the class representation objects, see help for the class `classRepresentation`.

Metadata Information

When a class is defined, an object is stored that contains the information about that class. The object, known as the metadata defining the class, is not stored under the name of the class (to allow programmers to write generating functions of that name), but under a specially constructed name. To examine the class definition, call `getClass`. The information in the metadata object includes:

**Slots:** The data contained in an object from an S4 class is defined by the slots in the class definition. Each slot in an object is a component of the object; like components (that is, elements) of a list, these may be extracted and set, using the function `slot()` or more often the operator `@`. However, they differ from list components in important ways. First, slots can only be referred to by name, not by position, and there is no partial matching of names as with list elements. All the objects from a particular class have the same set of slot names; specifically, the slot names that are contained in the class definition. Each slot in each object always is an object of the class specified for this slot in the definition of the current class. The word "is" corresponds to the \(R\) function of the same name (\texttt{is}), meaning that the class of the object in the slot must be the same as the class specified in the definition, or some class that extends the one in the definition (a subclass).

A special slot name, `.Data`, stands for the ‘data part’ of the object. An object from a class with a data part is defined by specifying that the class contains one of the \(R\) object types or one of the special pseudo-classes, \texttt{matrix} or \texttt{array}, usually because the definition of the class, or of one of its superclasses, has included the type or pseudo-class in its `contains` argument. A second special slot name, `.xData`, is used to enable inheritance from abnormal types such as "environment". See the section on inheriting from non-S4 classes for details on the representation and for the behavior of S3 methods with objects from these classes.

Some slot names correspond to attributes used in old-style S3 objects and in \(R\) objects without an explicit class, for example, the `names` attribute. If you define a class for which that attribute...
will be set, such as a subclass of named vectors, you should include "names" as a slot. See the
definition of class "namedList" for an example. Using the names() assignment to set such
names will generate a warning if there is no names slot and an error if the object in question
is not a vector type. A slot called "names" can be used anywhere, but only if it is assigned as
a slot, not via the default names() assignment.

**Superclasses:** The definition of a class includes the *superclasses* —the classes that this class ex-
tends. A class Fancy, say, extends a class Simple if an object from the Fancy class has all
the capabilities of the Simple class (and probably some more as well). In particular, and very
usefully, any method defined to work for a Simple object can be applied to a Fancy object as
well.

This relationship is expressed equivalently by saying that Simple is a superclass of Fancy, or
that Fancy is a subclass of Simple.

The direct superclasses of a class are those superclasses explicitly defined. Direct superclasses
can be defined in three ways. Most commonly, the superclasses are listed in the contains=
argument in the call to setClass that creates the subclass. In this case the subclass will
contain all the slots of the superclass, and the relation between the class is called simple, as
it in fact is. Superclasses can also be defined explicitly by a call to setIs; in this case, the
relation requires methods to be specified to go from subclass to superclass. Thirdly, a class
union is a superclass of all the members of the union. In this case too the relation is simple,
but notice that the relation is defined when the superclass is created, not when the subclass is
created as with the contains= mechanism.

The definition of a superclass will also potentially contain its own direct superclasses. These
are considered (and shown) as superclasses at distance 2 from the original class; their direct
superclasses are at distance 3, and so on. All these are legitimate superclasses for purposes
such as method selection.

When superclasses are defined by including the names of superclasses in the contains=
argument to setClass, an object from the class will have all the slots defined for its own class
and all the slots defined for all its superclasses as well.

The information about the relation between a class and a particular superclass is encoded as an
object of class SClassExtension. A list of such objects for the superclasses (and sometimes
for the subclasses) is included in the metadata object defining the class. If you need to compute
with these objects (for example, to compare the distances), call the function extends with
argument fullInfo=TRUE.

**Prototype:** The objects from a class created by a call to new are defined by the prototype object for
the class and by additional arguments in the call to new, which are passed to a method for that
class for the function initialize.

Each class representation object contains a prototype object for the class (although for a virtual
class the prototype may be NULL). The prototype object must have values for all the slots of
the class. By default, these are the prototypes of the corresponding slot classes. However, the
definition of the class can specify any valid object for any of the slots.

**Basic classes**

There are a number of 'basic' classes, corresponding to the ordinary kinds of data occurring in
R. For example, "numeric" is a class corresponding to numeric vectors. The other vector basic
classes are "logical", "integer", "complex", "character", "raw", "list" and "expression".
The prototypes for the vector classes are vectors of length 0 of the corresponding type. Notice that
basic classes are unusual in that the prototype object is from the class itself.

In addition to the vector classes there are also basic classes corresponding to objects in the language,
such as "function" and "call". These classes are subclasses of the virtual class "language".
Finally, there are object types and corresponding basic classes for “abnormal” objects, such as
"environment" and "externalptr". These objects do not follow the functional behavior of the language; in particular, they are not copied and so cannot have attributes or slots defined locally.

All these classes can be used as slots or as superclasses for any other class definitions, although they do not themselves come with an explicit class. For the abnormal object types, a special mechanism is used to enable inheritance as described below.

Inheriting from non-S4 Classes

A class definition can extend classes other than regular S4 classes, usually by specifying them in the `contains=` argument to `setClass`. Three groups of such classes behave distinctly:

1. S3 classes, which must have been registered by a previous call to `setOldClass` (you can check that this has been done by calling `getClass`, which should return a class that extends `oldClass`);

2. One of the R object types, typically a vector type, which then defines the type of the S4 objects, but also a type such as `environment` that can not be used directly as a type for an S4 object. See below.

3. One of the pseudo-classes `matrix` and `array`, implying objects with arbitrary vector types plus the `dim` and `dimnames` attributes.

This section describes the approach to combining S4 computations with older S3 computations by using such classes as superclasses. The design goal is to allow the S4 class to inherit S3 methods and default computations in as consistent a form as possible.

As part of a general effort to make the S4 and S3 code in R more consistent, when objects from an S4 class are used as the first argument to a non-default S3 method, either for an S3 generic function (one that calls `UseMethod`) or for one of the primitive functions that dispatches S3 methods, an effort is made to provide a valid object for that method. In particular, if the S4 class extends an S3 class or `matrix` or `array`, and there is an S3 method matching one of these classes, the S4 object will be coerced to a valid S3 object, to the extent that is possible given that there is no formal definition of an S3 class.

For example, suppose "myFrame" is an S4 class that includes the S3 class "data.frame" in the `contains=` argument to `setClass`. If an object from this S4 class is passed to a function, say `as.matrix`, that has an S3 method for "data.frame", the internal code for `UseMethod` will convert the object to a data frame; in particular, to an S3 object whose class attribute will be the vector corresponding to the S3 class (possibly containing multiple class names). Similarly for an S4 object inheriting from "matrix" or "array", the S4 object will be converted to a valid S3 matrix or array.

Note that the conversion is not applied when an S4 object is passed to the default S3 method. Some S3 generics attempt to deal with general objects, including S4 objects. Also, no transformation is applied to S4 objects that do not correspond to a selected S3 method; in particular, to objects from a class that does not contain either an S3 class or one of the basic types. See `asS4` for the transformation details.

In addition to explicit S3 generic functions, S3 methods are defined for a variety of operators and functions implemented as primitives. These methods are dispatched by some internal C code that operates partly through the same code as real S3 generic functions and partly via special considerations (for example, both arguments to a binary operator are examined when looking for methods). The same mechanism for adapting S4 objects to S3 methods has been applied to these computations as well, with a few exceptions such as generating an error if an S4 object that does not extend an appropriate S3 class or type is passed to a binary operator.

The remainder of this section discusses the mechanisms for inheriting from basic object types. See `matrix` or `array` for inheriting from the matrix and array pseudo-classes, or from time-series. For the corresponding details for inheritance from S3 classes, see `setOldClass`. 
An object from a class that directly and simply contains one of the basic object types in R, has implicitly a corresponding .Data slot of that type, allowing computations to extract or replace the data part while leaving other slots unchanged. If the type is one that can accept attributes and is duplicated normally, the inheritance also determines the type of the object; if the class definition has a .Data slot corresponding to a normal type, the class of the slot determines the type of the object (that is, the value of typeof(x)). For such classes, .Data is a pseudo-slot; that is, extracting or setting it modifies the non-slot data in the object. The functions getDataPart and setDataPart are a cleaner, but essentially equivalent way to deal with the data part.

Extending a basic type this way allows objects to use old-style code for the corresponding type as well as S4 methods. Any basic type can be used for .Data, but a few types are treated differently because they do not behave like ordinary objects; for example, "NULL", environments, and external pointers. Classes extend these types by having a slot, .xData, itself inherited from an internally defined S4 class. This slot actually contains an object of the inherited type, to protect computations from the reference semantics of the type. Coercing to the nonstandard object type then requires an actual computation, rather than the "simple" inclusion for other types and classes. The intent is that programmers will not need to take account of the mechanism, but one implication is that you should not explicitly use the type of an S4 object to detect inheritance from an arbitrary object type. Use is and similar functions instead.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)

See Also

Methods_Details for analogous discussion of methods, setClass for details of specifying class definitions, is, as, new, slot

className

Class names including the corresponding package

description

The function className() generates a valid references to a class, including the name of the package containing the class definition. The object returned, from class "className", is the unambiguous way to refer to a class, for example when calling setMethod, just in case multiple definitions of the class exist.

Function "multipleClasses" returns information about multiple definitions of classes with the same name from different packages.

Usage

className(class, package)

multipleClasses(details = FALSE)
Arguments

class, package  The character string name of a class and, optionally, of the package to which it belongs. If argument package is missing and the class argument has a package slot, that is used (in particular, passing in an object from class "className" returns itself in this case, but changes the package slot if the second argument is supplied).

If there is no package argument or slot, a definition for the class must exist and will be used to define the package. If there are multiple definitions, one will be chosen and a warning printed giving the other possibilities.

details  If FALSE, the default, multipleClasses() returns a character vector of those classes currently known with multiple definitions.
If TRUE, a named list of those class definitions is returned. Each element of the list is itself a list of the corresponding class definitions, with the package names as the names of the list. Note that identical class definitions will not be considered “multiple” definitions (see the discussion of the details below).

Details

The table of class definitions used internally can maintain multiple definitions for classes with the same name but coming from different packages. If identical class definitions are encountered, only one class definition is kept; this occurs most often with S3 classes that have been specified in calls to setOldClass. For true classes, multiple class definitions are unavoidable in general if two packages happen to have used the same name, independently.

Overriding a class definition in another package with the same name deliberately is usually a bad idea. Although R attempts to keep and use the two definitions (as of version 2.14.0), ambiguities are always possible. It is more sensible to define a new class that extends an existing class but has a different name.

Value

A call to className() returns an object from class "className".

A call to multipleClasses() returns either a character vector or a named list of class definitions. In either case, testing the length of the returned value for being greater than 0 is a check for the existence of multiply defined classes.

Objects from the Class

The class "className" extends "character" and has a slot "package", also of class "character".

Examples

## Not run:

className("vector") # will be found, from package "methods"
className("vector", "magic") # OK, even though the class doesn't exist

className("An unknown class") # Will cause an error

## End(Not run)
classRepresentation-class

Class Objects

Description

These are the objects that hold the definition of classes of objects. They are constructed and stored as meta-data by calls to the function `setClass`. Don’t manipulate them directly, except perhaps to look at individual slots.

Details

Class definitions are stored as metadata in various packages. Additional metadata supplies information on inheritance (the result of calls to `setIs`). Inheritance information implied by the class definition itself (because the class contains one or more other classes) is also constructed automatically.

When a class is to be used in an R session, this information is assembled to complete the class definition. The completion is a second object of class "classRepresentation", cached for the session or until something happens to change the information. A call to `getClass` returns the completed definition of a class; a call to `getClassDef` returns the stored definition (uncompleted).

In particular, completion fills in the upward- and downward-pointing inheritance information for the class, in slots `contains` and `subclasses` respectively. It’s in principle important to note that this information can depend on which packages are installed, since these may define additional subclasses or superclasses.

Slots

slots: A named list of the slots in this class; the elements of the list are the classes to which the slots must belong (or extend), and the names of the list gives the corresponding slot names.

contains: A named list of the classes this class ‘contains’; the elements of the list are objects of `SClassExtension`. The list may be only the direct extensions or all the currently known extensions (see the details).

virtual: Logical flag, set to TRUE if this is a virtual class.

prototype: The object that represents the standard prototype for this class; i.e., the data and slots returned by a call to `new` for this class with no special arguments. Don’t mess with the prototype object directly.

validity: Optionally, a function to be used to test the validity of objects from this class. See `validObject`.

access: Access control information. Not currently used.

className: The character string name of the class.

package: The character string name of the package to which the class belongs. Nearly always the package on which the metadata for the class is stored, but in operations such as constructing inheritance information, the internal package name rules.

subclasses: A named list of the classes known to extend this class'; the elements of the list are objects of class `SClassExtension`. The list is currently only filled in when completing the class definition (see the details).

versionKey: Object of class "externalptr"; eventually will perhaps hold some versioning information, but not currently used.

sealed: Object of class "logical"; is this class sealed? If so, no modifications are allowed.
Documentation

Using and Creating On-line Documentation for Classes and Methods

Description

Special documentation can be supplied to describe the classes and methods that are created by the software in the methods package. Techniques to access this documentation and to create it in R help files are described here.

Getting documentation on classes and methods

You can ask for on-line help for class definitions, for specific methods for a generic function, and for general discussion of methods for a generic function. These requests use the ? operator (see help for a general description of the operator). Of course, you are at the mercy of the implementer as to whether there is any documentation on the corresponding topics.

Documentation on a class uses the argument class on the left of the ?, and the name of the class on the right; for example,

class ? genericFunction

to ask for documentation on the class "genericFunction".

When you want documentation for the methods defined for a particular function, you can ask either for a general discussion of the methods or for documentation of a particular method (that is, the method that would be selected for a particular set of actual arguments).

Overall methods documentation is requested by calling the ? operator with methods as the left-side argument and the name of the function as the right-side argument. For example,

methods ? initialize

asks for documentation on the methods for the initialize function.

Asking for documentation on a particular method is done by giving a function call expression as the right-hand argument to the "?" operator. There are two forms, depending on whether you prefer to give the class names for the arguments or expressions that you intend to use in the actual call.

If you planned to evaluate a function call, say myFun(x, sqrt(wt)) and wanted to find out something about the method that would be used for this call, put the call on the right of the "?" operator:

?myFun(x, sqrt(wt))

A method will be selected, as it would be for the call itself, and documentation for that method will be requested. If myFun is not a generic function, ordinary documentation for the function will be requested.

If you know the actual classes for which you would like method documentation, you can supply these explicitly in place of the argument expressions. In the example above, if you want method documentation for the first argument having class "maybeNumber" and the second "logical", call the "?" operator, this time with a left-side argument method, and with a function call on the right using the class names as arguments:

method ? myFun("maybeNumber", "logical")
Once again, a method will be selected, this time corresponding to the specified classes, and method
documentation will be requested. This version only works with generic functions.

The two forms each have advantages. The version with actual arguments doesn’t require you to
figure out (or guess at) the classes of the arguments. On the other hand, evaluating the arguments
may take some time, depending on the example. The version with class names does require you to
pick classes, but it’s otherwise unambiguous. It has a subtler advantage, in that the classes supplied
may be virtual classes, in which case no actual argument will have specifically this class. The class
"maybeNumber", for example, might be a class union (see the example for setClassUnion).

In either form, methods will be selected as they would be in actual computation, including use of
inheritance and group generic functions. See selectMethod for the details, since it is the function
used to find the appropriate method.

Writing Documentation for Methods

The on-line documentation for methods and classes uses some extensions to the R documentation
format to implement the requests for class and method documentation described above. See the
document Writing R Extensions for the available markup commands (you should have consulted
this document already if you are at the stage of documenting your software).

In addition to the specific markup commands to be described, you can create an initial, overall file
with a skeleton of documentation for the methods defined for a particular generic function:

promptMethods("myFun")

will create a file, ‘myFun-methods.Rd’ with a skeleton of documentation for the methods defined
for function myFun. The output from promptMethods is suitable if you want to describe all or most
of the methods for the function in one file, separate from the documentation of the generic function
itself. Once the file has been filled in and moved to the ‘man’ subdirectory of your source package,
requests for methods documentation will use that file, both for specific methods documentation as
described above, and for overall documentation requested by

methods ? myFun

You are not required to use promptMethods, and if you do, you may not want to use the entire file
created:

• If you want to document the methods in the file containing the documentation for the generic
  function itself, you can cut-and-paste to move the \alias lines and the Methods section from
  the file created by promptMethods to the existing file.

• On the other hand, if these are auxiliary methods, and you only want to document the added or
  modified software, you should strip out all but the relevant \alias lines for the methods of inter-
  est, and remove all but the corresponding \item entries in the Methods section. Note that in
  this case you will usually remove the first \alias line as well, since that is the marker for gen-
  eral methods documentation on this function (in the example, ‘\alias{myfun-methods}’).

If you simply want to direct documentation for one or more methods to a particular R documentation
file, insert the appropriate alias.
Description

The “…” argument in R functions is treated specially, in that it matches zero, one or more actual arguments (and so, objects). A mechanism has been added to R to allow “…” as the signature of a generic function. Methods defined for such functions will be selected and called when all the arguments matching “…” are from the specified class or from some subclass of that class.

Using "..." in a Signature

Beginning with version 2.8.0 of R, S4 methods can be dispatched (selected and called) corresponding to the special argument “…”. Currently, “…” cannot be mixed with other formal arguments: either the signature of the generic function is “…” only, or it does not contain “…” (This restriction may be lifted in a future version.)

Given a suitable generic function, methods are specified in the usual way by a call to setMethod. The method definition must be written expecting all the arguments corresponding to “…” to be from the class specified in the method’s signature, or from a class that extends that class (i.e., a subclass of that class).

Typically the methods will pass “…” down to another function or will create a list of the arguments and iterate over that. See the examples below.

When you have a computation that is suitable for more than one existing class, a convenient approach may be to define a union of these classes by a call to setClassUnion. See the example below.

Method Selection and Dispatch for "..."

See Methods_Details for a general discussion. The following assumes you have read the “Method Selection and Dispatch” section of that documentation.

A method selecting on “…” is specified by a single class in the call to setMethod. If all the actual arguments corresponding to “…” have this class, the corresponding method is selected directly.

Otherwise, the class of each argument and that class’ superclasses are computed, beginning with the first “…” argument. For the first argument, eligible methods are those for any of the classes. For each succeeding argument that introduces a class not considered previously, the eligible methods are further restricted to those matching the argument’s class or superclasses. If no further eligible classes exist, the iteration breaks out and the default method, if any, is selected.

At the end of the iteration, one or more methods may be eligible. If more than one, the selection looks for the method with the least distance to the actual arguments. For each argument, any inherited method corresponds to a distance, available from the contains slot of the class definition. Since the same class can arise for more than one argument, there may be several distances associated with it. Combining them is inevitably arbitrary: the current computation uses the minimum distance. Thus, for example, if a method matched one argument directly, one as first generation superclass and another as a second generation superclass, the distances are 0, 1 and 2. The current selection computation would use distance 0 for this method. In particular, this selection criterion tends to use a method that matches exactly one or more of the arguments’ class.

As with ordinary method selection, there may be multiple methods with the same distance. A warning message is issued and one of the methods is chosen (the first encountered, which in this case is rather arbitrary).

Notice that, while the computation examines all arguments, the essential cost of dispatch goes up with the number of distinct classes among the arguments, likely to be much smaller than the number of arguments when the latter is large.
Implementation Details

Methods dispatching on “…” were introduced in version 2.8.0 of R. The initial implementation of the corresponding selection and dispatch is in an R function, for flexibility while the new mechanism is being studied. In this implementation, a local version of `standardGeneric` is inserted in the generic function’s environment. The local version selects a method according to the criteria above and calls that method, from the environment of the generic function. This is slightly different from the action taken by the C implementation when “…” is not involved. Aside from the extra computing time required, the method is evaluated in a true function call, as opposed to the special context constructed by the C version (which cannot be exactly replicated in R code.) However, situations in which different computational results would be obtained have not been encountered so far, and seem very unlikely.

Methods dispatching on arguments other than “…” are cached by storing the inherited method in the table of all methods, where it will be found on the next selection with the same combination of classes in the actual arguments (but not used for inheritance searches). Methods based on “…” are also cached, but not found quite as immediately. As noted, the selected method depends only on the set of classes that occur in the “…” arguments. Each of these classes can appear one or more times, so many combinations of actual argument classes will give rise to the same effective signature. The selection computation first computes and sorts the distinct classes encountered. This gives a label that will be cached in the table of all methods, avoiding any further search for inherited classes after the first occurrence. A call to `showMethods` will expose such inherited methods.

The intention is that the “…” features will be added to the standard C code when enough experience with them has been obtained. It is possible that at the same time, combinations of “…” with other arguments in signatures may be supported.

References

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

For the general discussion of methods, see `Methods_Details` and links from there.

Examples

```r
cc <- function(...)c(...)
setGeneric("cc")
setMethod("cc", "character", function(...)paste(...))
setClassUnion("Number", c("numeric", "complex"))
setMethod("cc", "Number", function(...) sum(...))
setClass("cdate", contains = "character", slots = c(date = "Date"))
setClass("vdate", contains = "vector", slots = c(date = "Date"))
cd1 <- new("cdate", "abcdef", date = Sys.Date())

cd2 <- new("vdate", "abcdef", date = Sys.Date())
```
stopifnot(identical(cc(letters, character(), cd1),
    paste(letters, character(), cd1))) # the "character" method

stopifnot(identical(cc(letters, character(), cd2),
    c(letters, character(), cd2)))
# the default, because "vdate" doesn’t extend "character"

stopifnot(identical(cc(1:10, 1+1i), sum(1:10, 1+1i))) # the "Number" method

stopifnot(identical(cc(1:10, 1+1i, TRUE), c(1:10, 1+1i, TRUE))) # the default

stopifnot(identical(cc(), c())) # no arguments implies the default method

setGeneric("numMax", function(...)standardGeneric("numMax"))

setMethod("numMax", "numeric", function(...)max(...))
# won't work for complex data

setMethod("numMax", "Number", function(...) paste(...))
# should not be selected w/o complex args

stopifnot(identical(numMax(1:10, pi, 1+1i), paste(1:10, pi, 1+1i))
stopifnot(identical(numMax(1:10, pi, 1), max(1:10, pi, 1)))

try(numMax(1:10, pi, TRUE)) # should be an error: no default method

## A generic version of paste(), dispatching on the "..." argument:
setGeneric("paste", signature = "...")

setMethod("paste", "Number", function(..., sep, collapse) c(...))

stopifnot(identical(paste(1:10, pi, 1), c(1:10, pi, 1)))

environment-class

Class "environment"

Description

A formal class for R environments.

Objects from the Class

Objects can be created by calls of the form new("environment", ...). The arguments in ..., if any, should be named and will be assigned to the newly created environment.

Methods

coerce signature(from = "ANY", to = "environment"): calls as.environment.

initialize signature(object = "environment"): Implements the assignments in the new environment. Note that the object argument is ignored; a new environment is always created, since environments are not protected by copying.
See Also

new.env

Description

Support Class to Implement R Objects using Reference Semantics

NOTE:
The software described here is an initial version. The eventual goal is to support reference-style classes with software in R itself or using inter-system interfaces. The current implementation (R version 2.12.0) is preliminary and subject to change, and currently includes only the R-only implementation. Developers are encouraged to experiment with the software, but the description here is more than usually subject to change.

Purpose of the Class

This class implements basic reference-style semantics for R objects. Objects normally do not come directly from this class, but from subclasses defined by a call to `setRefClass`. The documentation below is technical background describing the implementation, but applications should use the interface documented under `setRefClass`, in particular the $ operator and field accessor functions as described there.

A Basic Reference Class

The design of reference classes for R divides those classes up according to the mechanism used for implementing references, fields, and class methods. Each version of this mechanism is defined by a basic reference class, which must implement a set of methods and provide some further information used by `setRefClass`.

The required methods are for operators $ and $<- to get and set a field in an object, and for `initialize` to initialize objects.

To support these methods, the basic reference class needs to have some implementation mechanism to store and retrieve data from fields in the object. The mechanism needs to be consistent with reference semantics; that is, changes made to the contents of an object are global, seen by any code accessing that object, rather than only local to the function call where the change takes place. As described below, class `envRefClass` implements reference semantics through specialized use of environment objects. Other basic reference classes may use an interface to a language such as Java or C++ using reference semantics for classes.

Usually, the R user will be able to invoke class methods on the class, using the $ operator. The basic reference class method for $ needs to make this possible. Essentially, the operator must return an R function corresponding to the object and the class method name.

Class methods may include an implementation of data abstraction, in the sense that fields are accessed by “get” and “set” methods. The basic reference class provides this facility by setting the "fieldAccessorGenerator" slot in its definition to a function of one variable. This function will be called by `setRefClass` with the vector of field names as arguments. The generator function must return a list of defined accessor functions. An element corresponding to a get operation is invoked with no arguments and should extract the corresponding field; an element for a set operation will
evalSource

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be invoked with a single argument, the value to be assigned to the field. The implementation needs
to supply the object, since that is not an argument in the method invocation. The mechanism used
currently by envRefClass is described below.
Support Classes
Two virtual classes are supplied to test for reference objects: is(x, "refClass") tests whether
x comes from a class defined using the reference class mechanism described here; is(x,
"refObject") tests whether the object has reference semantics generally, including the previous classes and also classes inheriting from the R types with reference semantics, such as
"environment".
Installed class methods are "classMethodDefinition" objects, with slots that identify the name
of the function as a class method and the other class methods called from this method. The latter
information is determined heuristically when the class is defined by using the codetools recommended package. This package must be installed when reference classes are defined, but is not
needed in order to use existing reference classes.
Author(s)
John Chambers

evalSource

Use Function Definitions from a Source File without Reinstalling a
Package

Description
Definitions of functions and/or methods from a source file are inserted into a package, using the
trace mechanism. Typically, this allows testing or debugging modified versions of a few functions
without reinstalling a large package.
Usage
evalSource(source, package = "", lock = TRUE, cache = FALSE)
insertSource(source, package = "", functions = , methods = ,
force = )

Arguments
source

A file to be parsed and evaluated by evalSource to find the new function and
method definitions.
The argument to insertSource can be an object of class
"sourceEnvironment" returned from a previous call to evalSource If a
file name is passed to insertSource it calls evalSource to obtain the
corresponding object. See the section on the class for details.

package

Optionally, the name of the package to which the new code corresponds and into
which it will be inserted. Although the computations will attempt to infer the
package if it is omitted, the safe approach is to supply it. In the case of a package
that is not attached to the search list, the package name must be supplied.


functions, methods
Optional character-string names of functions to be used in the insertion. Names supplied in the functions argument are expected to be defined as functions in the source. For names supplied in the methods argument, a table of methods is expected (as generated by calls to `setMethod`, see the details section); methods from this table will be inserted by `insertSource`. In both cases, the revised function or method is inserted only if it differs from the version in the corresponding package as loaded.

If what is omitted, the results of evaluating the source file will be compared to the contents of the package (see the details section).

lock, cache
Optional arguments to control the actions taken by `evalSource`. If lock is TRUE, the environment in the object returned will be locked, and so will all its bindings. If cache is FALSE, the normal caching of method and class definitions will be suppressed during evaluation of the source file.

The default settings are generally recommended, the lock to support the credibility of the object returned as a snapshot of the source file, and the second so that method definitions can be inserted later by `insertSource` using the trace mechanism.

force
If FALSE, only functions currently in the environment will be redefined, using `trace`. If TRUE, other objects/functions will be simply assigned. By default, TRUE if neither the functions nor the methods argument is supplied.

Details
The source file is parsed and evaluated, suppressing by default the actual caching of method and class definitions contained in it, so that functions and methods can be tested out in a reversible way. The result, if all goes well, is an environment containing the assigned objects and metadata corresponding to method and class definitions in the source file.

From this environment, the objects are inserted into the package, into its namespace if it has one, for use during the current session or until reverting to the original version by a call to `untrace`. The insertion is done by calls to the internal version of `trace`, to make reversion possible.

Because the trace mechanism is used, only function-type objects will be inserted, functions themselves or S4 methods.

When the functions and methods arguments are both omitted, `insertSource` selects all suitable objects from the result of evaluating the source file.

In all cases, only objects in the source file that differ from the corresponding objects in the package are inserted. The definition of “differ” is that either the argument list (including default expressions) or the body of the function is not identical. Note that in the case of a method, there need be no specific method for the corresponding signature in the package: the comparison is made to the method that would be selected for that signature.

Nothing in the computation requires that the source file supplied be the same file as in the original package source, although that case is both likely and sensible if one is revising the package.

Nothing in the computations compares source files: the objects generated by evaluating source are compared as objects to the content of the package.

Value
An object from class "sourceEnvironment", a subclass of "environment" (see the section on the class) The environment contains the versions of all object resulting from evaluation of the source file. The class also has slots for the time of creation, the source file and the package name. Future extensions may use these objects for versioning or other code tools.
The object returned can be used in debugging (see the section on that topic) or as the source argument in a future call to `insertSource`. If only some of the revised functions were inserted in the first call, others can be inserted in a later call without re-evaluating the source file, by supplying the environment and optionally suitable functions and/or methods argument.

**Debugging**

Once a function or method has been inserted into a package by `insertSource`, it can be studied by the standard debugging tools; for example, `debug` or the various versions of `trace`. Calls to `trace` should take the extra argument `edit = env`, where `env` is the value returned by the call to `evalSource`. The trace mechanism has been used to install the revised version from the source file, and supplying the argument ensures that it is this version, not the original, that will be traced. See the example below.

To turn tracing off, but retain the source version, use `trace(x, edit = env)` as in the example. To return to the original version from the package, use `untrace(x)`.  

**Class** "sourceEnvironment"

Objects from this class can be treated as environments, to extract the version of functions and methods generated by `evalSource`. The objects also have the following slots:

- `packageName`: The character-string name of the package to which the source code corresponds.
- `dateCreated`: The date and time that the source file was evaluated (usually from a call to `Sys.time`).
- `sourceFile`: The character-string name of the source file used.

Note that using the environment does not change the `dateCreated`.

**See Also**

- `trace` for the underlying mechanism, and also for the `edit=` argument that can be used for somewhat similar purposes; that function and also `debug` and `setBreakpoint`, for techniques more oriented to traditional debugging styles. The present function is directly intended for the case that one is modifying some of the source for an existing package, although it can be used as well by inserting debugging code in the source (more useful if the debugging involved is non-trivial). As noted in the details section, the source file need not be the same one in the original package source.

**Examples**

```r
## Not run:
## Suppose package P0 has a source file "all.R"
## First, evaluate the source, and from it
## insert the revised version of methods for summary()
env <- insertSource("./P0/R/all.R", package = "P0",
                   methods = "summary")
## now test one of the methods, tracing the version from the source
trace("summary", signature = "myMat", browser, edit = env)
## After testing, remove the browser() call but keep the source
trace("summary", signature = "myMat", edit = env)
## Now insert all the (other) revised functions and methods
## without re-evaluating the source file.
## The package name is included in the object env.
insertSource(env)
## End(Not run)
```
findClass  

Find Class Definitions

Description

Functions to find classes: isClass tests for a class; findClass returns the name(s) of packages containing the class; getClasses returns the names of all the classes in an environment, typically a namespace. To examine the definition of a class, use getClass.

Usage

isClass(Class, formal=TRUE, where)

getClasses(where, inherits = missing(where))

findClass(Class, where, unique = "")

## The remaining functions are retained for compatibility
## but not generally recommended

removeClass(Class, where)

resetClass(Class, classDef, where)

sealClass(Class, where)

Arguments

Class

character string name for the class. The functions will usually take a class definition instead of the string. To restrict the class to those defined in a particular package, set the packageSlot of the character string.

where

the environment in which to search for the class definition. Defaults to the top-level environment of the calling function. When called from the command line, this has the effect of using all the package environments in the search list. To restrict the search to classes in a particular package, use where = asNamespace(pkg) with pkg the package name; to restrict it to the exported classes, use where = "package:pkg" after the package is attached to the search list.

formal

logical is a formal definition required? For S compatibility, and always treated as TRUE.

unique

if findClass expects a unique location for the class, unique is a character string explaining the purpose of the search (and is used in warning and error messages). By default, multiple locations are possible and the function always returns a list.

inherits

in a call to getClasses, should the value returned include all parent environments of where, or that environment only? Defaults to TRUE if where is omitted, and to FALSE otherwise.

classDef

For resetClass, the optional class definition.
Functions

isClass: Is this the name of a formally defined class?

getClasses: The names of all the classes formally defined on where. If called with no argument, all the classes visible from the calling function (if called from the top-level, all the classes in any of the environments on the search list). The where argument is used to search only in a particular package.

findClass: The list of environments in which a class definition of Class is found. If where is supplied, a list is still returned, either empty or containing the environment corresponding to where. By default when called from the R session, the global environment and all the currently attached packages are searched.

If unique is supplied as a character string, findClass will warn if there is more than one definition visible (using the string to identify the purpose of the call), and will generate an error if no definition can be found.

The remaining functions are retained for back-compatibility and internal use, but not generally recommended.

removeClass: Remove the definition of this class. This can’t be used if the class is in another package, and would rarely be needed in source code defining classes in a package.

resetClass: Reset the internal definition of a class. Not legitimate for a class definition not in this package and rarely needed otherwise.

sealClass: Seal the current definition of the specified class, to prevent further changes, by setting the corresponding slot in the class definition. This is rarely used, since classes in loaded packages are sealed by locking their namespace.

References


See Also

getClass, Classes_Details, Methods_Details, makeClassRepresentation

findMethods

Description

The function findMethods converts the methods defined in a table for a generic function (as used for selection of methods) into a list, for study or display. The list is actually from the class listOfMethods (see the section describing the class, below).

The list will be limited to the methods defined in environment where if that argument is supplied and limited to those including one or more of the specified classes in the method signature if that argument is supplied.

To see the actual table (an environment) used for methods dispatch, call getMethodsForDispatch. The names of the list returned by findMethods are the names of the objects in the table.
The function `findMethodSignatures` returns a character matrix whose rows are the class names from the signature of the corresponding methods; it operates either from a list returned by `findMethods`, or by computing such a list itself, given the same arguments as `findMethods`.

The function `hasMethods` returns `TRUE` or `FALSE` according to whether there is a non-empty table of methods for function `f` in the environment or search position `where` (or for the generic function generally if `where` is missing).

The defunct function `getMethods` is an older alternative to `findMethods`, returning information in the form of an object of class `MethodsList`, previously used for method dispatch. This class of objects is deprecated generally and will disappear in a future version of R.

Usage

```r
findMethods(f, where, classes = character(), inherited = FALSE, package = "")
findMethodSignatures(..., target = TRUE, methods = )
hasMethods(f, where, package)
```

## Deprecated in 2010 and defunct in 2015 for 'table = FALSE':
`getMethods(f, where, table = FALSE)`

Arguments

- `f`  
  A generic function or the character-string name of one.

- `where`  
  Optionally, an environment or position on the search list to look for methods metadata.
  If `where` is missing, `findMethods` uses the current table of methods in the generic function itself, and `hasMethods` looks for metadata anywhere in the search list.

- `table`  
  If `TRUE` in a call to `getMethods` the returned value is the table used for dispatch, including inherited methods discovered to date. Used internally, but since the default result is the now unused `mlist` object, the default will likely be changed at some point.

- `classes`  
  If supplied, only methods whose signatures contain at least one of the supplied classes will be included in the value returned.

- `inherited`  
  Logical flag; if `TRUE`, the table of all methods, inherited or defined directly, will be used; otherwise, only the methods explicitly defined. Option `TRUE` is meaningful only if `where` is missing.

- `...`  
  In the call to `findMethodSignatures`, any arguments that might be given to `findMethods`.

- `target`  
  Optional flag to `findMethodSignatures`; if `TRUE`, the signatures used are the target signatures (the classes for which the method will be selected); if `FALSE`, they will be the signatures are defined. The difference is only meaningful if `inherited` is `TRUE`.

- `methods`  
  In the call to `findMethodSignatures`, an optional list of methods, presumably returned by a previous call to `findMethods`. If missing, that function will be called with the `...` arguments.
In a call to `hasMethods`, the package name for the generic function (e.g., "base" for primitives). If missing this will be inferred either from the "package" attribute of the function name, if any, or from the package slot of the generic function. See ‘Details’.

Details

The functions obtain a table of the defined methods, either from the generic function or from the stored metadata object in the environment specified by `where`. In a call to `getMethods`, the information in the table is converted as described above to produce the returned value, except with the table argument.

Note that `hasMethods`, but not the other functions, can be used even if no generic function of this name is currently found. In this case package must either be supplied as an argument or included as an attribute of `f`, since the package name is part of the identification of the methods tables.

The Class for lists of methods

The class "listOfMethods" returns the methods as a named list of method definitions (or a primitive function, see the slot documentation below). The names are the strings used to store the corresponding objects in the environment from which method dispatch is computed. The current implementation uses the names of the corresponding classes in the method signature, separated by "#" if more than one argument is involved in the signature.

Slots

.Data: Object of class "list" The method definitions.

Arguments: Object of class "character". The names of the formal arguments in the signature of the generic function.

Signatures: Object of class "list". A list of the signatures of the individual methods. This is currently the result of splitting the names according to the "#" separator.

If the object has been constructed from a table, as when returned by `findMethods`, the signatures will all have the same length. However, a list rather than a character matrix is used for generality. Calling `findMethodSignatures` as in the example below will always convert to the matrix form.

Generic: Object of class "genericFunction". The generic function corresponding to these methods. There are plans to generalize this slot to allow reference to the function.

Names: Object of class "character". The names as noted are the class names separated by "#".

Extends

Class "namedList", directly.

Class "list", by class "namedList", distance 2.

Class "vector", by class "namedList", distance 3.

See Also

`showMethods, selectMethod, Methods_Details`
fixPre1.8

Description

Beginning with R version 1.8.0, the class of an object contains the identification of the package in which the class is defined. The function fixPre1.8 fixes and re-assigns objects missing that information (typically because they were loaded from a file saved with a previous version of R.)

Usage

fixPre1.8(names, where)

Arguments

names Character vector of the names of all the objects to be fixed and re-assigned.
where The environment from which to look for the objects, and for class definitions. Defaults to the top environment of the call to fixPre1.8, the global environment if the function is used interactively.

Details

The named object will be saved where it was found. Its class attribute will be changed to the full form required by R 1.8; otherwise, the contents of the object should be unchanged.

Objects will be fixed and re-assigned only if all the following conditions hold:

1. The named object exists.
2. It is from a defined class (not a basic datatype which has no actual class attribute).
3. The object appears to be from an earlier version of R.
4. The class is currently defined.
5. The object is consistent with the current class definition.

If any condition except the second fails, a warning message is generated.

Note that fixPre1.8 currently fixes only the change in class attributes. In particular, it will not fix binary versions of packages installed with earlier versions of R if these use incompatible features. Such packages must be re-installed from source, which is the wise approach always when major version changes occur in R.

Value

The names of all the objects that were in fact re-assigned.

Examples

mm <- findMethods("Ops")
findMethodSignatures(methods = mm)

---

fixPre1.8

Fix Objects Saved from R Versions Previous to 1.8

Description

Beginning with R version 1.8.0, the class of an object contains the identification of the package in which the class is defined. The function fixPre1.8 fixes and re-assigns objects missing that information (typically because they were loaded from a file saved with a previous version of R.)

Usage

fixPre1.8(names, where)

Arguments

names Character vector of the names of all the objects to be fixed and re-assigned.
where The environment from which to look for the objects, and for class definitions. Defaults to the top environment of the call to fixPre1.8, the global environment if the function is used interactively.

Details

The named object will be saved where it was found. Its class attribute will be changed to the full form required by R 1.8; otherwise, the contents of the object should be unchanged.

Objects will be fixed and re-assigned only if all the following conditions hold:

1. The named object exists.
2. It is from a defined class (not a basic datatype which has no actual class attribute).
3. The object appears to be from an earlier version of R.
4. The class is currently defined.
5. The object is consistent with the current class definition.

If any condition except the second fails, a warning message is generated.

Note that fixPre1.8 currently fixes only the change in class attributes. In particular, it will not fix binary versions of packages installed with earlier versions of R if these use incompatible features. Such packages must be re-installed from source, which is the wise approach always when major version changes occur in R.

Value

The names of all the objects that were in fact re-assigned.
Generic Function Objects

Description

Generic functions (objects from or extending class \texttt{genericFunction}) are extended function objects, containing information used in creating and dispatching methods for this function. They also identify the package associated with the function and its methods.

Objects from the Class

Generic functions are created and assigned by \texttt{setGeneric} or \texttt{setGroupGeneric} and, indirectly, by \texttt{setMethod}.

As you might expect \texttt{setGeneric} and \texttt{setGroupGeneric} create objects of class "\texttt{genericFunction}" and "\texttt{groupGenericFunction}" respectively.

Slots

\begin{itemize}
  \item \texttt{.Data}: Object of class "\texttt{function}", the function definition of the generic, usually created automatically as a call to \texttt{standardGeneric}.
  \item \texttt{generic}: Object of class "\texttt{character}", the name of the generic function.
  \item \texttt{package}: Object of class "\texttt{character}", the name of the package to which the function definition belongs (and \textit{not} necessarily where the generic function is stored). If the package is not specified explicitly in the call to \texttt{setGeneric}, it is usually the package on which the corresponding non-generic function exists.
  \item \texttt{group}: Object of class "\texttt{list}", the group or groups to which this generic function belongs. Empty by default.
  \item \texttt{valueClass}: Object of class "\texttt{character}"; if not an empty character vector, identifies one or more classes. It is asserted that all methods for this function return objects from these class (or from classes that extend them).
  \item \texttt{signature}: Object of class "\texttt{character}", the vector of formal argument names that can appear in the signature of methods for this generic function. By default, it is all the formal arguments, except for \ldots. Order matters for efficiency: the most commonly used arguments in specifying methods should come first.
  \item \texttt{default}: Object of class "\texttt{optionalMethod}" (a union of classes "\texttt{function}" and "\texttt{NULL}"), containing the default method for this function if any. Generated automatically and used to initialize method dispatch.
  \item \texttt{skeleton}: Object of class "\texttt{call}", a slot used internally in method dispatch. Don’t expect to use it directly.
\end{itemize}

Extends

Class "\texttt{function}", from data part.
Class "\texttt{OptionalMethods}", by class "\texttt{function}".
Class "\texttt{PossibleMethod}", by class "\texttt{function}".
GenericFunctions

Methods

Generic function objects are used in the creation and dispatch of formal methods; information from the object is used to create methods list objects and to merge or update the existing methods for this generic.

Description

The functions documented here manage collections of methods associated with a generic function, as well as providing information about the generic functions themselves.

Usage

- `isGeneric(f, where, fdef, getName = FALSE)`
- `isGroup(f, where, fdef)`
- `removeGeneric(f, where)`
- `dumpMethod(f, signature, file, where, def)`
- `findFunction(f, generic = TRUE, where = topenv(parent.frame()))`
- `dumpMethods(f, file, signature, methods, where)`
- `signature(...)`
- `removeMethods(f, where = topenv(parent.frame()), all = missing(where))`
- `setReplaceMethod(f, ..., where = topenv(parent.frame()))`
- `getGenerics(where, searchForm = FALSE)`

Arguments

- **f**: The character string naming the function.
- **where**: The environment, namespace, or search-list position from which to search for objects. By default, start at the top-level environment of the calling function, typically the global environment (i.e., use the search list), or the namespace of a package from which the call came. It is important to supply this argument when calling any of these functions indirectly. With package namespaces, the default is likely to be wrong in such calls.
- **signature**: The class signature of the relevant method. A signature is a named or unnamed vector of character strings. If named, the names must be formal argument names for the generic function. Signatures are matched to the arguments specified in the signature slot of the generic function (see the Details section of the `setMethod` documentation). The signature argument to `dumpMethods` is ignored (it was used internally in previous implementations).
- **file**: The file or connection on which to dump method definitions.
- **def**: The function object defining the method; if omitted, the current method definition corresponding to the signature.
Named or unnamed arguments to form a signature.

In testing or finding functions, should generic functions be included. Supply as FALSE to get only non-generic functions.

Optional, the generic function definition. Usually omitted in calls to isGeneric.

If TRUE, isGeneric returns the name of the generic. By default, it returns TRUE.

The methods object containing the methods to be dumped. By default, the methods defined for this generic (optionally on the specified where location).

In removeMethods, logical indicating if all (default) or only the first method found should be removed.

In getGenerics, if TRUE, the package slot of the returned result is in the form used by search(), otherwise as the simple package name (e.g. "package:base" vs "base").

Summary of Functions

**isGeneric**: Is there a function named f, and if so, is it a generic?

The getName argument allows a function to find the name from a function definition. If it is TRUE then the name of the generic is returned, or FALSE if this is not a generic function definition.

The behavior of isGeneric and getGeneric for primitive functions is slightly different. These functions don’t exist as formal function objects (for efficiency and historical reasons), regardless of whether methods have been defined for them. A call to isGeneric tells you whether methods have been defined for this primitive function, anywhere in the current search list, or in the specified position where. In contrast, a call to getGeneric will return what the generic for that function would be, even if no methods have been currently defined for it.

**removeGeneric**, **removeMethods**: Remove all the methods for the generic function of this name.

In addition, removeGeneric removes the function itself, removeMethods restores the non-generic function which was the default method. If there was no default method, removeMethods leaves a generic function with no methods.

**standardGeneric**: Dispatches a method from the current function call for the generic function f. It is an error to call standardGeneric anywhere except in the body of the corresponding generic function.

Note that standardGeneric is a primitive function in the base package for efficiency reasons, but rather documented here where it belongs naturally.

**dumpMethod**: Dump the method for this generic function and signature.

**findFirst**: return a list of either the positions on the search list, or the current top-level environment, on which a function object for name exists. The returned value is always a list, use the first element to access the first visible version of the function. See the example.

**NOTE**: Use this rather than find with mode="function", which is not as meaningful, and has a few subtle bugs from its use of regular expressions. Also, findFunction works correctly in the code for a package when attaching the package via a call to library.

**dumpMethods**: Dump all the methods for this generic.

**signature**: Returns a named list of classes to be matched to arguments of a generic function.

getGenerics: returns the names of the generic functions that have methods defined on where; this argument can be an environment or an index into the search list. By default, the whole search list is used.
The methods definitions are stored with package qualifiers; for example, methods for function "initialize" might refer to two different functions of that name, on different packages. The package names corresponding to the method list object are contained in the slot package of the returned object. The form of the returned name can be plain (e.g., "base"), or in the form used in the search list ("package:base") according to the value of searchForm.

Details

isGeneric: If the fdef argument is supplied, take this as the definition of the generic, and test whether it is really a generic, with f as the name of the generic. (This argument is not available in S-Plus.)
removeGeneric: If where supplied, just remove the version on this element of the search list; otherwise, removes the first version encountered.
standardGeneric: Generic functions should usually have a call to standardGeneric as their entire body. They can, however, do any other computations as well.

The usual setGeneric (directly or through calling setMethod) creates a function with a call to standardGeneric.
dumpMethod: The resulting source file will recreate the method.
findFunction: If generic is FALSE, ignore generic functions.
dumpMethods: If signature is supplied only the methods matching this initial signature are dumped. (This feature is not found in S-Plus: don’t use it if you want compatibility.)
signature: The advantage of using signature is to provide a check on which arguments you meant, as well as clearer documentation in your method specification. In addition, signature checks that each of the elements is a single character string.
removeMethods: Returns TRUE if f was a generic function, FALSE (silently) otherwise.

If there is a default method, the function will be re-assigned as a simple function with this definition. Otherwise, the generic function remains but with no methods (so any call to it will generate an error). In either case, a following call to setMethod will consistently re-establish the same generic function as before.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)

See Also

getMethod (also for selectMethod), setGeneric, setClass, showMethods

Examples

require(stats) # for lm

## get the function "myFun" -- throw an error if 0 or > 1 versions visible:
findFuncStrict <- function(fName) {
  allF <- findFunction(fName)
  if(length(allF) == 0)
    stop("No versions of ", fName, " visible")
  else if(length(allF) > 1)
    stop(fName," is ambiguous: ", length(allF), " versions")
  else
    get(fName, allF[[1]])
}

## get the function "myFun" -- throw an error if 0 or > 1 versions visible:
findFuncStrict <- function(fName) {
  allF <- findFunction(fName)
  if(length(allF) == 0)
    stop("No versions of ", fName, " visible")
  else if(length(allF) > 1)
    stop(fName," is ambiguous: ", length(allF), " versions")
  else
    get(fName, allF[[1]])
}
try(findFuncStrict("myFun"))# Error: no version
lm <- function(x) x+1
try(findFuncStrict("lm"))# Error: 2 versions
findFuncStrict("findFuncStrict")# just 1 version
rm(lm)

## method dumping ------------------------------------
setClass("A", slots = c(a="numeric"))
setMethod("plot", "A", function(x,y,...){ cat("A meth\n") })
dumpMethod("plot","A", file="")
## Not run:
setMethod("plot", "A",
function (x, y, ...)
{
    cat("AAAAA\n")
})
## End(Not run)
tmp <- tempfile()
dumpMethod("plot","A", file=tmp)
## now remove, and see if we can parse the dump
stopifnot(removeMethod("plot", "A"))
source(tmp)
stopifnot(is(getMethod("plot", "A"), "MethodDefinition"))

## same with dumpMethods():
setClass("B", contains="A")
setMethod("plot", "B", function(x,y,...){ cat("B ...
") })
dumpMethods("plot", file=tmp)
stopifnot(removeMethod("plot", "A"),
    removeMethod("plot", "B"))
source(tmp)
stopifnot(is(getMethod("plot", "A"), "MethodDefinition"),
    is(getMethod("plot", "B"), "MethodDefinition"))

getClass  

Get Class Definition

Description

Get the definition of a class.

Usage

getClass  (Class, .Force = FALSE, where)
getClassDef(Class, where, package, inherits = TRUE)
Arguments

Class
the character-string name of the class, often with a "package" attribute as noted below under package.

.Force
if TRUE, return NULL if the class is undefined; otherwise, an undefined class results in an error.

where
environment from which to begin the search for the definition; by default, start at the top-level (global) environment and proceed through the search list.

package
the name or environment of the package asserted to hold the definition. If it is a non-empty string it is used instead of where, as the first place to look for the class. Note that the package must be loaded but need not be attached. By default, the package attribute of the Class argument is used, if any. There will usually be a package attribute if Class comes from class(x) for some object.

inherits
logical; should the class definition be retrieved from any enclosing environment and also from the cache? If FALSE only a definition in the environment where will be returned.

Details

Class definitions are stored in metadata objects in a package namespace or other environment where they are defined. When packages are loaded, the class definitions in the package are cached in an internal table. Therefore, most calls to getClassDef will find the class in the cache or fail to find it at all, unless inherits is FALSE, in which case only the environment(s) defined by package or where are searched.

The class cache allows for multiple definitions of the same class name in separate environments, with of course the limitation that the package attribute or package name must be provided in the call to

Value

The object defining the class. If the class definition is not found, getClassDef returns NULL, while getClass, which calls getClassDef, either generates an error or, if .Force is TRUE, returns a simple definition for the class. The latter case is used internally, but is not typically sensible in user code.

The non-null returned value is an object of class classRepresentation.

Use functions such as setClass and setClassUnion to create class definitions.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)

See Also

classRepresentation, setClass, isClass.

Examples

gClass("numeric") # a built in class

cld <- getClass("thisIsAnUndefinedClass", .Force = TRUE)
cld # a NULL prototype
## If you are really curious:
getMethod

Get or Test for the Definition of a Method

Description

The function `selectMethod()` returns the method that would be selected for a call to function `f` if the arguments had classes as specified by `signature`. Failing to find a method is an error, unless argument `optional = TRUE`, in which case `NULL` is returned.

The function `findMethod()` returns a list of environments that contain a method for the specified function and `signature`; by default, these are a subset of the packages in the current search list. See section “Using `findMethod()`” for details.

The function `getMethod()` returns the method corresponding to the function and `signature` supplied similarly to `selectMethod`, but without using inheritance or group generics.

The functions `hasMethod()` and `existsMethod()` test whether `selectMethod()` or `getMethod()`, respectively, finds a matching method.

Usage

```r
selectMethod(f, signature, optional = FALSE, useInherited = ,
    mlist = , fdef = , verbose = , doCache = )
findMethod(f, signature, where)
getMethod(f, signature = character(), where, optional = FALSE,
    mlist, fdef)
existsMethod(f, signature = character(), where)
hasMethod(f, signature = character(), where)
```

Arguments

- `f`: a generic function or the character-string name of one.
- `signature`: the signature of classes to match to the arguments of `f`. See the details below.
- `where`: the environment in which to look for the method(s). By default, if the call comes from the command line, the table of methods defined in the generic function itself is used, except for `findMethod` (see the section below).
- `optional`: if the selection in `selectMethod` does not find a valid method an error is generated, unless `optional` is `TRUE`, in which case the value returned is `NULL`.
- `mlist`, `fdef`, `useInherited`, `verbose`, `doCache`: optional arguments to `getMethod` and `selectMethod` for internal use. Avoid these: some will work as expected and others will not, and none of them is required for normal use of the functions. But see the section “Methods for `as()`” for nonstandard inheritance.
**Details**

The `signature` argument specifies classes, corresponding to formal arguments of the generic function; to be precise, to the `signature` slot of the generic function object. The argument may be a vector of strings identifying classes, and may be named or not. Names, if supplied, match the names of those formal arguments included in the signature of the generic. That signature is normally all the arguments except `. . .`. However, generic functions can be specified with only a subset of the arguments permitted, or with the signature taking the arguments in a different order.

It’s a good idea to name the arguments in the signature to avoid confusion, if you’re dealing with a generic that does something special with its signature. In any case, the elements of the signature are matched to the formal signature by the same rules used in matching arguments in function calls (see `match.call`).

The strings in the signature may be class names, "missing" or "ANY". See Methods_Details for the meaning of these in method selection. Arguments not supplied in the signature implicitly correspond to class "ANY"; in particular, giving an empty signature means to look for the default method.

A call to `getMethod` returns the method for a particular function and signature. The search for the method makes no use of inheritance.

The function `selectMethod` also looks for a method given the function and signature, but makes full use of the method dispatch mechanism; i.e., inherited methods and group generics are taken into account just as they would be in dispatching a method for the corresponding signature, with the one exception that conditional inheritance is not used. Like `getMethod`, `selectMethod` returns `NULL` or generates an error if the method is not found, depending on the argument `optional`.

Both `selectMethod` and `getMethod` will normally use the current version of the generic function in the R session, which has a table of the methods obtained from all the packages loaded in the session. Optional arguments can cause a search for the generic function from a specified environment, but this is rarely a useful idea. In contrast, `findMethod` has a different default and the optional `where=` argument may be needed. See the section “Using `findMethod()`”.

The functions `existsMethod` and `hasMethod` return `TRUE` or `FALSE` according to whether a method is found, the first corresponding to `getMethod` (no inheritance) and the second to `selectMethod`.

**Value**

The call to `selectMethod` or `getMethod` returns the selected method, if one is found. (This class extends function, so you can use the result directly as a function if that is what you want.) Otherwise an error is thrown if `optional` is `FALSE` and `NULL` is returned if `optional` is `TRUE`.

The returned method object is a `MethodDefinition` object, except that the default method for a primitive function is required to be the primitive itself. Note therefore that the only reliable test that the search failed is `is.null()`.

The returned value of `findMethod` is a list of environments in which a corresponding method was found; that is, a table of methods including the one specified.

**Using `findMethod()`**

As its name suggests, this function is intended to behave like `find`, which produces a list of the packages on the current search list which have, and have exported, the object named. That’s what `findMethod` does also, by default. The “exported” part in this case means that the package’s namespace has an `exportMethods` directive for this generic function.

An important distinction is that the absence of such a directive does not prevent methods from the package from being called once the package is loaded. Otherwise, the code in the package could not use un-exported methods.
So, if your question is whether loading package `thisPkg` will define a method for this function and signature, you need to ask that question about the namespace of the package:

```r
findMethod(f, signature, where = asNamespace("thisPkg"))
```

If the package did not export the method, attaching it and calling `findMethod` with no `where` argument will not find the method.

Notice also that the length of the signature must be what the corresponding package used. If `thisPkg` had only methods for one argument, only length-1 signatures will match (no trailing "ANY"), even if another currently loaded package had signatures with more arguments.

### Methods for `as()`

The function `setAs` allows packages to define methods for coercing one class of objects to another class. This works internally by defining methods for the generic function `coerce(from, to)`, which can not be called directly.

The R evaluator selects methods for this purpose using a different form of inheritance. While methods can be inherited for the object being coerced, they cannot inherit for the target class, since the result would not be a valid object from that class. If you want to examine the selection procedure, you must supply the optional argument `useInherited = c(TRUE, FALSE)` to `selectMethod`.

### References


### See Also

`Methods_Details` for the details of method selection; `GenericFunctions` for other functions manipulating methods and generic function objects; `MethodDefinition` for the class that represents method definitions.

### Examples

```r
testFun <- function(x)x
setGeneric("testFun")
setMethod("testFun", "numeric", function(x)x+1)

hasMethod("testFun", "numeric") # TRUE

hasMethod("testFun", "integer") # TRUE, inherited

existsMethod("testFun", "integer") # FALSE

hasMethod("testFun") # TRUE, default method

hasMethod("testFun", "ANY")
```
The functions below produce the package associated with a particular environment or position on the search list, or of the package containing a particular function. They are primarily used to support computations that need to differentiate objects on multiple packages.

**Usage**

```r
getPackageName(where, create = TRUE)
setPackageName(pkg, env)
packageSlot(object)
packageSlot(object) <- value
```

**Arguments**

- `where`: the environment or position on the search list associated with the desired package.
- `object`: object providing a character string name, plus the package in which this object is to be found.
- `value`: the name of the package.
- `create`: flag, should a package name be created if none can be inferred? If `TRUE` and no non-empty package name is found, the current date and time are used as a package name, and a warning is issued. The created name is stored in the environment if that environment is not locked.
- `pkg, env`: make the string in `pkg` the internal package name for all computations that set class and method definitions in environment `env`.

**Details**

Package names are normally installed during loading of the package, by the `install` script or by the `library` function. (Currently, the name is stored as the object `.packageName` but don’t trust this for the future.)

**Value**

- `getPackageName` returns the character-string name of the package (without the extraneous "package:" found in the search list).
- `packageSlot` returns or sets the package name slot (currently an attribute, not a formal slot, but this may change someday).
- `setPackageName` can be used to establish a package name in an environment that would otherwise not have one. This allows you to create classes and/or methods in an arbitrary environment, but it is usually preferable to create packages by the standard R programming tools (`package.skeleton`, etc.)
hasArg

See Also

search, packageName

Examples

```r
## all the following usually return "base"
getPackageName(length(search()))
getPackageName(baseenv())
getPackageName(asNamespace("base"))
getPackageName("package:base")
```

hasArg | Look for an Argument in the Call

Description

Returns TRUE if name corresponds to an argument in the call, either a formal argument to the function, or a component of . . . , and FALSE otherwise.

Usage

```r
hasArg(name)
```

Arguments

name | The name of a potential argument, as an unquoted name or character string.

Details

The expression `hasArg(x)`, for example, is similar to `!missing(x)`, with two exceptions. First, `hasArg` will look for an argument named `x` in the call if `x` is not a formal argument to the calling function, but . . . is. Second, `hasArg` never generates an error if given a name as an argument, whereas `missing(x)` generates an error if `x` is not a formal argument.

Value

Always TRUE or FALSE as described above.

See Also

missing

Examples

```r
ftest <- function(x1, ...) c(hasArg(x1), hasArg("y2"))

ftest(1)  ## c(TRUE, FALSE)
ftest(1, 2)  ## c(TRUE, FALSE)
ftest(y2 = 2)  ## c(FALSE, TRUE)
ftest(y = 2)  ## c(FALSE, FALSE) (no partial matching)
ftest(y2 = 2, x = 1)  ## c(TRUE, TRUE) partial match x1
```
The implicit generic mechanism stores generic versions of functions in a table in a package. The package does not want the current version of the function to be a generic, however, and retains the non-generic version.

When a call to `setMethod` or `setGeneric` creates a generic version for one of these functions, the object in the table is used. This mechanism is only needed if special arguments were used to create the generic: e.g., the `signature` or the `valueClass` options.

Function `implicitGeneric()` returns the implicit generic version, `setGenericImplicit()` turns a generic implicit, `prohibitGeneric()` prevents your function from being made generic, and `registerImplicitGenerics()` saves a set of implicit generic definitions in the cached table of the current session.

### Usage

- `implicitGeneric(name, where, generic)`
- `setGenericImplicit(name, where, restore = TRUE)`
- `prohibitGeneric(name, where)`
- `registerImplicitGenerics(what, where)`

### Arguments

- **name**: Character string name of the function.
- **where**: Package or environment in which to register the implicit generics. When using the functions from the top level of your own package source, this argument should be omitted.
- **generic**: Obsolete, and likely to be deprecated.
- **restore**: Should the non-generic version of the function be restored?.
- **what**: Optional table of the implicit generics to register, but nearly always omitted, when it defaults to a standard metadata name.

### Details

Multiple packages may define methods for the same function, to apply to classes defined in that package. Arithmetic and other operators, `plot()` and many other basic computations are typical examples. It’s essential that all such packages write methods for the same definition of the generic function. So long as that generic uses the default choice for signature and other parameters, nothing needs to be done.

If the generic has special properties, these need to be ensured for all packages creating methods for it. The simplest solution is just to make the function generic in the package that originally owned it. If for some reason the owner(s) of that package are unwilling to do this, the alternative is to define the correct generic, save it in a special table and restore the non-generic version by calling `setGenericImplicit`.

Note that the package containing the function can define methods for the implicit generic as well; when the implicit generic is made a real generic, those methods will be included.
The usual reason for having a non-default implicit generic is to provide a non-default signature, and the usual reason for that is to allow lazy evaluation of some arguments. All arguments in the signature of a generic function must be evaluated at the time the function needs to select a method. In the base function `with()` in the example below, evaluation of the argument `expr` must be delayed; therefore, it is excluded from the signature.

If you want to completely prohibit anyone from turning your function into a generic, call `prohibitGeneric()`.

Function `implicitGeneric()` returns the implicit generic version of the named function. If there is no table of these or if this function is not in the table, the result of a simple call `setGeneric(name)` is returned.

Value

Function `implicitGeneric()` returns the implicit generic definition (and caches that definition the first time if it has to construct it).

The other functions exist for their side effect and return nothing useful.

Implicit Generics for Base Functions

Implicit generic versions exist for some functions in the packages supplied in the distribution of R itself. These are stored in the ‘methods’ package itself and will always be available.

As emphasized repeatedly in the documentation, `setGeneric()` calls for a function in another package should never have non-default settings for arguments such as `signature`. The reasoning applies specially to functions in supplied packages, since methods for these are likely to exist in multiple packages. A call to `implicitGeneric()` will show the generic version.

See Also

`setGeneric`

Examples

### How we would make the function `with()` into a generic:

```r
## Since the second argument, 'expr' is used literally, we want
## `with()` to only have "data" in the signature.

## Not run:
setGeneric("with", signature = "data")
## Now we could redefine methods for "with" if we wanted to.

## When ready, we store the generic as implicit, and restore the
## original
setGenericImplicit("with")

## End(Not run)

implicitGeneric("with")

# (This implicit generic is stored in the 'methods' package.)
```
inheritedSlotNames  Names of Slots Inherited From a Super Class

Description

For a class (or class definition, see getClass and the description of class classRepresentation), give the names which are inherited from “above”, i.e., super classes, rather than by this class’ definition itself.

Usage

inheritedSlotNames(Class, where = topoenv(parent.frame()))

Arguments

Class  character string or classRepresentation, i.e., resulting from getClass.
where  environment, to be passed further to isClass and getClass.

Value

character vector of slot names, or NULL.

See Also

slotNames, slot, setClass, etc.

Examples

.srch <- search()
library(stats4)
inheritedSlotNames("mle")

if(require("Matrix", quietly = TRUE)) withAutoprint({
inheritedSlotNames("Matrix")    # NULL
## whereas
inheritedSlotNames("sparseMatrix") # -- Dim & Dimnames
## i.e. inherited from "Matrix" class
cl <- getClass("dgCMatrix")    # six slots, etc
inheritedSlotNames(cl)         # *all* six slots are inherited
})
## Not run:

## detach package we've attached above:
for(n in rev(which(is.na(match(search(), .srch)))))
  try( detach(pos = n) )

## End(Not run)
Methods to Initialize New Objects from a Class

Description

The arguments to function `new` to create an object from a particular class can be interpreted specially for that class, by the definition of a method for function `initialize` for the class. This documentation describes some existing methods, and also outlines how to write new ones.

Methods

`initialize METHOD` The default method for `initialize` takes either named or unnamed arguments. Argument names must be the names of slots in this class definition, and the corresponding arguments must be valid objects for the slot (that is, have the same class as specified for the slot, or some superclass of that class). If the object comes from a superclass, it is not coerced strictly, so normally it will retain its current class (specifically, `as(object, Class, strict = FALSE)`).

Unnamed arguments must be objects of this class, of one of its superclasses, or one of its subclasses (from the class, from a class this class extends, or from a class that extends this class). If the object is from a superclass, this normally defines some of the slots in the object. If the object is from a subclass, the new object is that argument, coerced to the current class.

Unnamed arguments are processed first, in the order they appear. Then named arguments are processed. Therefore, explicit values for slots always override any values inferred from superclass or subclass arguments.

`initialize METHOD` Objects of a class that extends `traceable` are used to implement debug tracing (see class `traceable` and `trace`).

The `initialize` method for these classes takes special arguments `def, tracer, exit, at, print`. The first of these is the object to use as the original definition (e.g., a function). The others correspond to the arguments to `trace`.

`initialize METHOD` The `initialize` method for environments takes a named list of objects to be used to initialize the environment. Subclasses of "environment" inherit an initialize method through ".environment", which has the additional effect of allocating a new environment. If you define your own method for such a subclass, be sure either to call the existing method via `callNextMethod` or allocate an environment in your method, since environments are references and are not duplicated automatically.

`initialize METHOD` This is a method for internal use only. It takes an optional `functionDef` argument to provide a generic function with a signature slot to define the argument names. See `Methods_Details` for details.

Writing Initialization Methods

Initialization methods provide a general mechanism corresponding to generator functions in other languages.

The arguments to `initialize` are `.Object` and `...`. Nearly always, `initialize` is called from `new`, not directly. The `.Object` argument is then the prototype object from the class.

Two techniques are often appropriate for `initialize` methods: special argument names and `callNextMethod`. 
You may want argument names that are more natural to your users than the (default) slot names. These will be the formal arguments to your method definition, in addition to .Object (always) and ... (optionally). For example, the method for class "traceable" documented above would be created by a call to `setMethod` of the form:

```r
setMethod("initialize", "traceable",
function(.Object, def, tracer, exit, at, print) {
    ....
})
```

In this example, no other arguments are meaningful, and the resulting method will throw an error if other names are supplied.

When your new class extends another class, you may want to call the initialize method for this superclass (either a special method or the default). For example, suppose you want to define a method for your class, with special argument `x`, but you also want users to be able to set slots specifically. If you want `x` to override the slot information, the beginning of your method definition might look something like this:

```r
function(.Object, x, ...) {
    Object <- callNextMethod(.Object, ...)
    if(!missing(x)) { # do something with x

```

You could also choose to have the inherited method override, by first interpreting `x`, and then calling the next method.

---

### Description

The majority of applications using methods and classes will be in R packages implementing new computations for an application, using new classes of objects that represent the data and results. Computations will be implemented using methods that implement functional computations when one or more of the arguments is an object from these classes.

Calls to the functions `setClass()` define the new classes; calls to `setMethod` define the methods. These, along with ordinary R computations, are sufficient to get started for most applications.

Classes are defined in terms of the data in them and what other classes of data they inherit from. Section ‘Defining Classes’ outlines the basic design of new classes.

Methods are R functions, often implementing basic computations as they apply to the new classes of objects. Section ‘Defining Methods’ discusses basic requirements and special tools for defining methods.

The classes discussed here are the original functional classes. R also supports formal classes and methods similar to those in other languages such as Python, in which methods are part of class definitions and invoked on an object. These are more appropriate when computations expect references to objects that are persistent, making changes to the object over time. See ReferenceClasses and Chapter 9 of the reference for the choice between these and S4 classes.
Defining Classes

All objects in \( \mathcal{R} \) belong to a class; ordinary vectors and other basic objects are built-in (\texttt{builtin-class}). A new class is defined in terms of the named \textit{slots} that it has and/or in terms of existing classes that it inherits from, or \textit{contains} (discussed in 'Class Inheritance' below). A call to \texttt{setClass()} names a new class and uses the corresponding arguments to define it.

For example, suppose we want a class of objects to represent a collection of positions, perhaps from GPS readings. A natural way to think of these in \( \mathcal{R} \) would have vectors of numeric values for latitude, longitude and altitude. A class with three corresponding slots could be defined by:

\begin{verbatim}
Pos <- setClass("Pos", slots = c(latitude = "numeric", longitude = "numeric", altitude = "numeric"))
\end{verbatim}

The value returned is a function, typically assigned as here with the name of the class. Calling this function returns an object from the class; its arguments are named with the slot names. If a function in the class had read the corresponding data, perhaps from a CSV file or from a database, it could return an object from the class by:

\begin{verbatim}
Pos(latitude = x, longitude = y, altitude = z)
\end{verbatim}

The slots are accessed by the \texttt{@} operator; for example, if \( g \) is an object from the class, \( g@latitude \).

In addition to returning a generator function the call to \texttt{setClass()} assigns a definition of the class in a special metadata object in the package’s namespace. When the package is loaded into an \( \mathcal{R} \) session, the class definition is added to a table of known classes.

To make the class and the generating function publicly available, the package should include \texttt{POS} in \texttt{exportClasses()} and \texttt{export()} directives in its \texttt{NAMESPACE} file:

\begin{verbatim}
exportClasses(POS); export(POS)
\end{verbatim}

Defining Methods

Defining methods for an \( \mathcal{R} \) function makes that function \textit{generic}. Instead of a call to the function always being carried out by the same method, there will be several alternatives. These are selected by matching the classes of the arguments in the call to a table in the generic function, indexed by classes for one or more formal arguments to the function, known as the \textit{signatures} for the methods.

A method definition then specifies three things: the name of the function, the signature and the method definition itself. The definition must be a function with the same formal arguments as the generic.

For example, a method to make a plot of an object from class "Pos" could be defined by:

\begin{verbatim}
setMethod("plot", c("Pos", "missing"), function(x, y, ...) { plotPos(x, y) })
\end{verbatim}

This method will match a call to \texttt{plot()} if the first argument is from class "Pos" or a subclass of that. The second argument must be missing; only a missing argument matches that class in the signature. Any object will match class "ANY" in the corresponding position of the signature.

Class Inheritance

A class may inherit all the slots and methods of one or more existing classes by specifying the names of the inherited classes in the \texttt{contains =} argument to \texttt{setClass()}.

To define a class that extends class "Pos" to a class "GPS" with a slot for the observation times:

\begin{verbatim}
GPS <- setClass("GPS", slots = c(time = "POSIXt"), contains = "Pos")
\end{verbatim}

The inherited classes may be S4 classes, S3 classes or basic data types. S3 classes need to be identified as such by a call to \texttt{setOldClass()}; most S3 classes in the base package and many in the other built-in packages are already declared, as is "POSIXt". If it had not been, the application package should contain:
Inheriting from one of the R types is special. Objects from the new class will have the same type. A class `Currency` that contains numeric data plus a slot “unit” would be created by

```r
Currency <- setClass("Currency", slots = c(unit = "character"), contains = "numeric")
```

Objects created from this class will have type “numeric” and inherit all the built-in arithmetic and other computations for that type. Classes can only inherit from at most one such type; if the class does not inherit from a type, objects from the class will have type "S4".

### References

---

**is**  
_Is an Object from a Class?_

**Description**  
Functions to test inheritance relationships between an object and a class or between two classes (extends).

**Usage**  

```r
is(object, class2)
```

```r
extends(class1, class2, maybe = TRUE, fullInfo = FALSE)
```

**Arguments**  

- `object` any R object.
- `class1, class2` character strings giving the names of each of the two classes between which `is` relations are to be examined, or (more efficiently) the class definition objects for the classes.
- `fullInfo` In a call to `extends`, with `class2` missing, `fullInfo` is a flag, which if `TRUE` causes a list of objects of class `SClassExtension` to be returned, rather than just the names of the classes. Only the distance slot is likely to be useful in practice; see the ‘Selecting Superclasses’ section;  
- `maybe` What to return for conditional inheritance. But such relationships are rarely used and not recommended, so this argument should not be needed.

**Selecting Superclasses**  
A call to `selectSuperClasses(cl)` returns a list of superclasses, similarly to `extends(cl)`. Additional arguments restrict the class names returned to direct superclasses and/or to non-virtual classes.

Either way, programming with the result, particularly using `sapply`, can be useful.

To find superclasses with more generally defined properties, one can program with the result returned by `extends` when called with one class as argument. By default, the call returns a character vector including the name of the class itself and of all its superclasses. Alternatively, if
extends is called with `fullInfo = TRUE`, the return value is a named list, its names being the previous character vector. The elements of the list corresponding to superclasses are objects of class `SClassExtension`. Of the information in these objects, one piece can be useful: the number of generations between the classes, given by the "distance" slot.

Programming with the result of the call to `extends`, particularly using `sapply`, can select superclasses. The programming technique is to define a test function that returns TRUE for superclasses or relationships obeying some requirement. For example, to find only next-to-direct superclasses, use this function with the list of extension objects:

```r
function(what) is(what, "SClassExtension") && what@distance == 2
```
or, to find only superclasses from "myPkg", use this function with the simple vector of names:

```r
function(what) getClassDef(what)@package == "myPkg"
```
Giving such functions as an argument to `sapply` called on the output of `extends` allows you to find superclasses with desired properties. See the examples below.

Note
Prior to R 4.2.0 the code used the first elements of `class1` and `class2`, silently. These are now required to be length-one character vectors.

References

See Also
Although `inherits` is defined for S3 classes, it has been modified so that the result returned is nearly always equivalent to `is`, both for S4 and non-S4 objects. Since it is implemented in C, it is somewhat faster. The only non-equivalences arise from use of `setIs`, which should rarely be encountered.

Examples
```r
## Not run:
## this example can be run if package XRPython from CRAN is installed.
supers <- extends("PythonInterface")
## find all the superclasses from package XR
fromXR <- sapply(supers,
  function(what) getClassDef(what)@package == "XR")
## print them
supers[fromXR]

## find all the superclasses at distance 2
superRelations <- extends("PythonInterface", fullInfo = TRUE)
dist2 <- sapply(superRelations,
  function(what) is(what, "SClassExtension") && what@distance == 2)
## print them
names(superRelations)[dist2]

## End(Not run)
```
isSealedMethod

Check for a Sealed Method or Class

Description

These functions check for either a method or a class that has been sealed when it was defined, and which therefore cannot be re-defined.

Usage

isSealedMethod(f, signature, fdef, where)
isSealedClass(Class, where)

Arguments

f The quoted name of the generic function.
signature The class names in the method’s signature, as they would be supplied to setMethod.
fdef Optional, and usually omitted: the generic function definition for f.
Class The quoted name of the class.
where where to search for the method or class definition. By default, searches from the top environment of the call to isSealedMethod or isSealedClass, typically the global environment or the namespace of a package containing a call to one of the functions.

Details

In the R implementation of classes and methods, it is possible to seal the definition of either a class or a method. The basic classes (numeric and other types of vectors, matrix and array data) are sealed. So also are the methods for the primitive functions on those data types. The effect is that programmers cannot re-define the meaning of these basic data types and computations. More precisely, for primitive functions that depend on only one data argument, methods cannot be specified for basic classes. For functions (such as the arithmetic operators) that depend on two arguments, methods can be specified if one of those arguments is a basic class, but not if both are.

Programmers can seal other class and method definitions by using the sealed argument to setClass or setMethod.

Value

The functions return FALSE if the method or class is not sealed (including the case that it is not defined); TRUE if it is.

References

Chambers, John M. (1998) Programming with Data Springer (For the original S4 version.)
Examples

```r
### these are both TRUE
isSealedMethod("+", c("numeric", "character"))
isSealedClass("matrix")

setClass("track", slots = c(x="numeric", y="numeric"))
### but this is FALSE
isSealedClass("track")
### and so is this
isSealedClass("A Name for an undefined Class")
### and so are these, because only one of the two arguments is basic
isSealedMethod("+", c("track", "numeric"))
isSealedMethod("+", c("numeric", "track"))
```

Language-class

Classes to Represent Unevaluated Language Objects

Description

The virtual class "language" and the specific classes that extend it represent unevaluated objects, as produced for example by the parser or by functions such as `quote`.

Usage

```r
### each of these classes corresponds to an unevaluated object
### in the S language.
### The class name can appear in method signatures,
### and in a few other contexts (such as some calls to as()).
"("  
"<-"  
"call"  
"for"  
"if"  
"repeat"  
"while"  
"name"  
"{"

### Each of the classes above extends the virtual class
"language"
```

Objects from the Class

"language" is a virtual class; no objects may be created from it.

Objects from the other classes can be generated by a call to `new(Class, ...)`, where `Class` is the quoted class name, and the `...` arguments are either empty or a `single` object that is from this class (or an extension).
Methods

*coerce* signature(from = "ANY", to = "call"). A method exists for as(object, "call"), calling as.call().

Examples

showClass("language")

is( quote(sin(x)) ) # "call" "language"

(ff <- new("if")); is(ff) # "if" "language"

(ff <- new("for")); is(ff) # "for" "language"

LinearMethodsList-class

Class "LinearMethodsList"

Description

A version of methods lists that has been ‘linearized’ for producing summary information. The actual objects from class "MethodsList" used for method dispatch are defined recursively over the arguments involved.

Objects from the Class

The function `linearizeMlist` converts an ordinary methods list object into the linearized form.

Slots

methods: Object of class "list", the method definitions.

arguments: Object of class "list", the corresponding formal arguments, namely as many of the arguments in the signature of the generic function as are active in the relevant method table.

classes: Object of class "list", the corresponding classes in the signatures.

generic: Object of class "genericFunction"; the generic function to which the methods correspond.

Future Note

The current version of `linearizeMlist` does not take advantage of the `MethodDefinition` class, and therefore does more work for less effect than it could. In particular, we may move to redefine both the function and the class to take advantage of the stored signatures. Don’t write code depending precisely on the present form, although all the current information will be obtainable in the future.

See Also

Function `linearizeMlist` for the computation, and class `MethodsList` for the original, recursive form.
Description

Local reference classes are modified ReferenceClasses that isolate the objects to the local frame. Therefore, they do not propagate changes back to the calling environment. At the same time, they use the reference field semantics locally, avoiding the automatic duplication applied to standard R objects.

The current implementation has no special construction. To create a local reference class, call \code{setRefClass}() with a \code{contains} argument that includes \code{"localRefClass"}. See the example below.

Local reference classes operate essentially as do regular, functional classes in R; that is, changes are made by assignment and take place in the local frame. The essential difference is that replacement operations (like the change to the \code{twiddle} field in the example) do not cause duplication of the entire object, as would be the case for a formal class or for data with attributes or in a named list. The purpose is to allow large objects in some fields that are not changed along with potentially frequent changes to other fields, but without copying the large fields.

Usage

\begin{verbatim}
setRefClass(Class, fields = , contains = c("localRefClass",....),
    methods =, where =, ...)  
\end{verbatim}

Details

Localization of objects is only partially automated in the current implementation. Replacement expressions using the \code{$<-$} operator are safe.

However, if reference methods for the class themselves modify fields, using \code{<<-}, for example, then one must ensure that the object is local to the relevant frame before any such method is called. Otherwise, standard reference class behavior still prevails.

There are two ways to ensure locality. The direct way is to invoke the special method \code{x$ensureLocal()} on the object. The other way is to modify a field explicitly by \code{x$field <- ...}. It's only necessary that one or the other of these happens once for each object, in order to trigger the shallow copy that provides locality for the references. In the example below, we show both mechanisms.

However it's done, localization must occur before any methods make changes. (Eventually, some use of code tools should at least largely automate this process, although it may be difficult to guarantee success under arbitrary circumstances.)

Author(s)

John Chambers

Examples

\begin{verbatim}
## class "myIter" has a BigData field for the real (big) data
## and a "twiddle" field for some parameters that it twiddles
## ( for some reason)
\end{verbatim}
myIter <- setRefClass("myIter", contains = "localRefClass",
    fields = list(BigData = "numeric", twiddle = "numeric"))
tw <- rnorm(3)
x1 <- myIter(BigData = rnorm(1000), twiddle = tw) # OK, not REALLY big
twiddler <- function(x, n) {
    x$ensureLocal() # see the Details. Not really needed in this example
    for(i in seq_len(n)) {
        x$twiddle <- x$twiddle + rnorm(length(x$twiddle))
        ## then do something ....
        ## Snooping in gdb, etc will show that x$BigData is not copied
    }
    return(x)
}
x2 <- twiddler(x1, 10)
stopifnot(identical(x1$twiddle, tw), !identical(x1$twiddle, x2$twiddle))

---

makeClassRepresentation

**Create a Class Definition**

**Description**

Constructs an object of class `classRepresentation` to describe a particular class. Mostly a utility function, but you can call it to create a class definition without assigning it, as `setClass` would do.

**Usage**

```
makeClassRepresentation(name, slots=list(), superClasses=character(),
    prototype=NULL, package, validity, access,
    version, sealed, virtual=NA, where)
```

**Arguments**

- **name** character string name for the class
- **slots** named list of slot classes as would be supplied to `setClass`, but *without* the unnamed arguments for `superClasses` if any.
- **superClasses** what classes does this class extend
- **prototype** an object providing the default data for the class, e.g., the result of a call to `prototype`.
- **package** The character string name for the package in which the class will be stored; see `getPackageName`.
- **validity** Optional validity method. See `validObject` and the discussion of validity methods in the reference.
- **access** Access information. Not currently used.
- **version** Optional version key for version control. Currently generated, but not used.
sealed     Is the class sealed? See setClass.
virtual    Is this known to be a virtual class?
where      The environment from which to look for class definitions needed (e.g., for slots or superclasses). See the discussion of this argument under GenericFunctions.

References

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

setClass

method.skeleton

*Create a Skeleton File for a New Method*

Description

This function writes a source file containing a call to setMethod to define a method for the generic function and signature supplied. By default the method definition is in line in the call, but can be made an external (previously assigned) function.

Usage

method.skeleton(generic, signature, file, external = FALSE, where)

Arguments

generic     the character string name of the generic function, or the generic function itself. In the first case, the function need not currently be a generic, as it would not for the resulting call to setMethod.
signature   the method signature, as it would be given to setMethod
file        a character string name for the output file, or a writable connection. By default the generic function name and the classes in the signature are concatenated, with separating underscore characters. The file name should normally end in ".R". To write multiple method skeletons to one file, open the file connection first and then pass it to method.skeleton() in multiple calls.
external    flag to control whether the function definition for the method should be a separate external object assigned in the source file, or included in line in the call to setMethod. If supplied as a character string, this will be used as the name for the external function; by default the name concatenates the generic and signature names, with separating underscores.
where       The environment in which to look for the function; by default, the top-level environment of the call to method.skeleton.

Value

The file argument, invisibly, but the function is used for its side effect.
See Also

setMethod, package.skeleton

Examples

setClass("track", slots = c(x="numeric", y="numeric"))
method.skeleton("show", "track")  ## writes show_track.R
method.skeleton("Ops", c("track", "track"))  ## writes "Ops_track_track.R"

## write multiple method skeletons to one file
con <- file("./Math_track.R", "w")
method.skeleton("Math", "track", con)
method.skeleton("exp", "track", con)
method.skeleton("log", "track", con)
close(con)

MethodDefinition-class

Classes to Represent Method Definitions

Description

These classes extend the basic class "function" when functions are to be stored and used as method definitions.

Details

Method definition objects are functions with additional information defining how the function is being used as a method. The target slot is the class signature for which the method will be dispatched, and the defined slot the signature for which the method was originally specified (that is, the one that appeared in some call to setMethod).

Objects from the Class

The action of setting a method by a call to setMethod creates an object of this class. It's unwise to create them directly.

The class "SealedMethodDefinition" is created by a call to setMethod with argument sealed = TRUE. It has the same representation as "MethodDefinition".

Slots

.Data: Object of class "function"; the data part of the definition.
target: Object of class "signature"; the signature for which the method was wanted.
defined: Object of class "signature"; the signature for which a method was found. If the method was inherited, this will not be identical to target.
generic: Object of class "character"; the function for which the method was created.
Methods

Classes

- Extends "function", from data part.
- Extends "PossibleMethod", directly.
- Extends "OptionalMethods", by class "function".

See Also

- class MethodsList for the objects defining sets of methods associated with a particular generic function. The individual method definitions stored in these objects are from class MethodDefinition, or an extension. Class MethodWithNext for an extension used by callNextMethod.

Methods S4 Class Documentation

Description

You have navigated to an old link to documentation of S4 methods.

For basic use of classes and methods, see Introduction; to create new method definitions, see setMethod; for technical details on S4 methods, see Methods_Details.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)

MethodsList-class Class MethodsList, Defunct Representation of Methods

Description

This class of objects was used in the original implementation of the package to control method dispatch. Its use is now defunct, but object appear as the default method slot in generic functions. This and any other remaining uses will be removed in the future.

For the modern alternative, see listOfMethods.

The details in this documentation are retained to allow analysis of old-style objects.

Details

Suppose a function f has formal arguments x and y. The methods list object for that function has the object as .name("x") as its argument slot. An element of the methods named "track" is selected if the actual argument corresponding to x is an object of class "track". If there is such an element, it can generally be either a function or another methods list object.

In the first case, the function defines the method to use for any call in which x is of class "track". In the second case, the new methods list object defines the available methods depending on the remaining formal arguments, in this example, y.

Each method corresponds conceptually to a signature; that is a named list of classes, with names corresponding to some or all of the formal arguments. In the previous example, if selecting class "track" for x, finding that the selection was another methods list and then selecting class "numeric" for y would produce a method associated with the signature x = "track", y = "numeric".
Methods_Details

Slots

argument: Object of class "name". The name of the argument being used for dispatch at this level.

methods: A named list of the methods (and method lists) defined explicitly for this argument. The names are the names of classes, and the corresponding element defines the method or methods to be used if the corresponding argument has that class. See the details below.

allMethods: A named list, contains all the directly defined methods from the methods slot, plus any inherited methods. Ignored when methods tables are used for dispatch (see Methods_Details).

Extends

Class "OptionalMethods", directly.

Methods_Details

General Information on Methods

Description

This documentation covers some general topics on how methods work and how the methods package interacts with the rest of R. The information is usually not needed to get started with methods and classes, but may be helpful for moderately ambitious projects, or when something doesn’t work as expected.

For additional information see documentation for the important steps: (setMethod(), setClass() and setGeneric()). Also Methods_for_Nongenerics on defining formal methods for functions that are not currently generic functions; Methods_for_S3 for the relation to S3 classes and methods; Classes_Details for class definitions and Chapters 9 and 10 of the reference.

How Methods Work

A call to a generic function selects a method matching the actual arguments in the call. The body of the method is evaluated in the frame of the call to the generic function. A generic function is identified by its name and by the package to which it correspond. Unlike ordinary functions, the generic has a slot that specifies its package.

In an R session, there is one version of each such generic, regardless of where the call to that generic originated, and the generic function has a table of all the methods currently available for it; that is, all the methods in packages currently loaded into the session.

Methods are frequently defined for functions that are non-generic in their original package,. for example, for function plot() in package graphics. An identical version of the corresponding generic function may exist in several packages. All methods will be dispatched consistently from the R session.

Each R package with a call to setMethod in its source code will include a methods metadata object for that generic. When the package is loaded into an R session, the methods for each generic function are cached, that is, added to the environment of the generic function. This merged table of methods is used to dispatch or select methods from the generic, using class inheritance and possibly group generic functions (see GroupGenericFunctions) to find an applicable method. See the “Method Selection and Dispatch” section below. The caching computations ensure that only one version of each generic function is visible globally; although different attached packages may contain a copy of the generic function, these behave identically with respect to method selection.
In contrast, it is possible for the same function name to refer to more than one generic function, when these have different package slots. In the latter case, R considers the functions unrelated: A generic function is defined by the combination of name and package. See the “Generic Functions” section below.

The methods for a generic are stored according to the corresponding signature in the call to `setMethod` that defined the method. The signature associates one class name with each of a subset of the formal arguments to the generic function. Which formal arguments are available, and the order in which they appear, are determined by the "signature" slot of the generic function itself. By default, the signature of the generic consists of all the formal arguments except ..., in the order they appear in the function definition.

Trailing arguments in the signature of the generic will be inactive if no method has yet been specified that included those arguments in its signature. Inactive arguments are not needed or used in labeling the cached methods. (The distinction does not change which methods are dispatched, but ignoring inactive arguments improves the efficiency of dispatch.)

All arguments in the signature of the generic function will be evaluated when the function is called, rather than using lazy evaluation. Therefore, it’s important to exclude any arguments that need to be dealt with symbolically (such as the expr argument to function `with`). Note that only actual arguments are evaluated, not default expressions. A missing argument enters into the method selection as class "missing".

The cached methods are stored in an environment object. The names used for assignment are a concatenation of the class names for the active arguments in the method signature.

**Method Selection: Details**

When a call to a generic function is evaluated, a method is selected corresponding to the classes of the actual arguments in the signature. First, the cached methods table is searched for an exact match; that is, a method stored under the signature defined by the string value of `class(x)` for each non-missing argument, and "missing" for each missing argument. If no method is found directly for the actual arguments in a call to a generic function, an attempt is made to match the available methods to the arguments by using the superclass information about the actual classes. A method found by this search is cached in the generic function so that future calls with the same argument classes will not require repeating the search. In any likely application, the search for inherited methods will be a negligible overhead.

Each class definition may include a list of one or more direct superclasses of the new class. The simplest and most common specification is by the contains= argument in the call to `setClass`. Each class named in this argument is a superclass of the new class. A class will also have as a direct superclass any class union to which it is a member. Class unions are created by a call to `setClassUnion`. Additional members can be added to the union by a simple call to `setIs`. Superclasses specified by either mechanism are the direct superclasses.

Inheritance specified in either of these forms is simple in the sense that all the information needed for the superclass is asserted to be directly available from the object. R inherited from S a more general form of inheritance in which inheritance may require some transformation or be conditional on a test. This more general form has not proved to be useful in general practical situations. Since it also adds some computational costs non-simple inheritance is not recommended. See `setIs` for the general version.

The direct superclasses themselves may have direct superclasses and similarly through further generations. Putting all this information together produces the full list of superclasses for this class. The superclass list is included in the definition of the class that is cached during the R session. The distance between the two classes is defined to be the number of generations: 1 for direct superclasses (regardless of which mechanism defined them), then 2 for the direct superclasses of those classes, and so on. To see all the superclasses, with their distance, print the class definition by calling
**Methods_Details**

**getClass.** In addition, any class implicitly has class "ANY" as a superclass. The distance to "ANY" is treated as larger than the distance to any actual class. The special class "missing" corresponding to missing arguments has only "ANY" as a superclass, while "ANY" has no superclasses.

When a method is to be selected by inheritance, a search is made in the table for all methods corresponding to a combination of either the direct class or one of its superclasses, for each argument in the active signature. For an example, suppose there is only one argument in the signature and that the class of the corresponding object was "dgeMatrix" (from the recommended package Matrix). This class has (currently) three direct superclasses and through these additional superclasses at distances 2 through 4. A method that had been defined for any of these classes or for class "ANY" (the default method) would be eligible. Methods for the shortest difference are preferred. If there is only one best method in this sense, method selection is unambiguous.

When there are multiple arguments in the signature, each argument will generate a similar list of inherited classes. The possible matches are now all the combinations of classes from each argument (think of the function outer generating an array of all possible combinations). The search now finds all the methods matching any of this combination of classes. For each argument, the distance to the superclass defines which method(s) are preferred for that argument. A method is considered best for selection if it is among the best (i.e., has the least distance) for each argument.

The end result is that zero, one or more methods may be “best”. If one, this method is selected and cached in the table of methods. If there is more than one best match, the selection is ambiguous and a message is printed noting which method was selected (the first method lexicographically in the ordering) and what other methods could have been selected. Since the ambiguity is usually nothing the end user could control, this is not a warning. Package authors should examine their package for possible ambiguous inheritance by calling testInheritedMethods.

Cached inherited selections are not themselves used in future inheritance searches, since that could result in invalid selections. If you want inheritance computations to be done again (for example, because a newly loaded package has a more direct method than one that has already been used in this session), call resetGeneric. Because classes and methods involving them tend to come from the same package, the current implementation does not reset all generics every time a new package is loaded.

Besides being initiated through calls to the generic function, method selection can be done explicitly by calling the function selectMethod. Note that some computations may use this function directly, with optional arguments. The prime example is the use of coerce() methods by function as(). There has been some confusion from comparing coerce methods to a call to selectMethod with other options.

**Method Evaluation: Details**

Once a method has been selected, the evaluator creates a new context in which a call to the method is evaluated. The context is initialized with the arguments from the call to the generic function. These arguments are not rematched. All the arguments in the signature of the generic will have been evaluated (including any that are currently inactive); arguments that are not in the signature will obey the usual lazy evaluation rules of the language. If an argument was missing in the call, its default expression if any will not have been evaluated, since method dispatch always uses class missing for such arguments.

A call to a generic function therefore has two contexts: one for the function and a second for the method. The argument objects will be copied to the second context, but not any local objects created in a nonstandard generic function. The other important distinction is that the parent ("enclosing") environment of the second context is the environment of the method as a function, so that all R programming techniques using such environments apply to method definitions as ordinary functions.

For further discussion of method selection and dispatch, see the references in the sections indicated.
Generic Functions

In principle, a generic function could be any function that evaluates a call to standardGeneric(), the internal function that selects a method and evaluates a call to the selected method. In practice, generic functions are special objects that in addition to being from a subclass of class "function" also extend the class genericFunction. Such objects have slots to define information needed to deal with their methods. They also have specialized environments, containing the tables used in method selection.

The slots "generic" and "package" in the object are the character string names of the generic function itself and of the package from which the function is defined. As with classes, generic functions are uniquely defined in R by the combination of the two names. There can be generic functions of the same name associated with different packages (although inevitably keeping such functions cleanly distinguished is not always easy). On the other hand, R will enforce that only one definition of a generic function can be associated with a particular combination of function and package name, in the current session or other active version of R.

Tables of methods for a particular generic function, in this sense, will often be spread over several other packages. The total set of methods for a given generic function may change during a session, as additional packages are loaded. Each table must be consistent in the signature assumed for the generic function.

R distinguishes standard and nonstandard generic functions, with the former having a function body that does nothing but dispatch a method. For the most part, the distinction is just one of simplicity: knowing that a generic function only dispatches a method call allows some efficiencies and also removes some uncertainties.

In most cases, the generic function is the visible function corresponding to that name, in the corresponding package. There are two exceptions, implicit generic functions and the special computations required to deal with R's primitive functions. Packages can contain a table of implicit generic versions of functions in the package, if the package wishes to leave a function non-generic but to constrain what the function would be like if it were generic. Such implicit generic functions are created during the installation of the package, essentially by defining the generic function and possibly methods for it, and then reverting the function to its non-generic form. (See implicitGeneric for how this is done.) The mechanism is mainly used for functions in the older packages in R, which may prefer to ignore S4 methods. Even in this case, the actual mechanism is only needed if something special has to be specified. All functions have a corresponding implicit generic version defined automatically (an implicit, implicit generic function one might say). This function is a standard generic with the same arguments as the non-generic function, with the non-generic version as the default (and only) method, and with the generic signature being all the formal arguments except . . . .

The implicit generic mechanism is needed only to override some aspect of the default definition. One reason to do so would be to remove some arguments from the signature. Arguments that may need to be interpreted literally, or for which the lazy evaluation mechanism of the language is needed, must not be included in the signature of the generic function, since all arguments in the signature will be evaluated in order to select a method. For example, the argument expr to the function with is treated literally and must therefore be excluded from the signature.

One would also need to define an implicit generic if the existing non-generic function were not suitable as the default method. Perhaps the function only applies to some classes of objects, and the package designer prefers to have no general default method. In the other direction, the package designer might have some ideas about suitable methods for some classes, if the function were generic. With reasonably modern packages, the simple approach in all these cases is just to define the function as a generic. The implicit generic mechanism is mainly attractive for older packages that do not want to require the methods package to be available.
Generic functions will also be defined but not obviously visible for functions implemented as primitive functions in the base package. Primitive functions look like ordinary functions when printed but are in fact not function objects but objects of two types interpreted by the R evaluator to call underlying C code directly. Since their entire justification is efficiency, R refuses to hide primitives behind a generic function object. Methods may be defined for most primitives, and corresponding metadata objects will be created to store them. Calls to the primitive still go directly to the C code, which will sometimes check for applicable methods. The definition of “sometimes” is that methods must have been detected for the function in some package loaded in the session and isS4(x) is TRUE for the first argument (or for the second argument, in the case of binary operators). You can test whether methods have been detected by calling isGeneric for the relevant function and you can examine the generic function by calling getGeneric, whether or not methods have been detected. For more on generic functions, see the references and also section 2 of the R Internals document supplied with R.

Method Definitions

All method definitions are stored as objects from the MethodDefinition class. Like the class of generic functions, this class extends ordinary R functions with some additional slots: "generic", containing the name and package of the generic function, and two signature slots, “defined” and “target”, the first being the signature supplied when the method was defined by a call to setMethod. The “target” slot starts off equal to the "defined" slot. When an inherited method is cached after being selected, as described above, a copy is made with the appropriate "target" signature. Output from showMethods, for example, includes both signatures.

Method definitions are required to have the same formal arguments as the generic function, since the method dispatch mechanism does not rematch arguments, for reasons of both efficiency and consistency.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)


See Also

For more specific information, see setGeneric, setMethod, and setClass.

For the use of … in methods, see dotsMethods.
The original version, however, remains non-generic. Calls in that package or in other packages that use that version will not dispatch your methods except for special circumstances:

1. If the function is one of the primitive functions that accept methods, the internal C implementation will dispatch methods if one of the arguments is an S4 object, as should be the case.

2. If the other version of the function dispatches S3 methods and your methods are also registered as S3 methods, the method will usually be dispatched as that S3 method.

3. Otherwise, you will need to ensure that all calls to the function come from a package in which the function is generic, perhaps by copying code to your package.

Details and the underlying reasons are discussed in the following sections.

Generic and Non-Generic Calls

Creating methods for a function (any function) in a package means that calls to the function in that package will select methods according to the actual arguments. However, if the function was originally a non-generic in another package, calls to the function from that package will not dispatch methods. In addition, calls from any third package that imports the non-generic version will also not dispatch methods. This section considers the reason and how one might deal with the consequences.

The reason is simply the R namespace mechanism and its role in evaluating function calls. When a name (such as the name of a function) needs to be evaluated in a call to a function from some package, the evaluator looks first in the frame of the call, then in the namespace of the package and then in the imports to that package.

Defining methods for a function in a package ensures that calls to the function in that package will select the methods, because a generic version of the function is created in the namespace. Similarly, calls from another package that has or imports the generic version will select methods. Because the generic versions are identical, all methods will be available in all these packages.

However, calls from any package that imports the old version or just selects it from the search list will usually not select methods.

A an example, consider the function `data.frame()` in the base package. This function takes any number of objects as arguments and attempts to combine them as variables into a data frame object. It does this by calling `as.data.frame()`, also in the base package, for each of the objects.

A reasonable goal would be to extend the classes of objects that can be included in a data frame by defining methods for `as.data.frame()`. But calls to `data.frame()`, will still use the version of that function in the base package, which continues to call the non-generic `as.data.frame()` in that package.

The details of what happens and options for dealing with it depend on the form of the function: a primitive function; a function that dispatches S3 methods; or an ordinary R function.

Primitive functions are not actual R function objects. They go directly to internal C code. Some of them, however, have been implemented to recognize methods. These functions dispatch both S4 and S3 methods from the internal C code. There is no explicit generic function, either S3 or S4. The internal code looks for S4 methods if the first argument, or either of the arguments in the case of a binary operator, is an S4 object. If no S4 method is found, a search is made for an S3 method. So defining methods for these functions works as long as the relevant classes have been defined, which should always be the case.

A function dispatches S3 methods by calling `UseMethod()`, which does not look for formal methods regardless of whether the first argument is an S4 object or not. This applies to the `as.data.frame()` example above. To have methods called in this situation, your package must also define the method as an S3 method, if possible. See section ‘S3 “Generic” Functions’.
In the third possibility, the function is defined with no expectation of methods. For example, the base package has a number of functions that compute numerical decompositions of matrix arguments. Some, such as `cho1()` and `qr()` are implemented to dispatch S3 methods; others, such as `svd()` are implemented directly as a specific computation. A generic version of the latter functions can be written and called directly to define formal methods, but no code in another package that does not import this generic version will dispatch such methods.

In this case, you need to have the generic version used in all the indirect calls to the function supplying arguments that should dispatch methods. This may require supplying new functions that dispatch methods and then call the function they replace. For example, if S3 methods did not work for `as.data.frame()`, one could call a function that applied the generic version to all its arguments and then called `data.frame()` as a replacement for that function. If all else fails, it might be necessary to copy over the relevant functions so that they would find the generic versions.

**S3 “Generic” Functions**

S3 method dispatch looks at the class of the first argument. S3 methods are ordinary functions with the same arguments as the generic function. The “signature” of an S3 method is identified by the name to which the method is assigned, composed of the name of the generic function, followed by “.”, followed by the name of the class. For details, see UseMethod.

To implement a method for one of these functions corresponding to S4 classes, there are two possibilities: either an S4 method or an S3 method with the S4 class name. The S3 method is only possible if the intended signature has the first argument and nothing else. In this case, the recommended approach is to define the S3 method and also supply the identical function as the definition of the S4 method. If the S3 generic function was `f3(x, ...)` and the S4 class for the new method was "myClass":

```r
f3.myClass <- function(x, ...) { .... }  
setMethod("f3", "myClass", f3.myClass)
```

Defining both methods usually ensures that all calls to the original function will dispatch the intended method. The S4 method alone would not be called from other packages using the original version of the function. On the other hand, an S3 method alone will not be called if there is any eligible non-default S4 method.

S4 and S3 method selection are designed to follow compatible rules of inheritance, as far as possible. S3 classes can be used for any S4 method selection, provided that the S3 classes have been registered by a call to `setOldClass`, with that call specifying the correct S3 inheritance pattern. S4 classes can be used for any S3 method selection; when an S4 object is detected, S3 method selection uses the contents of `extends(class(x))` as the equivalent of the S3 inheritance (the inheritance is cached after the first call).

An existing S3 method may not behave as desired for an S4 subclass, in which case utilities such as `asS3` and `S3Part` may be useful. If the S3 method fails on the S4 object, `asS3(x)` may be passed instead; if the object returned by the S3 method needs to be incorporated in the S4 object, the replacement function for `S3Part` may be useful.

**References**


**See Also**

Methods_for_S3 for suggested implementation of methods that work for both S3 and S4 dispatch.
Methods_for_Nongenerics

Examples

```r
## A class that extends a registered S3 class inherits that class' S3
## methods.

setClass("myFrame", contains = "data.frame",
slots = c(timestamps = "POSIXt"))
df1 <- data.frame(x = 1:10, y = rnorm(10), z = sample(letters,10))
mydf1 <- new("myFrame", df1, timestamps = Sys.time())

## "myFrame" objects inherit "data.frame" S3 methods; e.g., for `[`

## IGNORE_RDIFF_BEGIN
mydf1[1:2, ]  # a data frame object (with extra attributes)
## IGNORE_RDIFF_END

## a method explicitly for "myFrame" class

setMethod("[",
signature(x = "myFrame"),
function (x, i, j, ..., drop = TRUE)
{
  S3Part(x) <- callNextMethod()
x@timestamps <- c(Sys.time(), as.POSIXct(x@timestamps))
  x
}
)

## IGNORE_RDIFF_BEGIN
mydf1[1:2, ]
## IGNORE_RDIFF_END

setClass("myDateTime", contains = "POSIXt")

now <- Sys.time() # class(now) is c("POSIXct", "POSIXt")
nowLt <- as.POSIXlt(now) # class(nowLt) is c("POSIXlt", "POSIXt")

mCt <- new("myDateTime", now)
mLt <- new("myDateTime", nowLt)

## S3 methods for an S4 object will be selected using S4 inheritance
## Objects mCt and mLt have different S3Class() values, but this is
## not used.

f3 <- function(x)UseMethod("f3") # an S3 generic to illustrate inheritance

f3.POSIXct <- function(x) "The POSIXct result"
f3.POSIXlt <- function(x) "The POSIXlt result"
f3.POSIXt <- function(x) "The POSIXt result"

stopifnot(identical(f3(mCt), f3.POSIXt(mCt)))
stopifnot(identical(f3(mLt), f3.POSIXt(mLt)))

## An S4 object selects S3 methods according to its S4 "inheritance"
```
setClass("classA", contains = "numeric", slots = c(realData = "numeric"))

Math.classA <- function(x) { (getFunction(.Generic))(x@realData) }
setMethod("Math", "classA", Math.classA)

x <- new("classA", log(1:10), realData = 1:10)
stopifnot(identical(abs(x), 1:10))
setClass("classB", contains = "classA")

y <- new("classB", x)
stopifnot(identical(abs(y), abs(x))) # (version 2.9.0 or earlier fails here)

## an S3 generic: just for demonstration purposes
f3 <- function(x, ...) UseMethod("f3")
f3.default <- function(x, ...) "Default f3"

## S3 method (only) for classA
f3.classA <- function(x, ...) "Class classA for f3"

## S3 and S4 method for numeric
f3.numeric <- function(x, ...) "Class numeric for f3"
setMethod("f3", "numeric", f3.numeric)

## The S3 method for classA and the closest inherited S3 method for classB
## are not found.

f3(x); f3(y) # both choose "numeric" method

## to obtain the natural inheritance, set identical S3 and S4 methods
setMethod("f3", "classA", f3.classA)

f3(x); f3(y) # now both choose "classA" method

## Need to define an S3 as well as S4 method to use on an S3 object
## or called from a package without the S4 generic

MathFun <- function(x) { # a smarter "data.frame" method for Math group
  for (i in seq_len(ncol(x))[sapply(x, is.numeric)])
    x[, i] <- (getFunction(.Generic))(x[, i])
  x
}
setMethod("Math", "data.frame", MathFun)

## S4 method works for an S4 class containing data.frame,
## but not for data.frame objects (not S4 objects)

try(logIris <- log(iris)) # gets an error from the old method

## Define an S3 method with the same computation
Math.data.frame <- MathFun

logIris <- log(iris)

Description

The S3 and S4 software in R are two generations implementing functional object-oriented programming. S3 is the original, simpler for initial programming but less general, less formal and less open to validation. The S4 formal methods and classes provide these features but require more programming.

In modern R, the two versions attempt to work together. This documentation outlines how to write methods for both systems by defining an S4 method for a function that dispatches S3 methods.

The systems can also be combined by using an S3 class with S4 method dispatch or in S4 class definitions. See setOldClass.

S3 Method Dispatch

The R evaluator will ‘dispatch’ a method from a function call either when the body of the function calls the special primitive UseMethod or when the call is to one of the builtin primitives such as the math functions or the binary operators.

S3 method dispatch looks at the class of the first argument or the class of either argument in a call to one of the primitive binary operators. In pure S3 situations, ‘class’ in this context means the class attribute or the implied class for a basic data type such as "numeric". The first S3 method that matches a name in the class is called and the value of that call is the value of the original function call. For details, see S3Methods.

In modern R, a function meth in a package is registered as an S3 method for function fun and class Class by including in the package’s NAMESPACE file the directive

S3method(fun, Class, meth)

By default (and traditionally), the third argument is taken to be the function fun.Class; that is, the name of the generic function, followed by ".", followed by the name of the class.

As with S4 methods, a method that has been registered will be added to a table of methods for this function when the corresponding package is loaded into the session. Older versions of R, copying the mechanism in S, looked for the method in the current search list, but packages should now always register S3 methods rather than requiring the package to be attached.

Methods for S4 Classes

Two possible mechanisms for implementing a method corresponding to an S4 class, there are two possibilities are to register it as an S3 method with the S4 class name or to define and set an S4 method, which will have the side effect of creating an S4 generic version of this function.
Methods_for_S3

For most situations either works, but the recommended approach is to do both: register the S3 method and supply the identical function as the definition of the S4 method. This ensures that the proposed method will be dispatched for any applicable call to the function.

As an example, suppose an S4 class "uncased" is defined, extending "character" and intending to ignore upper- and lower-case. The base function `unique` dispatches S3 methods. To define the class and a method for this function:

```r
setClass("uncased", contains = "character")
unique.uncased <- function(x, incomparables = FALSE, ...) nextMethod(tolower(x))
setMethod("unique", "uncased", unique.uncased)
```

In addition, the `NAMESPACE` for the package should contain:

```r
S3method(unique, uncased)
exportMethods(unique)
```

The result is to define identical S3 and S4 methods and ensure that all calls to `unique` will dispatch that method when appropriate.

Details

The reasons for defining both S3 and S4 methods are as follows:

1. An S4 method alone will not be seen if the S3 generic function is called directly. This will be the case, for example, if some function calls `unique()` from a package that does not make that function an S4 generic.

   However, primitive functions and operators are exceptions: The internal C code will look for S4 methods if and only if the object is an S4 object. S4 method dispatch would be used to dispatch any binary operator calls where either of the operands was an S4 object, for example.

2. An S3 method alone will not be called if there is any eligible non-default S4 method.

   So if a package defined an S3 method for `unique` for an S4 class but another package defined an S4 method for a superclass of that class, the superclass method would be chosen, probably not what was intended.

S4 and S3 method selection are designed to follow compatible rules of inheritance, as far as possible. S3 classes can be used for any S4 method selection, provided that the S3 classes have been registered by a call to `setOldClass`, with that call specifying the correct S3 inheritance pattern. S4 classes can be used for any S3 method selection; when an S4 object is detected, S3 method selection uses the contents of `extends(class(x))` as the equivalent of the S3 inheritance (the inheritance is cached after the first call).

For the details of S4 and S3 dispatch see `Methods_Details` and `S3Methods`.

References

MethodWithNext-class

Class MethodWithNext

Description

Class of method definitions set up for callNextMethod

Objects from the Class

Objects from this class are generated as a side-effect of calls to callNextMethod.

Slots

.Data: Object of class "function"; the actual function definition.

nextMethod: Object of class "PossibleMethod" the method to use in response to a callNextMethod() call.

excluded: Object of class "list"; one or more signatures excluded in finding the next method.

target: Object of class "signature", from class "MethodDefinition" defined: Object of class "signature", from class "MethodDefinition"

generic: Object of class "character"; the function for which the method was created.

Extends

Class "MethodDefinition", directly.
Class "function", from data part.
Class "PossibleMethod", by class "MethodDefinition".
Class "OptionalMethods", by class "MethodDefinition".

Methods

findNextMethod signature(method = "MethodWithNext"): used internally by method dispatch.

loadMethod signature(method = "MethodWithNext"): used internally by method dispatch.

show signature(object = "MethodWithNext")

See Also

callNextMethod, and class MethodDefinition.
new

Generate an Object from a Class

Description

A call to new returns a newly allocated object from the class identified by the first argument. This call in turn calls the method for the generic function initialize corresponding to the specified class, passing the ... arguments to this method. In the default method for initialize(), named arguments provide values for the corresponding slots and unnamed arguments must be objects from superclasses of this class.

A call to a generating function for a class (see setClass) will pass its ...arguments to a corresponding call to new().

Usage

new(Class, ...)
initialize(.Object, ...)

Arguments

Class either the name of a class, a character string, (the usual case) or the object describing the class (e.g., the value returned by getClass). Note that the character string passed from a generating function includes the package name as an attribute, avoiding ambiguity if two packages have identically named classes.

... arguments to specify properties of the new object, to be passed to initialize().

,Object An object: see the “Initialize Methods” section.

Initialize Methods

The generic function initialize is not called directly. A call to new begins by copying the prototype object from the class definition, and then calls initialize() with this object as the first argument, followed by the ...arguments.

The interpretation of the ... arguments in a call to a generator function or to new() can be specialized to particular classes, by defining an appropriate method for "initialize".

In the default method, unnamed arguments in the ... are interpreted as objects from a superclass, and named arguments are interpreted as objects to be assigned into the correspondingly named slots. Explicitly specified slots override inherited information for the same slot, regardless of the order in which the arguments appear.

The initialize methods do not have to have ... as their second argument (see the examples). Initialize methods are often written when the natural parameters describing the new object are not the names of the slots. If you do define such a method, you should include ... as a formal argument, and your method should pass such arguments along via callNextMethod. This helps the definition of future subclasses of your class. If these have additional slots and your method does not have this argument, it will be difficult for these slots to be included in an initializing call.

See initialize-methods for a discussion of some classes with existing methods.
Methods for initialize can be inherited only by simple inheritance, since it is a requirement that the method return an object from the target class. See the simpleInheritanceOnly argument to setGeneric and the discussion in setIS for the general concept.

Note that the basic vector classes, "numeric", etc. are implicitly defined, so one can use new for these classes. The ...arguments are interpreted as objects of this type and are concatenated into the resulting vector.

References


See Also

Classes_Details for details of class definitions, and setOldClass for the relation to S3 classes.

Examples

```r
## using the definition of class "track" from \link{setClass}

## a new object with two slots specified
t1 <- new("track", x = seq_along(ydata), y = ydata)

# a new object including an object from a superclass, plus a slot
t2 <- new("trackCurve", t1, smooth = ysmooth)

### define a method for initialize, to ensure that new objects have
### equal-length x and y slots. In this version, the slots must still be
### supplied by name.
setMethod("initialize", "track",
  function(.Object, ...) {
    .Object <- callNextMethod()
    if(length(.Object@x) != length(.Object@y))
      stop("specified x and y of different lengths")
    .Object
  })

### An alternative version that allows x and y to be supplied
### unnamed. A still more friendly version would make the default x
### a vector of the same length as y, and vice versa.
setMethod("initialize", "track",
  function(.Object, x = numeric(0), y = numeric(0), ...) {
    .Object <- callNextMethod(.Object, ...)
    if(length(x) != length(y))
      stop("specified x and y of different lengths")
    .Object@x <- x
    .Object@y <- y
    .Object
  })
```
nonStructure-class  A non-structure S4 Class for basic types

Description

S4 classes that are defined to extend one of the basic vector classes should contain the class `structure` if they behave like structures; that is, if they should retain their class behavior under math functions or operators, so long as their length is unchanged. On the other hand, if their class depends on the values in the object, not just its structure, then they should lose that class under any such transformations. In the latter case, they should be defined to contain `nonStructure`.

If neither of these strategies applies, the class likely needs some methods of its own for `Ops`, `Math`, and/or other generic functions. What is not usually a good idea is to allow such computations to drop down to the default, base code. This is inconsistent with most definitions of such classes.

Methods

Methods are defined for operators and math functions (groups `Ops`, `Math` and `Math2`). In all cases the result is an ordinary vector of the appropriate type.

References


See Also

`structure`

Examples

setClass("NumericNotStructure", contains = c("numeric","nonStructure"))
xx <- new("NumericNotStructure", 1:10)
xx + 1 # vector
log(xx) # vector
sample(xx) # vector

ObjectsWithPackage-class

A Vector of Object Names, with associated Package Names

Description

This class of objects is used to represent ordinary character string object names, extended with a package slot naming the package associated with each object.

Objects from the Class

The function `getGenerics` returns an object of this class.
**promptClass**

Slots

.Data: Object of class "character": the object names.
package: Object of class "character" the package names.

Extends

Class "character", from data part.
Class "vector", by class "character".

See Also

Methods for general background.

---

**promptClass**  
*Generate a Shell for Documentation of a Formal Class*

**Description**

Assembles all relevant slot and method information for a class, with minimal markup for Rd processing; no QC facilities at present.

**Usage**

promptClass(clName, filename = NULL, type = "class", keywords = "classes", where = topenv(parent.frame())),  
generatorName = clName)

**Arguments**

clName  
a character string naming the class to be documented.

filename  
usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is the topic name for the class documentation, followed by ".Rd". Can also be NA (see below).

type  
the documentation type to be declared in the output file.

keywords  
the keywords to include in the shell of the documentation. The keyword "classes" should be one of them.

where  
where to look for the definition of the class and of methods that use it.

generatorName  
the name for a generator function for this class; only required if a generator function was created and saved under a name different from the class name.

**Details**

The class definition is found on the search list. Using that definition, information about classes extended and slots is determined.

In addition, the currently available generics with methods for this class are found (using getGenerics). Note that these methods need not be in the same environment as the class definition; in particular, this part of the output may depend on which packages are currently in the search list.
As with other prompt-style functions, unless `filename` is NA, the documentation shell is written to a file, and a message about this is given. The file will need editing to give information about the meaning of the class. The output of `promptClass` can only contain information from the metadata about the formal definition and how it is used.

If `filename` is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n"), where `x` is the list-style representation.

If a generator function is found assigned under the class name or the optional `generatorName`, skeleton documentation for that function is added to the file.

**Value**

If `filename` is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

**Author(s)**

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**References**


Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

**See Also**

`prompt` for documentation of functions, `promptMethods` for documentation of method definitions.

For processing of the edited documentation, either use R CMD `Rdconv`, or include the edited file in the ‘man’ subdirectory of a package.

**Examples**

```r
## Not run: > promptClass("track")
A shell of class documentation has been written to the
file "track-class.Rd".

## End(Not run)
```
Arguments

- **f**: a character string naming the generic function whose methods are to be documented.
- **filename**: usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to the coded topic name for these methods (currently, f followed by "-methods.Rd"). Can also be FALSE or NA (see below).
- **methods**: optional "listOfMethods" object giving the methods to be documented. By default, the first methods object for this generic is used (for example, if the current global environment has some methods for f, these would be documented). If this argument is supplied, it is likely to be findMethods(f, where), with where some package containing methods for f.

Details

If filename is FALSE, the text created is returned, presumably to be inserted some other documentation file, such as the documentation of the generic function itself (see prompt).

If filename is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to cat(unlist(x), file = filename, sep = "\n"), where x is the list-style representation.

Otherwise, the documentation shell is written to the file specified by filename.

Value

If filename is FALSE, the text generated; if filename is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

References


Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

See Also

prompt and promptClass

ReferenceClasses

Objects With Fields Treated by Reference (OOP-style)

Description

The software described here allows packages to define reference classes that behave in the style of “OOP” languages such as Java and C++. This model for OOP differs from the functional model implemented by S4 (and S3) classes and methods, in which methods are defined for generic functions. Methods for reference classes are “encapsulated” in the class definition.

Computations with objects from reference classes invoke methods on them and extract or set their fields, using the `$` operator in R. The field and method computations potentially modify the
object. All computations referring to the objects see the modifications, in contrast to the usual
functional programming model in R.

A call to `setRefClass` in the source code for a package defines the class and returns a generator
object. Subsequent calls to the `$methods()` method of the generator will define methods for the
class. As with functional classes, if the class is exported from the package, it will be available when
the package is loaded.

Methods are R functions. In their usual implementation, they refer to fields and other methods of
the class directly by name. See the section on “Writing Reference Methods”.

As with functional classes, reference classes can inherit from other reference classes via a
`contains=` argument to `setRefClass`. Fields and methods will be inherited, except where the
new class overrides method definitions. See the section on “Inheritance”.

Usage

```r
setRefClass(Class, fields = , contains = , methods =,
            where = , inheritPackage = , ...)
```

```r
getRefClass(Class, where =)
```

Arguments

- **Class** character string name for the class.
  In the call to `getRefClass()` this argument can also be any object from the
  relevant class.
- **fields** either a character vector of field names or a named list of the fields. The resulting
  fields will be accessed with reference semantics (see the section on “Reference
  Objects”). If the argument is a list, each element of the list should usually be
  the character string name of a class, in which case the object in the field must be
  from that class or a subclass. An alternative, but not generally recommended, is
to supply an accessor function; see the section on “Implementation” for accessor
functions and the related internal mechanism.
  Note that fields are distinct from slots. Reference classes should not define class-
specific slots. See the note on slots in the “Implementation” section.
- **contains** optional vector of superclasses for this class. If a superclass is also a reference
  class, the fields and class-based methods will be inherited.
- **methods** a named list of function definitions that can be invoked on objects from this class.
  These can also be created by invoking the `$methods` method on the generator
  object returned. See the section on “Writing Reference Methods” for details.
- **where** for `setRefClass`, the environment in which to store the class definition. Should
  be omitted in calls from a package’s source code.
  For `getRefClass`, the environment from which to search for the definition. If
  the package is not loaded or you need to be specific, use `asNamespace` with the
  package name.
- **inheritPackage** Should objects from the new class inherit the package environment of a con-
tained superclass? Default FALSE. See the Section “Inter-Package Superclasses
  and External Methods”.
- **...** other arguments to be passed to `setClass`.
Value

`setRefClass()` returns a generator function suitable for creating objects from the class, invisibly. A call to this function takes any number of arguments, which will be passed on to the `initialize` method. If no `initialize` method is defined for the class or one of its superclasses, the default method expects named arguments with the name of one of the fields and unnamed arguments, if any, that are objects from one of the superclasses of this class (but only superclasses that are themselves reference classes have any effect).

The generator function is similar to the S4 generator function returned by `setClass`. In addition to being a generator function, however, it is also a reference class generator object, with reference class methods for various utilities. See the section on reference class generator objects below.

`getRefClass()` also returns the generator function for the class. Note that the package slot in the value is the correct package from the class definition, regardless of the `where` argument, which is used only to find the class if necessary.

Reference Objects

Normal objects in R are passed as arguments in function calls consistently with functional programming semantics; that is, changes made to an object passed as an argument are local to the function call. The object that supplied the argument is unchanged.

The functional model (sometimes called pass-by-value, although this is inaccurate for R) is suitable for many statistical computations and is implicit, for example, in the basic R software for fitting statistical models. In some other situations, one would like all the code dealing with an object to see the exact same content, so that changes made in any computation would be reflected everywhere. This is often suitable if the object has some “objective” reality, such as a window in a user interface.

In addition, commonly used languages, including Java, C++ and many others, support a version of classes and methods assuming reference semantics. The corresponding programming mechanism is to invoke a method on an object. In the R syntax we use "$" for this operation; one invokes a method, `m1` say, on an object `x` by the expression `x$m1(...)`. Methods in this paradigm are associated with the object, or more precisely with the class of the object, as opposed to methods in a function-based class/method system, which are fundamentally associated with the function (in R, for example, a generic function in an R session has a table of all its currently known methods). In this document “methods for a class” as opposed to “methods for a function” will make the distinction.

Objects in this paradigm usually have named fields on which the methods operate. In the R implementation, the fields are defined when the class is created. The field itself can optionally have a specified class, meaning that only objects from this class or one of its subclasses can be assigned to the field. By default, fields have class "ANY".

Fields are accessed by reference. In particular, invoking a method may modify the content of the fields.

Programming for such classes involves writing new methods for a particular class. In the R implementation, these methods are R functions, with zero or more formal arguments. For standard reference methods, the object itself is not an explicit argument to the method. Instead, fields and methods for the class can be referred to by name in the method definition. The implementation uses R environments to make fields and other methods available by name within the method. Specifically, the parent environment of the method is the object itself. See the section on “Writing Reference Methods”. This special use of environments is optional. If a method is defined with an initial formal argument `.self`, that will be passed in as the whole object, and the method follows the standard rules for any function in a package. See the section on “External Methods”
The goal of the software described here is to provide a uniform programming style in \texttt{R} for software dealing with reference classes, whether implemented directly in \texttt{R} or through an interface to one of the OOP languages.

**Writing Reference Methods**

Reference methods are functions supplied as elements of a named list, either when invoking \texttt{$methods()} on a generator object \texttt{g} or as the argument \texttt{methods} in a call to \texttt{setRefClass}. The two mechanisms have the same effect, but the first makes the code more readable.

Methods are written as ordinary \texttt{R} functions but have some special features and restrictions in their usual form. In contrast to some other languages (e.g., Python), the object itself does not need to be an argument in the method definition. The body of the function can contain calls to any other reference method, including those inherited from other reference classes and may refer to methods and to fields in the object by name.

Alternatively, a method may be an \textit{external} method. This is signalled by \texttt{.self} being the first formal argument to the method. The body of the method then works like any ordinary function. The methods are called like other methods (without the \texttt{.self} argument, which is supplied internally and always refers to the object itself). Inside the method, fields and other methods are accessed in the form \texttt{.self$\mathit{x}}. External methods exist so that reference classes can inherit the package environment of superclasses in other packages; see the section on “External Methods”.

Fields may be modified in a method by using the non-local assignment operator, \texttt{<<-}, as in the \texttt{$edit} and \texttt{$undo} methods in the example below. Note that non-local assignment is required: a local assignment with the \texttt{<-} operator just creates a local object in the function call, as it would in any \texttt{R} function. When methods are installed, a heuristic check is made for local assignments to field names and a warning issued if any are detected.

Reference methods should be kept simple; if they need to do some specialized \texttt{R} computation, that computation should use a separate \texttt{R} function that is called from the reference method. Specifically, methods can not use special features of the enclosing environment mechanism, since the method’s environment is used to access fields and other methods. In particular, methods should not use non-exported entries in the package’s namespace, because the methods may be inherited by a reference class in another package.

Two method names are interpreted specially, \texttt{initialize} and \texttt{finalize}. If an \texttt{initialize} method is defined, it will be invoked when an object is generated from the class. See the discussion of method \texttt{$new(...)} in the section “Initialization Methods”.

If a \texttt{finalize} method is defined, a function will be \texttt{registered} to invoke it before the environment in the object is discarded by the garbage collector; finalizers are registered with \texttt{atexit=TRUE}, and so are also run at the end of \texttt{R} sessions. See the matrix viewer example for both \texttt{initialize} and \texttt{finalize} methods.

Reference methods can not themselves be generic functions; if you want additional function-based method dispatch, write a separate generic function and call that from the method.

Two special object names are available. The entire object can be referred to in a method by the reserved name \texttt{.self}. The object \texttt{.refClassDef} contains the definition of the class of the object. These are accessed as fields but are read-only, with one exception. In principal, the \texttt{.self} field can be modified in the \texttt{$initialize} method, because the object is still being created at this stage. This is not recommended, as it can invalidate the object with respect to its class.

The methods available include methods inherited from superclasses, as discussed in the section “Inheritance”.

Only methods actually used will be included in the environment corresponding to an individual object. To declare that a method requires a particular other method, the first method should include a call to \texttt{$usingMethods()} with the name of the other method as an argument. Declaring the methods
this way is essential if the other method is used indirectly (e.g., via `sapply()` or `do.call()`). If it is called directly, code analysis will find it. Declaring the method is harmless in any case, however, and may aid readability of the source code.

Documentation for the methods can be obtained by the `$help` method for the generator object. Methods for classes are not documented in the Rd format used for R functions. Instead, the `$help` method prints the calling sequence of the method, followed by self-documentation from the method definition, in the style of Python. If the first element of the body of the method is a literal character string (possibly multi-line), that string is interpreted as documentation. See the method definitions in the example.

**Initialization Methods**

If the class has a method defined for `$initialize()`, this method will be called once the reference object has been created. You should write such a method for a class that needs to do some special initialization. In particular, a reference method is recommended rather than a method for the S4 generic function `initialize()`, because some special initialization is required for reference objects before the initialization of fields. As with S4 classes, methods are written for `$initialize()` and not for `$new()`, both for the previous reason and also because `$new()` is invoked on the generator object and would be a method for that class.

The default method for `$initialize()` is equivalent to invoking the method `$initFields(...)`. Named arguments assign initial values to the corresponding fields. Unnamed arguments must be objects from this class or a reference superclass of this class. Fields will be initialized to the contents of the fields in such objects, but named arguments override the corresponding inherited fields. Note that fields are simply assigned. If the field is itself a reference object, that object is not copied. The new and previous object will share the reference. Also, a field assigned from an unnamed argument counts as an assignment for locked fields. To override an inherited value for a locked field, the new value must be one of the named arguments in the initializing call. A later assignment of the field will result in an error.

Initialization methods need some care in design. The generator for a reference class will be called with no arguments, for example when copying the object. To ensure that these calls do not fail, the method must have defaults for all arguments or check for `missing()`. The method should include `...` as an argument and pass this on via `$callSuper()` (or `$initFields()` if you know that your superclasses have no initialization methods). This allows future class definitions that subclass this class, with additional fields.

**Inheritance**

Reference classes inherit from other reference classes by using the standard R inheritance; that is, by including the superclasses in the `contains=` argument when creating the new class. The names of the reference superclasses are in slot `refSuperClasses` of the class definition. Reference classes can inherit from ordinary S4 classes also, but this is usually a bad idea if it mixes reference fields and non-reference slots. See the comments in the section on “Implementation”.

Class fields are inherited. A class definition can override a field of the same name in a superclass only if the overriding class is a subclass of the class of the inherited field. This ensures that a valid object in the field remains valid for the superclass as well.

Inherited methods are installed in the same way as directly specified methods. The code in a method can refer to inherited methods in the same way as directly specified methods.

A method may override a method of the same name in a superclass. The overriding method can call the superclass method by `$callSuper(...)` as described below.
Methods Provided for all Objects

All reference classes inherit from the class "envRefClass". All reference objects can use the following methods.

$callSuper(...) Calls the method inherited from a reference superclass. The call is meaningful only from within another method, and will be resolved to call the inherited method of the same name. The arguments to $callSuper are passed to the superclass version. See the matrix viewer class in the example.

Note that the intended arguments for the superclass method must be supplied explicitly; there is no convention for supplying the arguments automatically, in contrast to the similar mechanism for functional methods.

$copy(shallow = FALSE) Creates a copy of the object. With reference classes, unlike ordinary R objects, merely assigning the object with a different name does not create an independent copy. If shallow is FALSE, any field that is itself a reference object will also be copied, and similarly recursively for its fields. Otherwise, while reassigning a field to a new reference object will have no side effect, modifying such a field will still be reflected in both copies of the object. The argument has no effect on non-reference objects in fields. When there are reference objects in some fields but it is asserted that they will not be modified, using shallow = TRUE will save some memory and time.

$field(name, value) With one argument, returns the field of the object with character string name. With two arguments, the corresponding field is assigned value. Assignment checks that name specifies a valid field, but the single-argument version will attempt to get anything of that name from the object's environment.

The $field() method replaces the direct use of a field name, when the name of the field must be calculated, or for looping over several fields.

lexport(Class) Returns the result of coercing the object to Class (typically one of the superclasses of the object’s class). Calling the method has no side effect on the object itself.

$getRefClass(); $getClass() These return respectively the generator object and the formal class definition for the reference class of this object, efficiently.

import(value, Class = class(value)) Import the object value into the current object, replacing the corresponding fields in the current object. Object value must come from one of the superclasses of the current object’s class. If argument Class is supplied, value is first coerced to that class.

$initFields(...) Initialize the fields of the object from the supplied arguments. This method is usually only called from a class with a $initialize() method. It corresponds to the default initialization for reference classes. If there are slots and non-reference superclasses, these may be supplied in the ... argument as well.

Typically, a specialized $initialize() method carries out its own computations, then invokes $initFields() to perform standard initialization, as shown in the matrixViewer class in the example below.

$show() This method is called when the object is printed automatically, analogously to the show function. A general method is defined for class "envRefClass". User-defined reference classes will often define their own method: see the Example below.

Note two points in the example. As with any show() method, it is a good idea to print the class explicitly to allow for subclasses using the method. Second, to call the function show() from the method, as opposed to the $show() method itself, refer to methods::show() explicitly.

$trace(what, ...), $untrace(what) Apply the tracing and debugging facilities of the trace function to the reference method what.
All the arguments of the `trace` function can be supplied, except for `signature`, which is not meaningful.

The reference method can be invoked on either an object or the generator for the class. See the section on Debugging below for details.

$usingMethods(...) Reference methods used by this method are named as the arguments either quoted or unquoted. In the code analysis phase of installing the present method, the declared methods will be included. It is essential to declare any methods used in a nonstandard way (e.g., via an apply function). Methods called directly do not need to be declared, but it is harmless to do so. $usingMethods() does nothing at run time.

Objects also inherit two reserved fields:

`.self` a reference to the entire object;
`refClassDef` the class definition.

The defined fields should not override these, and in general it is unwise to define a field whose name begins with ".", since the implementation may use such names for special purposes.

**External Methods; Inter-Package Superclasses**

The environment of a method in a reference class is the object itself, as an environment. This allows the method to refer directly to fields and other methods, without using the whole object and the "$" operator. The parent of that environment is the namespace of the package in which the reference class is defined. Computations in the method have access to all the objects in the package’s namespace, exported or not.

When defining a class that contains a reference superclass in another package, there is an ambiguity about which package namespace should have that role. The argument `inheritPackage` to `setRefClass()` controls whether the environment of new objects should inherit from an inherited class in another package or continue to inherit from the current package’s namespace.

If the superclass is “lean”, with few methods, or exists primarily to support a family of subclasses, then it may be better to continue to use the new package’s environment. On the other hand, if the superclass was originally written as a standalone, this choice may invalidate existing superclass methods. For the superclass methods to continue to work, they must use only exported functions in their package and the new package must import these.

Either way, some methods may need to be written that do not assume the standard model for reference class methods, but behave essentially as ordinary functions would in dealing with reference class objects.

The mechanism is to recognize external methods. An external method is written as a function in which the first argument, named `.self`, stands for the reference class object. This function is supplied as the definition for a reference class method. The method will be called, automatically, with the first argument being the current object and the other arguments, if any, passed along from the actual call.

Since an external method is an ordinary function in the source code for its package, it has access to all the objects in the namespace. Fields and methods in the reference class must be referred to in the form `.self$name`.

If for some reason you do not want to use `.self` as the first argument, a function f() can be converted explicitly as `externalRefMethod(f)`, which returns an object of class "externalRefMethod" that can be supplied as a method for the class. The first argument will still correspond to the whole object.

External methods can be supplied for any reference class, but there is no obvious advantage unless they are needed. They are more work to write, harder to read and (slightly) slower to execute.
NOTE: If you are the author of a package whose reference classes are likely to be subclassed in other packages, you can avoid these questions entirely by writing methods that only use exported functions from your package, so that all the methods will work from another package that imports yours.

Reference Class Generators

The call to `setRefClass` defines the specified class and returns a "generator function" object for that class. This object has class "refObjectGenerator"; it inherits from "function" via "classGeneratorFunction" and can be called to generate new objects from the reference class.

The returned object is also a reference class object, although not of the standard construction. It can be used to invoke reference methods and access fields in the usual way, but instead of being implemented directly as an environment it has a subsidiary generator object as a slot, a standard reference object (of class "refGeneratorSlot"). Note that if one wanted to extend the reference class generator capability with a subclass, this should be done by subclassing "refGeneratorSlot", not "refObjectGenerator".

The fields are def, the class definition, and className, the character string name of the class. Methods generate objects from the class, to access help on reference methods, and to define new reference methods for the class. The currently available methods are:

$new(...) This method is equivalent to calling the generator function returned by `setRefClass`.

$help(topic) Prints brief help on the topic. The topics recognized are reference method names, quoted or not.

The information printed is the calling sequence for the method, plus self-documentation if any. Reference methods can have an initial character string or vector as the first element in the body of the function defining the method. If so, this string is taken as self-documentation for the method (see the section on “Writing Reference Methods” for details).

If no topic is given or if the topic is not a method name, the definition of the class is printed.

$methods(...) With no arguments, returns the names of the reference methods for this class. With one character string argument, returns the method of that name.

Named arguments are method definitions, which will be installed in the class, as if they had been supplied in the methods argument to `setRefClass()`. Supplying methods in this way, rather than in the call to `setRefClass()`, is recommended for the sake of clearer source code. See the section on “Writing Reference Methods” for details.

All methods for a class should be defined in the source code that defines the class, typically as part of a package. In particular, methods can not be redefined in a class in an attached package with a namespace: The class method checks for a locked binding of the class definition.

The new methods can refer to any currently defined method by name (including other methods supplied in this call to $methods()). Note though that previously defined methods are not re-analyzed meaning that they will not call the new method (unless it redefines an existing method of the same name).

To remove a method, supply NULL as its new definition.

$fields() Returns a list of the fields, each with its corresponding class. Fields for which an accessor function was supplied in the definition have class "activeBindingFunction".

$lock(...) The fields named in the arguments are locked; specifically, after the lock method is called, the field may be set once. Any further attempt to set it will generate an error.

If called with no arguments, the method returns the names of the locked fields. Fields that are defined by an explicit accessor function can not be locked (on the other hand, the accessor function can be defined to generate an error if called with an argument).
All code to lock fields should normally be part of the definition of a class; that is, the read-only nature of the fields is meant to be part of the class definition, not a dynamic property added later. In particular, fields can not be locked in a class in an attached package with a namespace: The class method checks for a locked binding of the class definition. Locked fields can not be subsequently unlocked.

$\text{trace}(\text{what}, \ldots, \text{classMethod} = \text{FALSE})$ Establish a traced version of method $\text{what}$ for objects generated from this class. The generator object tracing works like the $\text{\$trace()}$ method for objects from the class, with two differences. Since it changes the method definition in the class object itself, tracing applies to all objects, not just the one on which the trace method is invoked.

Second, the optional argument $\text{classMethod} = \text{TRUE}$ allows tracing on the methods of the generator object itself. By default, what is interpreted as the name of a method in the class for which this object is the generator.

$\text{\$accessors}(\ldots)$ A number of systems using the OOP programming paradigm recommend or enforce getter and setter methods corresponding to each field, rather than direct access by name. If you like this style and want to extract a field named abc by $\text{x\$getAbc()}$ and assign it by $\text{x\$setAbc(value)}$, the $\text{\$accessors}$ method is a convenience function that creates such getter and setter methods for the specified fields. Otherwise there is no reason to use this mechanism. In particular, it has nothing to do with the general ability to define fields by functions as described in the section on “Reference Objects”.

**Implementation; Reference Classes as S4 Classes**

Reference classes are implemented as S4 classes with a data part of type "environment". Fields correspond to named objects in the environment. A field associated with a function is implemented as an active binding. In particular, fields with a specified class are implemented as a special form of active binding to enforce valid assignment to the field.

As a related feature, the element in the $\text{fields= list}$ supplied to $\text{setRefClass}$ can be an accessor function, a function of one argument that returns the field if called with no argument or sets it to the value of the argument otherwise. Accessor functions are used internally and for inter-system interface applications, but not generally recommended as they blur the concept of fields as data within the object.

A field, say $\text{data}$, can be accessed generally by an expression of the form $\text{x$\$data}$ for any object from the relevant class. In an internal method for this class, the field can be accessed by the name $\text{data}$. A field that is not locked can be set by an expression of the form $\text{x$\$data <- value}$ Inside an internal method, a field can be assigned by an expression of the form $\text{x <- value}$. Note the non-local assignment operator. The standard $\text{R}$ interpretation of this operator works to assign it in the environment of the object. If the field has an accessor function defined, getting and setting will call that function.

When a method is invoked on an object, the function defining the method is installed in the object’s environment, with the same environment as the environment of the function.

Reference classes can have validity methods in the same sense as any S4 class (see $\text{setValidity}$). Such methods are often a good idea; they will be called by calling $\text{validObject}$ and a validity method, if one is defined, will be called when a reference object is created (from version 3.4 of $\text{R}$ on). Just remember that these are S4 methods. The function will be called with the object as its argument. Fields and methods must be accessed using $\$. 

**Note:** Slots. Because of the implementation, new reference classes can inherit from non-reference S4 classes as well as reference classes, and can include class-specific slots in the definition. This is usually a bad idea, if the slots from the non-reference class are thought of as alternatives to fields. Slots will as always be treated functionally. Therefore, changes to the slots and the fields
will behave inconsistently, mixing the functional and reference paradigms for properties of the same object, conceptually unclear and prone to errors. In addition, the initialization method for the class will have to sort out fields from slots, with a good chance of creating anomalous behavior for subclasses of this class.

Inheriting from a class union, however, is a reasonable strategy (with all members of the union likely to be reference classes).

Debugging

The standard R debugging and tracing facilities can be applied to reference methods. Reference methods can be passed to `debug` and its relatives from an object to debug further method invocations on that object; for example, `debug(xx$edit)`.

Somewhat more flexible use is available for a reference method version of the `trace` function. A corresponding `$trace()` reference method is available for either an object or for the reference class generator (`xx$trace()` or `mEdit$trace()` in the example below). Using `$trace()` on an object sets up a tracing version for future invocations of the specified method for that object. Using `$trace()` on the generator for the class sets up a tracing version for all future objects from that class (and sometimes for existing objects from the class if the method is not declared or previously invoked).

In either case, all the arguments to the standard `trace` function are available, except for `signature=` which is meaningless since reference methods can not be S4 generic functions. This includes the typical style `trace(what, browser)` for interactive debugging and `trace(what, edit = TRUE)` to edit the reference method interactively.

References


Examples

```r
## a simple editor for matrix objects. Method $edit() changes some
## range of values; method $undo() undoes the last edit.
mEdit <- setRefClass("mEdit",
   fields = list( data = "matrix",
                  edits = "list"))

## The basic edit, undo methods
mEdit$methods{
   edit = function(i, j, value) {
      ## the following string documents the edit method
      #'Replaces the range [i, j] of the
      #object by value.
      backup <-
      list(i, j, data[i,j])
      data[i,j] <<- value
      edits <<- c(edits, list(backup))
      invisible(value)
   },
   undo = function() {
      #'Undoes the last edit() operation
      and update the edits field accordingly.
      prev <- edits
```
if(length(prev)) prev <- prev[[length(prev)]]
else stop("No more edits to undo")
edit(prev[[1]], prev[[2]], prev[[3]])
## trim the edits list
length(edits) <<- length(edits) - 2
invisible(prev)
})

## A method to automatically print objects
mEdit$methods(
  show = function() {
    'Method for automatically printing matrix editors'
    cat("Reference matrix editor object of class",
    classLabel(class(.self)), "\n")
    cat("Data: \n")
    methods::show(data)
    cat("Undo list is of length", length(edits), "\n")
  }
)

xMat <- matrix(1:12,4,3)
xx <- mEdit(data = xMat)
xx$edit(2, 2, 0)
xx
xx$undo()
mEdit$help("undo")
stopifnot(all.equal(xx$data, xMat))

utils::str(xx) # show fields and names of methods

## A method to save the object
mEdit$methods(
  save = function(file) {
    'Save the current object on the file
    in R external object format.'
    base::save(.self, file = file)
  }
)

tf <- tempfile()
xx$save(tf)

## Not run:
## Inheriting a reference class: a matrix viewer
mv <- setRefClass("matrixViewer",
  fields = c("viewerDevice", "viewerFile"),
  contains = "mEdit",
  methods = list( view = function() {
    dd <- dev.cur(); dev.set(viewerDevice)
deAskNewPage(FALSE)
    matplot(data, main = paste("After",length(edits),"edits"))
    dev.set(dd),
    edit = # invoke previous method, then replot
    function(i, j, value) {
      callSuper(i, j, value)
removeMethod

Remove a Method

Description

Remove the method for a given function and signature. Obsolete for ordinary applications: Method definitions in a package should never need to remove methods and it’s very bad practice to remove methods that were defined in other packages.

Usage

removeMethod(f, signature, where)

Arguments

f, signature, where

As for setMethod().

Value

TRUE if a method was found to be removed.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)
representation

Construct a Representation or a Prototype for a Class Definition

Description

These are old utility functions to construct, respectively a list designed to represent the slots and superclasses and a list of prototype specifications. The `representation()` function is no longer useful, since the arguments `slots` and `contains` to `setClass` are now recommended.

The `prototype()` function may still be used for the corresponding argument, but a simple list of the same arguments works as well.

Usage

```r
representation(...)
prototype(...)
```

Arguments

...  

The call to `representation` takes arguments that are single character strings.Unnamed arguments are classes that a newly defined class extends; named arguments name the explicit slots in the new class, and specify what class each slot should have.

In the call to `prototype`, if an unnamed argument is supplied, it unconditionally forms the basis for the prototype object. Remaining arguments are taken to correspond to slots of this object. It is an error to supply more than one unnamed argument.

Details

The `representation` function applies tests for the validity of the arguments. Each must specify the name of a class.

The classes named don’t have to exist when `representation` is called, but if they do, then the function will check for any duplicate slot names introduced by each of the inherited classes.

The arguments to `prototype` are usually named initial values for slots, plus an optional first argument that gives the object itself. The unnamed argument is typically useful if there is a data part to the definition (see the examples below).

Value

The value of `representation` is just the list of arguments, after these have been checked for validity.

The value of `prototype` is the object to be used as the prototype. Slots will have been set consistently with the arguments, but the construction does not use the class definition to test validity of the contents (it hardly can, since the prototype object is usually supplied to create the definition).

References


Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)
S3Part

See Also

setClass

Examples

## representation for a new class with a directly define slot "smooth"
## which should be a "numeric" object, and extending class "track"
representation("track", smooth = "numeric")

### >>> This *is* old syntax -- use 'contains=*, slots=*' instead <<<
### ========== ---------- ------ ======

setClass("Character", representation("character"))
setClass("TypedCharacter", representation("Character", type = "character"),
prototype(character(0), type = "plain"))

###

setClass("num1", representation(comment = "character"),
contains = "numeric",
prototype = prototype(pi, comment = "Start with pi"))

S3Part

S4 Classes that Contain S3 Classes

Description

A regular (S4) class may contain an S3 class, if that class has been registered (by calling setOldClass). The functions described here provide information about contained S3 classes. See the section ‘Functions’.

In modern R, these functions are not usually needed to program with objects from the S4 class. Standard computations work as expected, including method selection for both S4 and S3. To coerce an object to its contained S3 class, use either of the expressions:

as(object, S3Class); as(object, "S3")

where S3Class evaluates to the name of the contained class. These return slightly different objects, which in rare cases may need to be distinguished. See the section “Contained S3 Objects”.

Usage

S3Part(object, strictS3 = FALSE, S3Class)
S3Class(object)
isXS3Class(classDef)
slotsFromS3(object)
## the replacement versions of the functions are not recommended
## Create a new object from the class or use the replacement version of as().

S3Part(object, strictS3 = FALSE, needClass = ) <- value

S3Class(object) <- value

**Arguments**

- **object**: an object from some class that extends a registered S3 class, or a basic vector, matrix or array object type. For most of the functions, an S3 object can also be supplied, with the interpretation that it is its own S3 part.

- **strictS3**: If TRUE, the value returned by S3Part will be an S3 object, with all the S4 slots removed. Otherwise, an S4 object will always be returned; for example, from the S4 class created by setOldClass as a proxy for an S3 class, rather than the underlying S3 object.

- **S3Class**: the character vector to be stored as the S3 class slot in the object. Usually, and by default, retains the slot from object, but an S3 superclass is allowed.

- **classDef**: a class definition object, as returned by getClass.

The remaining arguments apply only to the replacement versions, which are not recommended.

- **needClass**: Require that the replacement value be this class or a subclass of it.

- **value**: For S3Part<-, the replacement value for the S3 part of the object. For S3Class<-, the character vector that will be used as a proxy for class(x) in S3 method dispatch.

**Functions**

- **S3Part**: Returns an object from the S3 class that appeared in the contains= argument to setClass. If called with strictS3 = TRUE, S3Part() constructs the underlying S3 object by eliminating all the formally defined slots and turning off the S4 bit of the object. With strictS3 = FALSE the object returned is from the corresponding S4 class. For consistency and generality, S3Part() works also for classes that extend the basic vector, matrix and array classes.

  A call to is equivalent coercing the object to class “S3” for the strict case, or to whatever the specific S3 class was, for the non-strict case. The as() calls are usually easier for readers to understand.

- **S3Class**: Returns the character vector of S3 class(es) stored in the object, if the class has the corresponding .S3Class slot. Currently, the function defaults to class otherwise.

- **isXS3Class**: Returns TRUE or FALSE according to whether the class defined by ClassDef extends S3 classes (specifically, whether it has the slot for holding the S3 class).

- **slotsFromS3**: returns a list of the relevant slot classes, or an empty list for any other object.

  The function slotsFromS3() is a generic function used internally to access the slots associated with the S3 part of the object. Methods for this function are created automatically when setOldClass is called with the S4Class argument. Usually, there is only one S3 slot, containing the S3 class, but the S4Class argument may provide additional slots, in the case that the S3 class has some guaranteed attributes that can be used as formal S4 slots. See the corresponding section in the documentation of setOldClass.
Contained S3 Objects

Registering an S3 class defines an S4 class. Objects from this class are essentially identical in content to an object from the S3 class, except for two differences. The value returned by `class()` will always be a single string for the S4 object, and `isS4()` will return TRUE or FALSE in the two cases. See the example below. It is barely possible that some S3 code will not work with the S4 object; if so, use `as(x, "S3")`.

Objects from a class that extends an S3 class will have some basic type and possibly some attributes. For an S3 class that has an equivalent S4 definition (e.g., "data.frame"), an extending S4 class will have a data part and slots. For other S3 classes (e.g., "lm") an object from the extending S4 class will be some sort of basic type, nearly always a vector type (e.g., "list" for "lm"), but the data part will not have a formal definition.

Registering an S3 class by a call to `setOldClass` creates a class of the same name with a slot ".S3Class" to hold the corresponding S3 vector of class strings. New S4 classes that extend such classes also have the same slot, set to the S3 class of the contained S3 object, which may be an (S3) subclass of the registered class. For example, an S4 class might contain the S3 class "lm", but an object from the class might contain an object from class "mlm", as in the "xlm"example below.

R is somewhat arbitrary about what it treats as an S3 class: "ts" is, but "matrix" and "array" are not. For classes that extend those, assuming they contain an S3 class is incorrect and will cause some confusion—not usually disastrous, but the better strategy is to stick to the explicit "class". Thus `as(x, "matrix")` rather than `as(x, "S3")` or `S3Part(x)`.

S3 and S4 Objects: Conversion Mechanisms

Objects in R have an internal bit that indicates whether or not to treat the object as coming from an S4 class. This bit is tested by `isS4` and can be set on or off by `asS4`. The latter function, however, does no checking or interpretation; you should only use it if you are very certain every detail has been handled correctly.

As a friendlier alternative, methods have been defined for coercing to the virtual classes "S3" and "S4". The expressions `as(object, "S3")` and `as(object, "S4")` return S3 and S4 objects, respectively. In addition, they attempt to do conversions in a valid way, and also check validity when coercing to S4.

The expression `as(object, "S3")` can be used in two ways. For objects from one of the registered S3 classes, the expression will ensure that the class attribute is the full multi-string S3 class implied by `class(object)`. If the registered class has known attribute/slots, these will also be provided.

As a friendlier alternative, methods have been defined for coercing to the virtual classes "S3" and "S4". The expressions `as(object, "S3")` and `as(object, "S4")` return S3 and S4 objects, respectively. In addition, they attempt to do conversions in a valid way, and also check validity when coercing to S4.

Another use of `as(object, "S3")` is to take an S4 object and turn it into an S3 object with corresponding attributes. This is only meaningful with S4 classes that have a data part. If you want to operate on the object without invoking S4 methods, this conversion is usually the safest way.

The expression `as(object, "S4")` will use the attributes in the object to create an object from the S4 definition of `class(object)`. This is a general mechanism to create partially defined version of S4 objects via S3 computations (not much different from invoking `new` with corresponding arguments, but usable in this form even if the S4 object has an initialize method with different arguments).

References

Chambers, John M. (2016) *Extending R*, Chapman & Hall. (Chapters 9 and 10, particularly Section 10.8)

See Also

`setOldClass`
Examples

## an "mlm" object, regressing two variables on two others

```r
sepal <- as.matrix(datasets::iris[, c("Sepal.Width", "Sepal.Length")])
fit <- lm(sepal ~ Petal.Length + Petal.Width + Species, data = datasets::iris)
class(fit) # S3 class: "mlm", "lm"
```

## a class that contains "mlm"

```r
myReg <- setClass("myReg", slots = c(title = "character"), contains = "mlm")
fit2 <- myReg(fit, title = "Sepal Regression for iris data")
```

fit2 # shows the inherited "mlm" object and the title

```r
identical(S3Part(fit2), as(fit2, "mlm"))
class(as(fit2, "mlm")) # the S4 class, "mlm"
class(as(fit2, "S3")) # the S3 class, c("mlm", "lm")
```

## An object may contain an S3 class from a subclass of that declared:

```r
xlm <- setClass("xlm", slots = c(eps = "numeric"), contains = "lm")
xfit <- xlm(fit, eps = .Machine$double.eps)
```

xfit@.S3Class # c("mlm", "lm")

---

**S4 Group Generic Functions**

Description

Methods can be defined for group generic functions. Each group generic function has a number of member generic functions associated with it.

Methods defined for a group generic function cause the same method to be defined for each member of the group, but a method explicitly defined for a member of the group takes precedence over a method defined, with the same signature, for the group generic.

The functions shown in this documentation page all reside in the methods package, but the mechanism is available to any programmer, by calling `setGroupGeneric` (provided package methods is attached).

Usage

```r
## S4 group generics:
Arith(e1, e2)
Compare(e1, e2)
Ops(e1, e2)
Logic(e1, e2)
Math(x)
Math2(x, digits)
```
Summary(x, ..., na.rm = FALSE)
Complex(z)

Arguments

- x, z, e1, e2: objects.
- digits: number of digits to be used in `round` or `signif`.
- ...: further arguments passed to or from methods.
- na.rm: logical: should missing values be removed?

Details

Methods can be defined for the group generic functions by calls to `setMethod` in the usual way. Note that the group generic functions should never be called directly – a suitable error message will result if they are. When metadata for a group generic is loaded, the methods defined become methods for the members of the group, but only if no method has been specified directly for the member function for the same signature. The effect is that group generic definitions are selected before inherited methods but after directly specified methods. For more on method selection, see Methods_Details.

There are also S3 groups Math, Ops, Summary and Complex, see ?S3groupGeneric, with no corresponding R objects, but these are irrelevant for S4 group generic functions.

The members of the group defined by a particular generic can be obtained by calling `getGroupMembers`. For the group generic functions currently defined in this package the members are as follows:

- **Arith**: `+`, `-`, `*`, `/`, `%%`, `%/%`, `^`
- **Compare**: `==`, `>`, `<`, `!=`, `<=`, `>=`
- **Logic**: `&`, `|`
- **Ops**: "Arith", "Compare", "Logic"
- **Math**: `abs`, `sign`, `sqrt`, `ceiling`, `floor`, `trunc`, `cummax`, `cummin`, `cumprod`, `cumsum`, `log`, `log10`, `log2`, `log1p`, `acos`, `acosh`, `asin`, `asinh`, `atan`, `atanh`, `exp`, `expm1`, `cos`, `cosh`, `cospi`, `sin`, `sinh`, `sinpi`, `tan`, `tanh`, `tanpi`, `gamma`, `lgamma`, `digamma`, `trigamma`
- **Math2**: "round", "signif"
- **Summary**: "max", "min", "range", "prod", "sum", "any", "all"
- **Complex**: "Arg", "Conj", "Im", "Mod", "Re"

Note that Ops merely consists of three sub groups.

All the functions in these groups (other than the group generics themselves) are basic functions in R. They are not by default S4 generic functions, and many of them are defined as primitives. However, you can still define formal methods for them, both individually and via the group generics. It all works more or less as you might expect, admittedly via a bit of trickery in the background. See Methods_Details for details.

Note that two members of the Math group, `log` and `trunc`, have ... as an extra formal argument. Since methods for Math will have only one formal argument, you must set a specific method for these functions in order to call them with the extra argument(s).

For further details about group generic functions see section 10.5 of the second reference.
SClassExtension-class

References


See Also

The function `callGeneric` is nearly always relevant when writing a method for a group generic. See the examples below and in section 10.5 of *Software for Data Analysis*.

See `S3groupGeneric` for S3 group generics.

Examples

```r
setClass("testComplex", slots = c(zz = "complex"))
## method for whole group "Complex"
setMethod("Complex", "testComplex",
          function(z) c("groupMethod", callGeneric(z@zz)))
## exception for Arg():
setMethod("Arg", "testComplex",
          function(z) c("ArgMethod", Arg(z@zz)))
z1 <- 1+2i
z2 <- new("testComplex", zz = z1)
stopifnot(identical(Mod(z2), c("groupMethod", Mod(z1))))
stopifnot(identical(Arg(z2), c("ArgMethod", Arg(z1))))
```

SClassExtension-class  
*Class to Represent Inheritance (Extension) Relations*

Description

An object from this class represents a single ‘is’ relationship; lists of these objects are used to represent all the extensions (superclasses) and subclasses for a given class. The object contains information about how the relation is defined and methods to coerce, test, and replace correspondingly.

Objects from the Class

Objects from this class are generated by `setIs`, from direct calls and from the `contains=` information in a call to `setClass`, and from class unions created by `setClassUnion`. In the last case, the information is stored in defining the subclasses of the union class (allowing unions to contain sealed classes).

Slots

- `subClass`, `superClass`: The classes being extended: corresponding to the `from`, and `to` arguments to `setIs`.
- `package`: The package to which that class belongs.
- `coerce`: A function to carry out the as() computation implied by the relation. Note that these functions should not be used directly. They only deal with the `strict=TRUE` calls to the `as` function, with the full method constructed from this mechanically.
test: The function that would test whether the relation holds. Except for explicitly specified test arguments to setIs, this function is trivial.

replace: The method used to implement as(x, Class) <- value.

simple: A "logical" flag, TRUE if this is a simple relation, either because one class is contained in the definition of another, or because a class has been explicitly stated to extend a virtual class. For simple extensions, the three methods are generated automatically.

by: If this relation has been constructed transitively, the first intermediate class from the subclass.

dataPart: A "logical" flag, TRUE if the extended class is in fact the data part of the subclass. In this case the extended class is a basic class (i.e., a type).

distance: The distance between the two classes, 1 for directly contained classes, plus the number of generations between otherwise.

Methods

No methods defined with class "SClassExtension" in the signature.

See Also

is, as, and the classRepresentation class.

selectSuperClasses Super Classes (of Specific Kinds) of a Class

Description

Return superclasses of ClassDef, possibly only non-virtual or direct or simple ones.

These functions are designed to be fast, and consequently only work with the contains slot of the corresponding class definitions.

Usage

```
selectSuperClasses(Class, dropVirtual = FALSE, namesOnly = TRUE, 
directOnly = TRUE, simpleOnly = directOnly, 
where = topenv(parent.frame()))

.selectSuperClasses(ext, dropVirtual = FALSE, namesOnly = TRUE, 
directOnly = TRUE, simpleOnly = directOnly)
```

Arguments

- **Class**
  - name of the class or (more efficiently) the class definition object (see getClass).
- **dropVirtual**
  - logical indicating if only non-virtual superclasses should be returned.
- **namesOnly**
  - logical indicating if only a vector names instead of a named list class-extensions should be returned.
- **directOnly**
  - logical indicating if only a direct super classes should be returned.
- **simpleOnly**
  - logical indicating if only simple class extensions should be returned.
- **where**
  - (only used when Class is not a class definition) environment where the class definition of Class is found.
- **ext**
  - for .selectSuperClasses() only, a list of class extensions, typically getClassDef(..)@contains.
setAs

Value

a character vector (if namesOnly is true, as per default) or a list of class extensions (as the contains slot in the result of getClass).

Note

The typical user level function is selectSuperClasses() which calls .selectSuperClasses(); i.e., the latter should only be used for efficiency reasons by experienced useRs.

See Also

is, getClass; further, the more technical class classRepresentation documentation.

Examples

setClass("Root")
setClass("Base", contains = "Root", slots = c(length = "integer"))
setClass("A", contains = "Base", slots = c(x = "numeric"))
setClass("B", contains = "Base", slots = c(y = "character"))
setClass("C", contains = c("A", "B"))

extends("C") #--> "C" "A" "B" "Base" "Root"
selectSuperClasses("C") # "A" "B"
selectSuperClasses("C", directOnly=FALSE) # "A" "B" "Base" "Root"
selectSuperClasses("C", dropVirtual=TRUE, directOnly=FALSE)# ditto w/o "Root"

Description

A call to setAs defines a method for coercing an object of class from to class to. The methods will then be used by calls to as for objects with class from, including calls that replace part of the object.

Methods for this purpose work indirectly, by defining methods for function coerce. The coerce function is not to be called directly, and method selection uses class inheritance only on the first argument.

Usage

setAs(from, to, def, replace, where = topenv(parent.frame()))

Arguments

from, to The classes between which the coerce methods def and replace perform coercion.
def function of one argument. It will get an object from class from and had better return an object of class to. The convention is that the name of the argument is from; if another argument name is used, setAs will attempt to substitute from.
replace if supplied, the function to use as a replacement method, when \texttt{as} is used on the left of an assignment. Should be a function of two arguments, from, value, although \texttt{setAs} will attempt to substitute if the arguments differ.

\textit{The remaining argument will not be used in standard applications.}

where the position or environment in which to store the resulting methods. Do not use this argument when defining a method in a package. Only the default, the namespace of the package, should be used in normal situations.

Inheritance and Coercion

Objects from one class can turn into objects from another class either automatically or by an explicit call to the \texttt{as} function. Automatic conversion is special, and comes from the designer of one class of objects asserting that this class extends another class. The most common case is that one or more class names are supplied in the \texttt{contains=} argument to \texttt{setClass}, in which case the new class extends each of the earlier classes (in the usual terminology, the earlier classes are superclasses of the new class and it is a subclass of each of them).

This form of inheritance is called \textit{simple} inheritance in R. See \texttt{setClass} for details. Inheritance can also be defined explicitly by a call to \texttt{setIs}. The two versions have slightly different implications for coerce methods. Simple inheritance implies that inherited slots behave identically in the subclass and the superclass. Whenever two classes are related by simple inheritance, corresponding coerce methods are defined for both direct and replacement use of \texttt{as}. In the case of simple inheritance, these methods do the obvious computation: they extract or replace the slots in the object that correspond to those in the superclass definition.

The implicitly defined coerce methods may be overridden by a call to \texttt{setAs}; note, however, that the implicit methods are defined for each subclass-superclass pair, so that you must override each of these explicitly, not rely on inheritance.

When inheritance is defined by a call to \texttt{setIs}, the coerce methods are provided explicitly, not generated automatically. Inheritance will apply (to the \texttt{from} argument, as described in the section below). You could also supply methods via \texttt{setAs} for non-inherited relationships, and now these also can be inherited.

For further on the distinction between simple and explicit inheritance, see \texttt{setIs}.

How Functions 'as' and 'setAs' Work

The function \texttt{as} turns object into an object of class \texttt{Class}. In doing so, it applies a “coerce method”, using S4 classes and methods, but in a somewhat special way. Coerce methods are methods for the function \texttt{coerce} or, in the replacement case the function \texttt{`coerce<-`}. These functions have two arguments in method signatures, \texttt{from} and \texttt{to}, corresponding to the class of the object and the desired coerce class. These functions must not be called directly, but are used to store tables of methods for the use of \texttt{as}, directly and for replacements. In this section we will describe the direct case, but except where noted the replacement case works the same way, using \texttt{`coerce<-`} and the \texttt{replace} argument to \texttt{setAs}, rather than \texttt{coerce} and the \texttt{def} argument.

Assuming the object is not already of the desired class, \texttt{as} first looks for a method in the table of methods for the function \texttt{coerce} for the signature \texttt{c(from = class(object), to = Class)}, in the same way method selection would do its initial lookup. To be precise, this means the table of both direct and inherited methods, but inheritance is used specially in this case (see below).

If no method is found, as looks for one. First, if either \texttt{Class} or \texttt{class(object)} is a superclass of the other, the class definition will contain the information needed to construct a coerce method. In the usual case that the subclass contains the superclass (i.e., has all its slots), the method is constructed either by extracting or replacing the inherited slots. Non-simple extensions (the result of a call to \texttt{setIs}) will usually contain explicit methods, though possibly not for replacement.
If no subclass/superclass relationship provides a method, `as` looks for an inherited method, but applying, inheritance for the argument from only, not for the argument to (if you think about it, you'll probably agree that you wouldn't want the result to be from some class other than the Class specified). Thus, `selectMethod("coerce", sig, useInherited=c(from=TRUE, to=FALSE))` replicates the method selection used by `as()`.

In nearly all cases the method found in this way will be cached in the table of coerce methods (the exception being subclass relationships with a test, which are legal but discouraged). So the detailed calculations should be done only on the first occurrence of a coerce from `class(object)` to `Class`.

Note that `coerce` is not a standard generic function. It is not intended to be called directly. To prevent accidentally caching an invalid inherited method, calls are routed to an equivalent call to `as`, and a warning is issued. Also, calls to `selectMethod` for this function may not represent the method that `as` will choose. You can only trust the result if the corresponding call to `as` has occurred previously in this session.

With this explanation as background, the function `setAs` does a fairly obvious computation: It constructs and sets a method for the function `coerce` with signature `c(from, to)`, using the `def` argument to define the body of the method. The function supplied as `def` can have one argument (interpreted as an object to be coerced) or two arguments (the `from` object and the `to` class). Either way, `setAs` constructs a function of two arguments, with the second defaulting to the name of the `to` class. The method will be called from `as` with the object as the `from` argument and no `to` argument, with the default for this argument being the name of the intended `to` class, so the method can use this information in messages.

The direct version of the `as` function also has a `strict=` argument that defaults to `TRUE`. Calls during the evaluation of methods for other functions will set this argument to `FALSE`. The distinction is relevant when the object being coerced is from a simple subclass of the `to` class; if `strict=False` in this case, nothing need be done. For most user-written coerce methods, when the two classes have no subclass/superclass, the `strict=` argument is irrelevant.

The `replace` argument to `setAs` provides a method for `"coerce<-"`. As with all replacement methods, the last argument of the method must have the name `value` for the object on the right of the assignment. As with the `coerce` method, the first two arguments are `from`, `to`; there is no `strict=` option for the replace case.

The function `coerce` exists as a repository for such methods, to be selected as described above by the `as` function. Actually dispatching the methods using `standardGeneric` could produce incorrect inherited methods, by using inheritance on the `to` argument; as mentioned, this is not the logic used for `as`. To prevent selecting and caching invalid methods, calls to `coerce` are currently mapped into calls to `as`, with a warning message.

**Basic Coercion Methods**

Methods are pre-defined for coercing any object to one of the basic datatypes. For example, `as(x, "numeric")` uses the existing `as.numeric` function. These built-in methods can be listed by `showMethods("coerce")`.

**References**


**See Also**

If you think of using `try(as(x, cl))`, consider `canCoerce(x, cl)` instead.
Examples

```r
## using the definition of class "track" from \link{setClass}

setAs("track", "numeric", function(from) from@y)

t1 <- new("track", x=1:20, y=(1:20)^2)

as(t1, "numeric")
```

```r
## The next example shows:
## 1. A virtual class to define setAs for several classes at once.
## 2. as() using inherited information

setClass("ca", slots = c(a = "character", id = "numeric"))
setClass("cb", slots = c(b = "character", id = "numeric"))

setClass("id")
setIs("ca", "id")
setIs("cb", "id")

setAs("id", "numeric", function(from) from@id)

CA <- new("ca", a = "A", id = 1)
CB <- new("cb", b = "B", id = 2)

setAs("cb", "ca", function(from, to )new(to, a=from@b, id = from@id))

as(CB, "numeric")
```

---

**setClass**  
Create a Class Definition

**Description**

Create a class definition and return a generator function to create objects from the class. Typical usage will be of the style:

```
myClass <- setClass("myClass", slots=....., contains=.....)
```

where the first argument is the name of the new class and, if supplied, the arguments slots= and contains= specify the slots in the new class and existing classes from which the new class should inherit. Calls to setClass() are normally found in the source of a package; when the package is loaded the class will be defined in the package's namespace. Assigning the generator function with the name of the class is convenient for users, but not a requirement.

**Usage**

```
setClass(Class, representation, prototype, contains=character(),
         validity, access, where, version, sealed, package,
         S3methods = FALSE, slots)
```
**Arguments**

- **Class**: character string name for the class.
- **slots**: The names and classes for the slots in the new class. This argument must be supplied by name, `slots=`, in the call, for back compatibility with other arguments no longer recommended.

  The argument must be vector with a names attribute, the names being those of the slots in the new class. Each element of the vector specifies an existing class; the corresponding slot must be from this class or a subclass of it. Usually, this is a character vector naming the classes. It’s also legal for the elements of the vector to be class representation objects, as returned by `getClass`.

  As a limiting case, the argument may be an unnamed character vector; the elements are taken as slot names and all slots have the unrestricted class "ANY".

- **contains**: A vector specifying existing classes from which this class should inherit. The new class will have all the slots of the superclasses, with the same requirements on the classes of these slots. This argument must be supplied by name, `contains=`, in the call, for back compatibility with other arguments no longer recommended.

  See the section 'Virtual Classes' for the special superclass "VIRTUAL".

- **prototype, where, validity, sealed, package**: These arguments are currently allowed, but either they are unlikely to be useful or there are modern alternatives that are preferred.

  - **prototype**: supplies an object with the default data for the slots in this class. A more flexible approach is to write a method for `initialize()`.
  - **where**: supplies an environment in which to store the definition. Should not be used: For calls to `setClass()` appearing in the source code for a package the definition will be stored in the namespace of the package.
  - **validity**: supplied a validity-checking method for objects from this class. For clearer code, use a separate call to `setValidity()`.
  - **sealed**: if TRUE, the class definition will be sealed, so that another call to `setClass` will fail on this class name. But the definition is automatically sealed after the namespace is loaded, so explicit sealing it is not needed.
  - **package**: supplies an optional package name for the class, but the class attribute should be the package in which the class definition is assigned, as it is by default.

- **representation, access, version, S3methods**: All these arguments are deprecated from version 3.0.0 of R and should be avoided.

  - **representation**: is an argument inherited from S that included both `slots` and `contains`, but the use of the latter two arguments is clearer and recommended.
  - **access** and **version** are included for historical compatibility with S-Plus, but ignored.
  - **S3methods**: is a flag indicating that old-style methods will be written involving this class; ignored now.

**Value**

A generator function suitable for creating objects from the class is returned, invisibly. A call to this function generates a call to `new` for the class. The call takes any number of arguments, which will be passed on to the `initialize` method. If no `initialize` method is defined for the class or one of its superclasses, the default method expects named arguments with the name of one of the slots and unnamed arguments that are objects from one of the contained classes.
Typically the generator function is assigned the name of the class, for programming clarity. This is not a requirement and objects from the class can also be generated directly from `new`. The advantages of the generator function are a slightly simpler and clearer call, and that the call will contain the package name of the class (eliminating any ambiguity if two classes from different packages have the same name).

If the class is virtual, an attempt to generate an object from either the generator or `new()` will result in an error.

**Basic Use: Slots and Inheritance**

The two essential arguments other than the class name are slots and contains, defining the explicit slots and the inheritance (superclasses). Together, these arguments define all the information in an object from this class; that is, the names of all the slots and the classes required for each of them. The name of the class determines which methods apply directly to objects from this class. The superclass information specifies which methods apply indirectly, through inheritance. See Methods_Details for inheritance in method selection.

The slots in a class definition will be the union of all the slots specified directly by `slots` and all the slots in all the contained classes. There can only be one slot with a given name. A class may override the definition of a slot with a given name, but only if the newly specified class is a subclass of the inherited one. For example, if the contained class had a slot a with class "ANY", then a subclass could specify a with class "numeric", but if the original specification for the slot was class "character", the new call to `setClass` would generate an error.

Slot names "class" and "Class" are not allowed. There are other slot names with a special meaning; these names start with the "." character. To be safe, you should define all of your own slots with names starting with an alphabetic character.

Some inherited classes will be treated specially—object types, S3 classes and a few special cases—whether inherited directly or indirectly. See the next three sections.

**Virtual Classes**

Classes exist for which no actual objects can be created, the virtual classes.

The most common and useful form of virtual class is the class union, a virtual class that is defined in a call to `setClassUnion()` rather than a call to `setClass()`. This call lists the members of the union—subclasses that extend the new class. Methods that are written with the class union in the signature are eligible for use with objects from any of the member classes. Class unions can include as members classes whose definition is otherwise sealed, including basic R data types.

Calls to `setClass()` will also create a virtual class, either when only the Class argument is supplied (no slots or superclasses) or when the contains= argument includes the special class name "VIRTUAL".

In the latter case, a virtual class may include slots to provide some common behavior without fully defining the object—see the class `traceable` for an example. Note that "VIRTUAL" does not carry over to subclasses; a class that contains a virtual class is not itself automatically virtual.

**Inheriting from Object Types**

In addition to containing other S4 classes, a class definition can contain either an S3 class (see the next section) or a built-in R pseudo-class—one of the R object types or one of the special R pseudo-classes "matrix" and "array". A class can contain at most one of the object types, directly or indirectly. When it does, that contained class determines the "data part" of the class. This appears as a pseudo-slot, ".Data" and can be treated as a slot but actually determines the type of objects from this slot.
Objects from the new class try to inherit the built-in behavior of the contained type. In the case of normal \texttt{R} data types, including vectors, functions, and expressions, the implementation is relatively straightforward. For any object \(x\) from the class, \texttt{typeof(x)} will be the contained basic type; and a special pseudo-slot, \texttt{.Data}, will be shown with the corresponding class. See the "numWithId" example below.

Classes may also inherit from "vector", "matrix" or "array". The data part of these objects can be any vector data type.

For an object from any class that does not contain one of these types or classes, \texttt{typeof(x)} will be "S4".

Some \texttt{R} data types do not behave normally, in the sense that they are non-local references or other objects that are not duplicated. Examples include those corresponding to classes "environment", "externalptr", and "name". These can not be the types for objects with user-defined classes (either S4 or S3) because setting an attribute overwrites the object in all contexts. It is possible to define a class that inherits from such types, through an indirect mechanism that stores the inherited object in a reserved slot, ".xData". See the example for class "stampedEnv" below. An object from such a class does not have a ".Data" pseudo-slot.

For most computations, these classes behave transparently as if they inherited directly from the anomalous type. S3 method dispatch and the relevant \texttt{as.type()} functions should behave correctly, but code that uses the type of the object directly will not. For example, \texttt{as.environment(e1)} would work as expected with the "stampedEnv" class, but \texttt{typeof(e1)} is "S4".

**Inheriting from S3 Classes**

Old-style S3 classes have no formal definition. Objects are “from” the class when their class attribute contains the character string considered to be the class name.

Using such classes with formal classes and methods is necessarily a risky business, since there are no guarantees about the content of the objects or about consistency of inherited methods. Given that, it is still possible to define a class that inherits from an S3 class, providing that class has been registered as an old class (see \texttt{setOldClass}).

Broadly speaking, both S3 and S4 method dispatch try to behave sensibly with respect to inheritance in either system. Given an S4 object, S3 method dispatch and the \texttt{inherits} function should use the S4 inheritance information. Given an S3 object, an S4 generic function will dispatch S4 methods using the S3 inheritance, provided that inheritance has been declared via \texttt{setOldClass}. For details, see \texttt{setOldClass} and Section 10.8 of the reference.

**Classes and Packages**

Class definitions normally belong to packages (but can be defined in the global environment as well, by evaluating the expression on the command line or in a file sourced from the command line). The corresponding package name is part of the class definition; that is, part of the \texttt{classRepresentation} object holding that definition. Thus, two classes with the same name can exist in different packages, for most purposes.

When a class name is supplied for a slot or a superclass in a call to \texttt{setClass}, a corresponding class definition will be found, looking from the namespace of the current package, assuming the call in question appears directly in the source for the package, as it should to avoid ambiguity. The class definition must be already defined in this package, in the imports directives of the package’s \texttt{DESCRIPTION} and \texttt{NAMESPACE} files or in the basic classes defined by the methods package. (The ‘methods’ package must be included in the imports directives for any package that uses S4 methods and classes, to satisfy the "CMD check" utility.)
setClass

If a package imports two classes of the same name from separate packages, the packageSlot of the name argument needs to be set to the package name of the particular class. This should be a rare occurrence.

References


See Also

Classes_Details for a general discussion of classes, Methods_Details for an analogous discussion of methods, makeClassRepresentation

Examples

## A simple class with two slots
track <- setClass("track", slots = c(x="numeric", y="numeric"))

## an object from the class
t1 <- track(x = 1:10, y = 1:10 + rnorm(10))

## A class extending the previous, adding one more slot
trackCurve <- setClass("trackCurve",
  slots = c(smooth = "numeric"),
  contains = "track")

## an object containing a superclass object
t1s <- trackCurve(t1, smooth = 1:10)

## A class similar to "trackCurve", but with different structure
## allowing matrices for the "y" and "smooth" slots
setClass("trackMultiCurve",
  slots = c(x="numeric", y="matrix", smooth="matrix"),
  prototype = list(x=numeric(), y=matrix(0,0,0),
    smooth= matrix(0,0,0)))

## A class that extends the built-in data type "numeric"
numWithId <- setClass("numWithId", slots = c(id = "character"),
  contains = "numeric")
numWithId(1:3, id = "An Example")

## inherit from reference object of type "environment"
stampedEnv <- setClass("stampedEnv", contains = "environment",
  slots = c(update = "POSIXct"))
setMethod("[[<-", c("stampedEnv", "character", "missing"),
  function(x, i, j, ..., value) {
    ev <- as(x, "environment")
    ev[[i]] <- value #update the object in the environment
    x$update <- Sys.time() # and the update time
  }}

e1 <- stampedEnv(update = Sys.time())

e1[["noise"]]<- rnorm(10)
**setClassUnion**

Classes Defined as the Union of Other Classes

**Description**

A class may be defined as the union of other classes; that is, as a virtual class defined as a superclass of several other classes. Class unions are useful in method signatures or as slots in other classes, when we want to allow one of several classes to be supplied.

**Usage**

```r
setClassUnion(name, members, where)
isClassUnion(Class)
```

**Arguments**

- `name`: the name for the new union class.
- `members`: the names of the classes that should be members of this union.
- `where`: where to save the new class definition. In calls from a package’s source code, should be omitted to save the definition in the package’s namespace.
- `Class`: the name or definition of a class.

**Details**

The classes in `members` must be defined before creating the union. However, members can be added later on to an existing union, as shown in the example below. Class unions can be members of other class unions.

Class unions are the only way to create a new superclass of a class whose definition is sealed. The namespace of all packages is sealed when the package is loaded, protecting the class and other definitions from being overwritten from another class or from the global environment. A call to `setIs` that tried to define a new superclass for class "numeric", for example, would cause an error.

Class unions are the exception; the class union "maybeNumber" in the examples defines itself as a new superclass of "numeric". Technically, it does not alter the metadata object in the other package’s namespace and, of course, the effect of the class union depends on loading the package it belongs to. But, basically, class unions are sufficiently useful to justify the exemption.

The different behavior for class unions is made possible because the class definition object for class unions has itself a special class, "ClassUnionRepresentation", an extension of class `classRepresentation`.

**References**

Examples

```r
## a class for either numeric or logical data
setClassUnion("maybeNumber", c("numeric", "logical"))

## use the union as the data part of another class
setClass("withId", contains = "maybeNumber", slots = c(id = "character"))

w1 <- new("withId", 1:10, id = "test 1")
w2 <- new("withId", sqrt(w1)%%1 < .01, id = "Perfect squares")

## add class "complex" to the union "maybeNumber"
setIs("complex", "maybeNumber")

w3 <- new("withId", complex(real = 1:10, imaginary = sqrt(1:10)))

## a class union containing the existing class union "OptionalFunction"
setClassUnion("maybeCode",
  c("expression", "language", "OptionalFunction"))

is(quote(sqrt(1:10)), "maybeCode") ## TRUE
```

setGeneric

Create a Generic Version of a Function

Description

Create a generic version of the named function so that methods may be defined for it. A call to `setMethod` will call `setGeneric` automatically if applied to a non-generic function.

An explicit call to `setGeneric` is usually not required, but doesn’t hurt and makes explicit that methods are being defined for a non-generic function.

Standard calls will be of the form:

```r
setGeneric(name)
```

where `name` specifies an existing function, possibly in another package. An alternative when creating a new generic function in this package is:

```r
setGeneric(name, def)
```

where the function definition `def` specifies the formal arguments and becomes the default method.

Usage

```r
setGeneric(name, def= , group=list(), valueClass=character(),
  where= , package= , signature= , useAsDefault= ,
  genericFunction= , simpleInheritanceOnly = )
```

Arguments

- `name` The character string name of the generic function.
def An optional function object, defining the non-generic version, to become the default method. This is equivalent in effect to assigning `def` as the function and then using the one-argument call to `setGeneric`

*The following arguments are specialized, optionally used when creating a new generic function with non-standard features. They should not be used when the non-generic is in another package.*

group The name of the group generic function to which this function belongs. See `Methods_Details` for details of group generic functions in method selection and `S4groupGeneric` for existing groups.

valueClass A character vector specifying one or more class names. The value returned by the generic function must have (or extend) this class, or one of the classes; otherwise, an error is generated.

signature The vector of names from among the formal arguments to the function, that will be allowed in the signature of methods for this function, in calls to `setMethod`.

By default and usually, this will be all formal arguments except `...`. A non-standard signature for the generic function may be used to exclude arguments that take advantage of lazy evaluation; in particular, if the argument may *not* be evaluated then it cannot be part of the signature.

While `...` cannot be used as part of a general signature, it is possible to have this as the *only* element of the signature. Methods will then be selected if their signature matches all the `...` arguments. See the documentation for topic `dotsMethods` for details. It is not possible to mix `...` and other arguments in the signature.

It’s usually a mistake to omit arguments from the signature in the belief that this improves efficiency. For method selection, the arguments that are used in the signatures for the *methods* are what counts, and then only seriously on the first call to the function with that combination of classes.

simpleInheritanceOnly

Supply this argument as `TRUE` to require that methods selected be inherited through simple inheritance only; that is, from superclasses specified in the `contains=` argument to `setClass`, or by simple inheritance to a class union or other virtual class. Generic functions should require simple inheritance if they need to be assured that they get the complete original object, not one that has been transformed. Examples of functions requiring simple inheritance are `initialize`, because by definition it must return an object from the same class as its argument, and `show`, because it claims to give a full description of the object provided as its argument.

useAsDefault Override the usual default method mechanism. Only relevant when defining a nonstandard generic function. See the section ‘Specialized Local Generics’.

*The remaining arguments are obsolete for normal applications.*

package The name of the package with which this function is associated. Should be determined automatically from the non-generic version.

where Where to store the resulting objects as side effects. The default, to store in the package’s namespace, is the only safe choice.

genericFunction Obsolete.

**Value**

The `setGeneric` function exists for its side effect: saving the generic function to allow methods to be specified later. It returns name.
Basic Use

The `setGeneric` function is called to initialize a generic function as preparation for defining some methods for that function.

The simplest and most common situation is that name specifies an existing function, usually in another package. You now want to define methods for this function. In this case you should supply only name, for example:

```r
setGeneric("colSums")
```

There must be an existing function of this name (in this case in package "base"). The non-generic function can be in the same package as the call, typically the case when you are creating a new function plus methods for it. When the function is in another package, it must be available by name, for example through an `importFrom()` directive in this package’s `NAMESPACE` file. Not required for functions in "base", which are implicitly imported.

A generic version of the function will be created in the current package. The existing function becomes the default method, and the package slot of the new generic function is set to the location of the original function ("base" in the example).

Two special types of non-generic should be noted. Functions that dispatch S3 methods by calling `UseMethod` are ordinary functions, not objects from the "genericFunction" class. They are made generic like any other function, but some special considerations apply to ensure that S4 and S3 method dispatch is consistent (see Methods_for_S3).

Primitive functions are handled in C code and don’t exist as normal functions. A call to `setGeneric` is allowed in the simple form, but no actual generic function object is created. Method dispatch will take place in the C code. See the section on Primitive Functions for more details.

It’s an important feature that the identical generic function definition is created in every package that uses the same `setGeneric()` call. When any of these packages is loaded into an R session, this function will be added to a table of generic functions, and will contain a methods table of all the available methods for the function.

Calling `setGeneric()` is not strictly necessary before calling `setMethod()`. If the function specified in the call to `setMethod` is not generic, `setMethod` will execute the call to `setGeneric` itself. In the case that the non-generic is in another package, does not dispatch S3 methods and is not a primitive, a message is printed noting the creation of the generic function the first time `setMethod` is called.

The second common use of `setGeneric()` is to create a new generic function, unrelated to any existing function. See the `asRObject()` example below. This case can be handled just like the previous examples, with only the difference that the non-generic function exists in the current package. Again, the non-generic version becomes the default method. For clarity it’s best for the assignment to immediately precede the call to `setGeneric()` in the source code.

Exactly the same result can be obtained by supplying the default as the `def` argument instead of assigning it. In some applications, there will be no completely general default method. While there is a special mechanism for this (see the ‘Specialized Local Generics’ section), the recommendation is to provide a default method that signals an error, but with a message that explains as clearly as you can why a non-default method is needed.

Specialized Local Generics

The great majority of calls to `setGeneric()` should either have one argument to ensure that an existing function can have methods, or arguments name and def to create a new generic function and optionally a default method.

It is possible to create generic functions with nonstandard signatures, or functions that do additional computations besides method dispatch or that belong to a group of generic functions.
None of these mechanisms should be used with a non-generic function from a different package, because the result is to create a generic function that may not be consistent from one package to another. When any such options are used, the new generic function will be assigned with a package slot set to the current package, not the one in which the non-generic version of the function is found.

There is a mechanism to define a specialized generic version of a non-generic function, the implicitGeneric construction. This defines the generic version, but then reverts the function to its non-generic form, saving the implicit generic in a table to be activated when methods are defined. However, the mechanism can only legitimately be used either for a non-generic in the same package or by the "methods" package itself. And in the first case, there is no compelling reason not to simply make the function generic, with the non-generic as the default method. See implicitGeneric for details.

The body of a generic function usually does nothing except for dispatching methods by a call to standardGeneric. Under some circumstances you might just want to do some additional computation in the generic function itself. As long as your function eventually calls standardGeneric that is permissible. See the example "authorNames" below.

In this case, the def argument will define the nonstandard generic, not the default method. An existing non-generic of the same name and calling sequence should be pre-assigned. It will become the default method, as usual. (An alternative is the useAsDefault argument.)

By default, the generic function can return any object. If valueClass is supplied, it should be a vector of class names; the value returned by a method is then required to satisfy is(object, Class) for one of the specified classes. An empty (i.e., zero length) vector of classes means anything is allowed. Note that more complicated requirements on the result can be specified explicitly, by defining a non-standard generic function.

If the def argument calls standardGeneric() (with or without additional computations) and there is no existing non-generic version of the function, the generic is created without a default method. This is not usually a good idea: better to have a default method that signals an error with a message explaining why the default case is not defined.

A new generic function can be created belonging to an existing group by including the group argument. The argument list of the new generic must agree with that of the group. See setGroupGeneric for defining a new group generic. For the role of group generics in dispatching methods, see GroupGenericFunctions and section 10.5 of the second reference.

Generic Functions and Primitive Functions

A number of the basic R functions are specially implemented as primitive functions, to be evaluated directly in the underlying C code rather than by evaluating an R language definition. Most have implicit generics (see implicitGeneric), and become generic as soon as methods (including group methods) are defined on them. Others cannot be made generic.

Calling setGeneric() for the primitive functions in the base package differs in that it does not, in fact, generate an explicit generic function. Methods for primitives are selected and dispatched from the internal C code, to satisfy concerns for efficiency. The same is true for a few non-primitive functions that dispatch internally. These include unlist and as.vector.

Note, that the implementation restrict methods for primitive functions to signatures in which at least one of the classes in the signature is a formal S4 class. Otherwise the internal C code will not look for methods. This is a desirable restriction in principle, since optional packages should not be allowed to change the behavior of basic R computations on existing data types.

To see the generic version of a primitive function, use getGeneric(name). The function isGeneric will tell you whether methods are defined for the function in the current session.

Note that S4 methods can only be set on those primitives which are 'internal generic', plus %*%.
setGroupGeneric

Create a Group Generic Version of a Function

Description

The setGroupGeneric function behaves like setGeneric except that it constructs a group generic function, differing in two ways from an ordinary generic function. First, this function cannot be called directly, and the body of the function created will contain a stop call with this information. Second, the group generic function contains information about the known members of the group, used to keep the members up to date when the group definition changes, through changes in the search list or direct specification of methods, etc.

All members of the group must have the identical argument list.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)

See Also

Methods_Details and the links there for a general discussion, dotsMethods for methods that dispatch on .... and setMethod for method definitions.

Examples

## Specify that this package will define methods for plot()
setGeneric("plot")

## create a new generic function, with a default method
setGeneric("props", function(object) attributes(object))

### A non-standard generic function. It insists that the methods
### return a non-empty character vector (a stronger requirement than
### valueClass = "character" in the call to setGeneric)
setGeneric("authorNames",
function(text) {
  value <- standardGeneric("authorNames")
  if(!(is(value, "character") && any(nchar(value)>0)))
    stop("authorNames methods must return non-empty strings")
  value
})

## the asRObject generic function, from package XR
## Its default method just returns object
## See the reference, Chapter 12 for methods
setGeneric("asRObject", function(object, evaluator) {
  object
})
setIs

Usage

```r
setGroupGeneric(name, def= , group=list(), valueClass=character(),
  knownMembers=list(), package= , where= )
```

Arguments

- **name**: the character string name of the generic function.
- **def**: A function object. There isn’t likely to be an existing nongeneric of this name, so some function needs to be supplied. Any known member or other function with the same argument list will do, because the group generic cannot be called directly.
- **group**, **valueClass**: arguments to pass to `setGeneric`
- **knownMembers**: the names of functions that are known to be members of this group. This information is used to reset cached definitions of the member generics when information about the group generic is changed.
- **package**, **where**: passed to `setGeneric`, but obsolete and to be avoided.

Value

The `setGroupGeneric` function exists for its side effect: saving the generic function to allow methods to be specified later. It returns `name`.

References


See Also

`Methods_Details` and the links there for a general discussion, `dotsMethods` for methods that dispatch on . . . , and `setMethod` for method definitions.

Examples

```r
## Not run:
## the definition of the "Logic" group generic in the methods package
setGroupGeneric("Logic", function(e1, e2) NULL,
  knownMembers = c("&", "|"))
## End(Not run)
```

---

**setIs**

Specify a Superclass Explicitly

Description

`setIs` is an explicit alternative to the `contains=` argument to `setClass`. It is only needed to create relations with explicit test or coercion. These have not proved to be of much practical value, so this function should not likely be needed in applications.

Where the programming goal is to define methods for transforming one class of objects to another, it is usually better practice to call `setAs()`, which requires the transformations to be done explicitly.
setIs

Usage

```r
setIs(class1, class2, test=NULL, coerce=NULL, replace=NULL, 
by = character(), where = toplevel(parent.frame()), classDef =, 
extensionObject = NULL, doComplete = TRUE)
```

Arguments

class1, class2  the names of the classes between which is relations are to be examined defined, or (more efficiently) the class definition objects for the classes.

coerce, replace functions optionally supplied to coerce the object to class2, and to alter the object so that `is(object, class2)` is identical to `value`. See the details section below.

test  a conditional relationship is defined by supplying this function. Conditional relations are discouraged and are not included in selecting methods. See the details section below.

The remaining arguments are for internal use and/or usually omitted.

extensionObject alternative to the test, coerce, replace, by arguments; an object from class SClassExtension describing the relation. (Used in internal calls.)

doComplete  when `TRUE`, the class definitions will be augmented with indirect relations as well. (Used in internal calls.)

by  In a call to setIs, the name of an intermediary class. Coercion will proceed by first coercing to this class and from there to the target class. (The intermediate coercions have to be valid.)

where  In a call to setIs, where to store the metadata defining the relationship. Default is the global environment for calls from the top level of the session or a source file evaluated there. When the call occurs in the top level of a file in the source of a package, the default will be the namespace or environment of the package. Other uses are tricky and not usually a good idea, unless you really know what you are doing.

classDef  Optional class definition for class, required internally when setIs is called during the initial definition of the class by a call to `setClass`. Don’t use this argument, unless you really know why you’re doing so.

Details

Arranging for a class to inherit from another class is a key tool in programming. In R, there are three basic techniques, the first two providing what is called “simple” inheritance, the preferred form:

1. By the `contains=` argument in a call to `setClass`. This is and should be the most common mechanism. It arranges that the new class contains all the structure of the existing class, and in particular all the slots with the same class specified. The resulting class extension is defined to be simple, with important implications for method definition (see the section on this topic below).

2. Making class1 a subclass of a virtual class either by a call to `setClassUnion` to make the subclass a member of a new class union, or by a call to setIs to add a class to an existing class union or as a new subclass of an existing virtual class. In either case, the implication should be that methods defined for the class union or other superclass all work correctly for
the subclass. This may depend on some similarity in the structure of the subclasses or simply indicate that the superclass methods are defined in terms of generic functions that apply to all the subclasses. These relationships are also generally simple.

3. Supplying coerce and replace arguments to setAs. R allows arbitrary inheritance relationships, using the same mechanism for defining coerce methods by a call to setAs. The difference between the two is simply that setAs will require a call to as for a conversion to take place, whereas after the call to setIs, objects will be automatically converted to the superclass.

The automatic feature is the dangerous part, mainly because it results in the subclass potentially inheriting methods that do not work. See the section on inheritance below. If the two classes involved do not actually inherit a large collection of methods, as in the first example below, the danger may be relatively slight.

If the superclass inherits methods where the subclass has only a default or remotely inherited method, problems are more likely. In this case, a general recommendation is to use the setAs mechanism instead, unless there is a strong counter reason. Otherwise, be prepared to override some of the methods inherited.

With this caution given, the rest of this section describes what happens when coerce= and replace= arguments are supplied to setIs.

The coerce and replace arguments are functions that define how to coerce a class1 object to class2, and how to replace the part of the subclass object that corresponds to class2. The first of these is a function of one argument which should be from, and the second of two arguments (from, value). For details, see the section on coerce functions below.

When by is specified, the coerce process first coerces to this class and then to class2. It’s unlikely you would use the by argument directly, but it is used in defining cached information about classes.

The value returned (invisibly) by setIs is the revised class definition of class1.

**Coerce, replace, and test functions**

The coerce argument is a function that turns a class1 object into a class2 object. The replace argument is a function of two arguments that modifies a class1 object (the first argument) to replace the part of it that corresponds to class2 (supplied as value, the second argument). It then returns the modified object as the value of the call. In other words, it acts as a replacement method to implement the expression as(object, class2) <- value.

The easiest way to think of the coerce and replace functions is by thinking of the case that class1 contains class2 in the usual sense, by including the slots of the second class. (To repeat, in this situation you would not call setIs, but the analogy shows what happens when you do.)

The coerce function in this case would just make a class2 object by extracting the corresponding slots from the class1 object. The replace function would replace in the class1 object the slots corresponding to class2, and return the modified object as its value.

For additional discussion of these functions, see the documentation of the setAs function. (Unfortunately, argument def to that function corresponds to argument coerce here.)

The inheritance relationship can also be conditional, if a function is supplied as the test argument. This should be a function of one argument that returns TRUE or FALSE according to whether the object supplied satisfies the relation is(object, class2). Conditional relations between classes are discouraged in general because they require a per-object calculation to determine their validity. They cannot be applied as efficiently as ordinary relations and tend to make the code that uses them harder to interpret. **NOTE: conditional inheritance is not used to dispatch methods.** Methods for conditional superclasses will not be inherited. Instead, a method for the subclass should be defined that tests the conditional relationship.
Inherited methods

A method written for a particular signature (classes matched to one or more formal arguments to the function) naturally assumes that the objects corresponding to the arguments can be treated as coming from the corresponding classes. The objects will have all the slots and available methods for the classes.

The code that selects and dispatches the methods ensures that this assumption is correct. If the inheritance was “simple”, that is, defined by one or more uses of the contains= argument in a call to setIs, no extra work is generally needed. Classes are inherited from the superclass, with the same definition.

When inheritance is defined by a general call to setIs, extra computations are required. This form of inheritance implies that the subclass does not just contain the slots of the superclass, but instead requires the explicit call to the coerce and/or replace method. To ensure correct computation, the inherited method is supplemented by calls to as before the body of the method is evaluated.

The calls to as generated in this case have the argument strict = FALSE, meaning that extra information can be left in the converted object, so long as it has all the appropriate slots. (It’s this option that allows simple subclass objects to be used without any change.) When you are writing your coerce method, you may want to take advantage of that option.

Methods inherited through non-simple extensions can result in ambiguities or unexpected selections. If class2 is a specialized class with just a few applicable methods, creating the inheritance relation may have little effect on the behavior of class1. But if class2 is a class with many methods, you may find that you now inherit some undesirable methods for class1, in some cases, fail to inherit expected methods. In the second example below, the non-simple inheritance from class "factor" might be assumed to inherit S3 methods via that class. But the S3 class is ambiguous, and in fact is "character" rather than "factor".

For some generic functions, methods inherited by non-simple extensions are either known to be invalid or sufficiently likely to be so that the generic function has been defined to exclude such inheritance. For example initialize methods must return an object of the target class; this is straightforward if the extension is simple, because no change is made to the argument object, but is essentially impossible. For this reason, the generic function insists on only simple extensions for inheritance. See the simpleInheritanceOnly argument to setGeneric for the mechanism. You can use this mechanism when defining new generic functions.

If you get into problems with functions that do allow non-simple inheritance, there are two basic choices. Either back off from the setIs call and settle for explicit coercing defined by a call to setAs; or, define explicit methods involving class1 to override the bad inherited methods. The first choice is the safer, when there are serious problems.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)

Examples

### Two examples of setIs() with coerce= and replace= arguments
### The first one works fairly well, because neither class has many
### inherited methods do be disturbed by the new inheritance

### The second example does NOT work well, because the new superclass,
### "factor", causes methods to be inherited that should not be.

### First example:
### a class definition (see \link{setClass} for class "track")
setClass("trackCurve", contains = "track",
  slots = c(smooth = "numeric"))
## A class similar to "trackCurve", but with different structure
## allowing matrices for the "y" and "smooth" slots
setClass("trackMultiCurve",
  slots = c(x="numeric", y="matrix", smooth="matrix"),
  prototype = structure(list(), x=numeric(), y=matrix(0,0,0),
    smooth= matrix(0,0,0)))
## Automatically convert an object from class "trackCurve" into
## "trackMultiCurve", by making the y, smooth slots into 1-column matrices
setIs("trackCurve",
  "trackMultiCurve",
  coerce = function(obj) {
    new("trackMultiCurve",
      x = obj@x,
      y = as.matrix(obj@y),
      smooth = as.matrix(obj@smooth))
  },
  replace = function(obj, value) {
    obj@y <- as.matrix(value@y)
    obj@x <- value@x
    obj@smooth <- as.matrix(value@smooth)
    obj})

## Second Example:
## A class that adds a slot to "character"
setClass("stringsDated", contains = "character",
  slots = c(stamp="POSIXt"))
## Convert automatically to a factor by explicit coerce
setIs("stringsDated", "factor",
  coerce = function(from) factor(from@.Data),
  replace= function(from, value) {
    from@.Data <- as.character(value); from })
ll <- sample(letters, 10, replace = TRUE)
l1 <- new("stringsDated", ll, stamp = Sys.time())
levels(as(l1, "factor"))
levels(l1) # will be NULL--see comment in section on inheritance above.

## In contrast, a class that simply extends "factor"
## has no such ambiguities
setClass("factorDated", contains = "factor",
  slots = c(stamp="POSIXt"))
f1 <- new("factorDated", factor(ll), stamp = Sys.time())
identical(levels(f1), levels(as(f1, "factor")))
Description

These functions provide a mechanism for packages to specify computations to be done during the loading of a package namespace. Such actions are a flexible way to provide information only available at load time (such as locations in a dynamically linked library).

A call to setLoadAction() or setLoadActions() specifies one or more functions to be called when the corresponding namespace is loaded, with the ...argument names being used as identifying names for the actions.

getLoadActions reports the currently defined load actions, given a package's namespace as its argument.

hasLoadAction returns TRUE if a load action corresponding to the given name has previously been set for the where namespace.

evalOnLoad() and evalqOnLoad() schedule a specific expression for evaluation at load time.

Usage

setLoadAction(action, aname=, where=)

setLoadActions(..., .where=)

getLoadActions(where=)

hasLoadAction(aname, where=)

evalOnLoad(expr, where=, aname=)

evalqOnLoad(expr, where=, aname=)

Arguments

action, ... functions of one or more arguments, to be called when this package is loaded. The functions will be called with one argument (the package namespace) so all following arguments must have default values.

If the elements of ...are named, these names will be used for the corresponding load metadata.

where, .where the namespace of the package for which the list of load actions are defined. This argument is normally omitted if the call comes from the source code for the package itself, but will be needed if a package supplies load actions for another package.

aname the name for the action. If an action is set without supplying a name, the default uses the position in the sequence of actions specified (".1", etc.).

eexpr an expression to be evaluated in a load action in environment where. In the case of evalqOnLoad(), the expression is interpreted literally, in that of evalOnLoad() it must be precomputed, typically as an object of type "language".

Details

The evalOnLoad() and evalqOnLoad() functions are for convenience. They construct a function to evaluate the expression and call setLoadAction() to schedule a call to that function.
Each of the functions supplied as an argument to `setLoadAction()` or `setLoadActions()` is saved as metadata in the namespace, typically that of the package containing the call to `setLoadActions()`. When this package’s namespace is loaded, each of these functions will be called. Action functions are called in the order they are supplied to `setLoadActions()`. The objects assigned have metadata names constructed from the names supplied in the call; unnamed arguments are taken to be named by their position in the list of actions (".1", etc.).

Multiple calls to `setLoadAction()` or `setLoadActions()` can be used in a package’s code; the actions will be scheduled after any previously specified, except if the name given to `setLoadAction()` is that of an existing action. In typical applications, `setLoadActions()` is more convenient when calling from the package’s own code to set several actions. Calls to `setLoadAction()` are more convenient if the action name is to be constructed, which is more typical when one package constructs load actions for another package.

Actions can be revised by assigning with the same name, actual or constructed, in a subsequent call. The replacement must still be a valid function, but can of course do nothing if the intention was to remove a previously specified action.

The functions must have at least one argument. They will be called with one argument, the namespace of the package. The functions will be called at the end of processing of S4 metadata, after dynamically linking any compiled code, the call to `.onLoad()`, if any, and caching method and class definitions, but before the namespace is sealed. (Load actions are only called if methods dispatch is on.)

Functions may therefore assign or modify objects in the namespace supplied as the argument in the call. The mechanism allows packages to save information not available until load time, such as values obtained from a dynamically linked library.

Load actions should be contrasted with user load hooks supplied by `setHook()`. User hooks are generally provided from outside the package and are run after the namespace has been sealed. Load actions are normally part of the package code, and the list of actions is normally established when the package is installed.

Load actions can be supplied directly in the source code for a package. It is also possible and useful to provide facilities in one package to create load actions in another package. The software needs to be careful to assign the action functions in the correct environment, namely the namespace of the target package.

**Value**

`setLoadAction()` and `setLoadActions()` are called for their side effect and return no useful value.

`getLoadActions()` returns a named list of the actions in the supplied namespace.

`hasLoadAction()` returns `TRUE` if the specified action name appears in the actions for this package.

**See Also**

`setHook` for safer (since they are run after the namespace is sealed) and more comprehensive versions in the base package.

**Examples**

```r
## Not run:
## in the code for some package

## ... somewhere else
setLoadActions(function(ns)
```
setMethod

Create and Save a Method

Description

Create a method for a generic function, corresponding to a signature of classes for the arguments. Standard usage will be of the form:

setMethod(f, signature, definition)

where f is the name of the function, signature specifies the argument classes for which the method applies and definition is the function definition for the method.

Usage

setMethod(f, signature=character(), definition,
where = topenv(parent.frame()),
valueClass = NULL, sealed = FALSE)

Arguments

f  The character-string name of the generic function. The unquoted name usually works as well (evaluating to the generic function), except for a few functions in the base package.

signature  The classes required for some of the arguments. Most applications just require one or two character strings matching the first argument(s) in the signature. More complicated cases follow R’s rule for argument matching. See the details below; however, if the signature is not trivial, you should use method.skeleton to generate a valid call to setMethod.

definition  A function definition, which will become the method called when the arguments in a call to f match the classes in signature, directly or through inheritance. The definition must be a function with the same formal arguments as the generic; however, setMethod() will handle methods that add arguments, if ... is a formal argument to the generic. See the Details section.

where, valueClass, sealed

These arguments are allowed but either obsolete or rarely appropriate.

where: where to store the definition; should be the default, the namespace for the package.

tests: obsolete.

sealed: prevents the method being redefined, but should never be needed when the method is defined in the source code of a package.
Value

The function exists for its side-effect. The definition will be stored in a special metadata object and incorporated in the generic function when the corresponding package is loaded into an R session.

Method Selection: Avoiding Ambiguity

When defining methods, it’s important to ensure that methods are selected correctly; in particular, packages should be designed to avoid ambiguous method selection.

To describe method selection, consider first the case where only one formal argument is in the active signature; that is, there is only one argument, \( x \) say, for which methods have been defined. The generic function has a table of methods, indexed by the class for the argument in the calls to `setMethod`. If there is a method in the table for the class of \( x \) in the call, this method is selected. If not, the next best methods would correspond to the direct superclasses of \( \text{class}(x) \) — those appearing in the `contains=` argument when that class was defined. If there is no method for any of these, the next best would correspond to the direct superclasses of the first set of superclasses, and so on.

The first possible source of ambiguity arises if the class has several direct superclasses and methods have been defined for more than one of those; R will consider these equally valid and report an ambiguous choice. If your package has the class definition for \( \text{class}(x) \), then you need to define a method explicitly for this combination of generic function and class.

When more than one formal argument appears in the method signature, R requires the “best” method to be chosen unambiguously for each argument. Ambiguities arise when one method is specific about one argument while another is specific about a different argument. A call that satisfies both requirements is then ambiguous: The two methods look equally valid, which should be chosen? In such cases the package needs to add a third method requiring both arguments to match.

The most common examples arise with binary operators. Methods may be defined for individual operators, for special groups of operators such as `Arith` or for group `Ops`.

Exporting Methods

If a package defines methods for generic functions, those methods should be exported if any of the classes involved are exported; in other words, if someone using the package might expect these methods to be called. Methods are exported by including an `exportMethods()` directive in the `NAMESPACE` file for the package, with the arguments to the directive being the names of the generic functions for which methods have been defined.

Exporting methods is always desirable in the sense of declaring what you want to happen, in that you do expect users to find such methods. It can be essential in the case that the method was defined for a function that is not originally a generic function in its own package (for example, `plot()` in the `graphics` package). In this case it may be that the version of the function in the \( \text{R} \) session is not generic, and your methods will not be called.

Exporting methods for a function also exports the generic version of the function. Keep in mind that this does not conflict with the function as it was originally defined in another package; on the contrary, it’s designed to ensure that the function in the \( \text{R} \) session dispatches methods correctly for your classes and continues to behave as expected when no specific methods apply. See Methods_Details for the actual mechanism.

Details

The call to `setMethod` stores the supplied method definition in the metadata table for this generic function in the environment, typically the global environment or the namespace of a package. In the
case of a package, the table object becomes part of the namespace or environment of the package. When the package is loaded into a later session, the methods will be merged into the table of methods in the corresponding generic function object.

Generic functions are referenced by the combination of the function name and the package name; for example, the function "show" from the package "methods". Metadata for methods is identified by the two strings; in particular, the generic function object itself has slots containing its name and its package name. The package name of a generic is set according to the package from which it originally comes; in particular, and frequently, the package where a non-generic version of the function originated. For example, generic functions for all the functions in package base will have "base" as the package name, although none of them is an S4 generic on that package. These include most of the base functions that are primitives, rather than true functions; see the section on primitive functions in the documentation for setGeneric for details.

Multiple packages can have methods for the same generic function; that is, for the same combination of generic function name and package name. Even though the methods are stored in separate tables in separate environments, loading the corresponding packages adds the methods to the table in the generic function itself, for the duration of the session.

The class names in the signature can be any formal class, including basic classes such as "numeric", "character", and "matrix". Two additional special class names can appear: "ANY", meaning that this argument can have any class at all; and "missing", meaning that this argument must not appear in the call in order to match this signature. Don't confuse these two: if an argument isn't mentioned in a signature, it corresponds implicitly to class "ANY", not to "missing". See the example below.

Old-style ('S3') classes can also be used, if you need compatibility with these, but you should definitely declare these classes by calling setOldClass if you want S3-style inheritance to work.

Method definitions can have default expressions for arguments, but only if the generic function must have some default expression for the same argument. (This restriction is imposed by the way R manages formal arguments.) If so, and if the corresponding argument is missing in the call to the generic function, the default expression in the method is used. If the method definition has no default for the argument, then the expression supplied in the definition of the generic function itself is used, but note that this expression will be evaluated using the enclosing environment of the method, not of the generic function. Method selection does not evaluate default expressions. All actual (non-missing) arguments in the signature of the generic function will be evaluated when a method is selected—when the call to standardGeneric(f) occurs. Note that specifying class "missing" in the signature does not require any default expressions.

It is possible to have some differences between the formal arguments to a method supplied to setMethod and those of the generic. Roughly, if the generic has ... as one of its arguments, then the method may have extra formal arguments, which will be matched from the arguments matching ... in the call to f. (What actually happens is that a local function is created inside the method, with the modified formal arguments, and the method is re-defined to call that local function.)

Method dispatch tries to match the class of the actual arguments in a call to the available methods collected for f. If there is a method defined for the exact same classes as in this call, that method is used. Otherwise, all possible signatures are considered corresponding to the actual classes or to superclasses of the actual classes (including "ANY"). The method having the least distance from the actual classes is chosen; if more than one method has minimal distance, one is chosen (the lexicographically first in terms of superclasses) but a warning is issued. All inherited methods chosen are stored in another table, so that the inheritance calculations only need to be done once per session per sequence of actual classes. See Methods_Details and Section 10.7 of the reference for more details.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10.)
See Also

Methods_for_Nongenerics discusses method definition for functions that are not generic functions in their original package: Methods_for_S3 discusses the integration of formal methods with the older S3 methods.

method.skeleton, which is the recommended way to generate a skeleton of the call to setMethod, with the correct formal arguments and other details.

Methods_Details and the links there for a general discussion, dotsMethods for methods that dispatch on "...", and setGeneric for generic functions.

Examples

## examples for a simple class with two numeric slots.
## (Run example(setMethod) to see the class and function definitions)

## methods for plotting track objects
##
## First, with only one object as argument, plot the two slots
## y must be included in the signature, it would default to "ANY"
setMethod("plot", signature(x="track", y="missing"),
  function(x, y, ...) plot(x@x, x@y, ...)
)

## plot numeric data on either axis against a track object
## (reducing the track object to the cumulative distance along the track)
## Using a short form for the signature, which matches like formal arguments
setMethod("plot", c("track", "numeric"),
  function(x, y, ...) plot(cumdist(x@x, x@y), y, xlab = "Distance",...)
)

## and similarly for the other axis
setMethod("plot", c("numeric", "track"),
  function(x, y, ...) plot(x, cumdist(y@x, y@y), ylab = "Distance",...)
)

t1 <- new("track", x=1:20, y=(1:20)^2)
plot(t1)
plot(qnorm(ppoints(20)), t1)

## Now a class that inherits from "track", with a vector for data at
## the points
setClass("trackData", contains = c("numeric", "track"))

tc1 <- new("trackData", t1, rnorm(20))

## a method for plotting the object
## This method has an extra argument, allowed because ... is an
## argument to the generic function.
setMethod("plot", c("trackData", "missing"),
  function(x, y, maxRadius = max(par("cin")), ...) {
    plot(x@x, x@y, type = "n", ...)
    symbols(x@x, x@y, circles = abs(x), inches = maxRadius)
  })
setOldClass

## Without other methods for "trackData", methods for "track"
## will be selected by inheritance

plot(qnorm(ppoints(20)), tc1)

## defining methods for primitive function.
## Although "[" and "length" are not ordinary functions
## methods can be defined for them.
setMethod("[", "track",
  function(x, i, j, ..., drop) {
    x@x <- x@x[i]; x@y <- x@y[i]
    x
  })
plot(t1[1:15])

setMethod("length", "track", function(x)length(x@y))
length(t1)

## Methods for binary operators
## A method for the group generic "Ops" will apply to all operators
## unless a method for a more specific operator has been defined.

## For one trackData argument, go on with just the data part
setMethod("Ops", signature(e1 = "trackData"),
  function(e1, e2) callGeneric(e1@.Data, e2))

setMethod("Ops", signature(e2 = "trackData"),
  function(e1, e2) callGeneric(e1, e2@.Data))

## At this point, the choice of a method for a call with BOTH
## arguments from "trackData" is ambiguous. We must define a method.

setMethod("Ops", signature(e1 = "trackData", e2 = "trackData"),
  function(e1, e2) callGeneric(e1@.Data, e2@.Data))

## (well, really we should only do this if the "track" part
## of the two arguments matched)
tc1 +1
1/tc1

all(tc1 == tc1)

setOldClass

Register Old-Style (S3) Classes and Inheritance

Description

Register an old-style (a.k.a. ‘S3’) class as a formally defined class. Simple usage will be of the form:
setOldClass(Classes)

where Classes is the character vector that would be the class attribute of the S3 object. Calls to setOldClass() in the code for a package allow the class to be used as a slot in formal (S4) classes and in signatures for methods (see Methods_for_S3). Formal classes can also contain a registered S3 class (see S3Part for details).

If the S3 class has a known set of attributes, an equivalent S4 class can be specified by S4Class= in the call to setOldClass(); see the section “Known Attributes”.

Usage

setOldClass(Classes, prototype, where, test = FALSE, S4Class)

Arguments

Classes  A character vector, giving the names for S3 classes, as they would appear on the right side of an assignment of the class attribute in S3 computations.

In addition to S3 classes, an object type or other valid data part can be specified, if the S3 class is known to require its data to be of that form.

S4Class  optionally, the class definition or the class name of an S4 class. The new class will have all the slots and other properties of this class, plus any S3 inheritance implied by multiple names in the Classes argument. See the section on “S3 classes with known attributes” below.

prototype, where, test  These arguments are currently allowed, but not recommended in typical applications.

prototype: An optional object to use as the prototype. If the S3 class is not to be VIRTUAL (the default), the use of S4Class= is preferred.

where: Where to store the class definitions. Should be the default (the package namespace) for normal use in an application package.

test: flag, if TRUE, arrange to test inheritance explicitly for each object, needed if the S3 class can have a different set of class strings, with the same first string. Such classes are inherently malformed, are rare, and should be avoided.

Details

The name (or each of the names) in Classes will be defined as an S4 class, extending class oldClass, which is the ‘root’ of all old-style classes. S3 classes with multiple names in their class attribute will have a corresponding inheritance as formal classes. See the “mlm” example.

S3 classes have no formal definition, and therefore no formally defined slots. If no S4 class is supplied as a model, the class created will be a virtual class. If a virtual class (any virtual class) is used for a slot in another class, then the initializing method for the class needs to put something legal in that slot; otherwise it will be set to NULL.

See Methods_for_S3 for the details of method dispatch and inheritance with mixed S3 and S4 methods.

Some S3 classes cannot be represented as an ordinary combination of S4 classes and superclasses, because objects with the same initial string in the class attribute can have different strings following. Such classes are fortunately rare. They violate the basic idea of object-oriented programming and should be avoided. If you must deal with them, it is still possible to register such classes as S4 classes, but now the inheritance has to be verified for each object, and you must call setOldClass with argument test=TRUE.
Pre-Defined Old Classes

Many of the widely used S3 classes in the standard R distribution come pre-defined for use with S4. These don’t need to be explicitly declared in your package (although it does no harm to do so).

The list .OldClassesList contains the old-style classes that are defined by the methods package. Each element of the list is a character vector, with multiple strings if inheritance is included. Each element of the list was passed to setOldClass when creating the methods package; therefore, these classes can be used in setMethod calls, with the inheritance as implied by the list.

S3 Classes with known attributes

A further specification of an S3 class can be made if the class is guaranteed to have some attributes of known class (where as with slots, “known” means that the attribute is an object of a specified class, or a subclass of that class).

In this case, the call to setOldClass() can supply an S4 class definition representing the known structure. Since S4 slots are implemented as attributes (largely for just this reason), the known attributes can be specified in the representation of the S4 class. The usual technique will be to create an S4 class with the desired structure, and then supply the class name or definition as the argument S4Class= to setOldClass().

See the definition of class "ts" in the examples below and the data.frame example in Section 10.2 of the reference. The call to setClass to create the S4 class can use the same class name, as here, so long as the call to setOldClass follows in the same package. For clarity it should be the next expression in the same file.

In the example, we define "ts" as a vector structure with a numeric slot for "tsp". The validity of this definition relies on an assertion that all the S3 code for this class is consistent with that definition; specifically, that all "ts" objects will behave as vector structures and will have a numeric "tsp" attribute. We believe this to be true of all the base code in R, but as always with S3 classes, no guarantee is possible.

The S4 class definition can have virtual superclasses (as in the "ts" case) if the S3 class is asserted to behave consistently with these (in the example, time-series objects are asserted to be consistent with the structure class).

Failures of the S3 class to live up to its asserted behavior will usually go uncorrected, since S3 classes inherently have no definition, and the resulting invalid S4 objects can cause all sorts of grief. Many S3 classes are not candidates for known slots, either because the presence or class of the attributes are not guaranteed (e.g., dimnames in arrays, although these are not even S3 classes), or because the class uses named components of a list rather than attributes (e.g., "1m"). An attribute that is sometimes missing cannot be represented as a slot, not even by pretending that it is present with class "NULL", because attributes, unlike slots, can not have value NULL.

One irregularity that is usually tolerated, however, is to optionally add other attributes to those guaranteed to exist (for example, "terms" in "data.frame" objects returned by model.frame). Validity checks by validObject ignore extra attributes; even if this check is tightened in the future, classes extending S3 classes would likely be exempted because extra attributes are so common.

References

Chambers, John M. (2016) Extending R, Chapman & Hall. (Chapters 9 and 10, particularly Section 10.8)

See Also

setClass, setMethod
Examples

require(stats)

## "lm" and "mlm" are predefined; if they were not this would do it:
## Not run:
setOldClass(c("mlm", "lm"))
## End(Not run)

## Define a new generic function to compute the residual degrees of freedom
setGeneric("dfResidual",
        function(model) stop(gettextf(
            "This function only works for fitted model objects, not class %s",
            class(model))))

setMethod("dfResidual", "lm", function(model)model$df.residual)

## dfResidual will work on mlm objects as well as lm objects
myData <- data.frame(time = 1:10, y = (1:10)^.5)
myLm <- lm(cbind(y, y^3) ~ time, myData)

## two examples extending S3 class "lm": class "xlm" directly
## and "ylm" indirectly
setClass("xlm", slots = c(eps = "numeric"), contains = "lm")
setClass("ylm", slots = c(header = "character"), contains = "xlm")
yml = new("ylm", myLm, header = "Example", eps = 0.)
## for more examples, see ?\link{S3Class}.

## Not run:
## The code in R that defines "ts" as an S4 class
setClass("ts", contains = "structure", slots = c(tsp = "numeric"),
        prototype(NA, tsp = rep(1,3)))
    # prototype to be a legal S3 time-series
## and now registers it as an S3 class
setOldClass("ts", S4Class = "ts", where = envir)
## End(Not run)

show

Show an Object

Description

Display the object, by printing, plotting or whatever suits its class. This function exists to be specialized by methods. The default method calls showDefault.

Formal methods for show will usually be invoked for automatic printing (see the details).
show

Usage

show(object)

Arguments

object Any R object

Details

Objects from an S4 class (a class defined by a call to setClass) will be displayed automatically is if by a call to show. S4 objects that occur as attributes of S3 objects will also be displayed in this form; conversely, S3 objects encountered as slots in S4 objects will be printed using the S3 convention, as if by a call to print.

Methods defined for show will only be inherited by simple inheritance, since otherwise the method would not receive the complete, original object, with misleading results. See the simpleInheritanceOnly argument to setGeneric and the discussion in setIs for the general concept.

Value

show returns an invisible NULL.

See Also

showMethods prints all the methods for one or more functions.

Examples

## following the example shown in the setMethod documentation ...
setClass("track", slots = c(x="numeric", y="numeric"))
setClass("trackCurve", contains = "track", slots = c(smooth = "numeric"))
t1 <- new("track", x=1:20, y=(1:20)^2)
tc1 <- new("trackCurve", t1)
setMethod("show", "track", 
function(object)print(rbind(x = object@x, y=object@y))
)
## The method will now be used for automatic printing of t1

x 1  2  3  4  5  6  7  8  9  10  11  12  13  14  15  16  17  18  19  20
y 1  4  9 16 25 36 49 64 81 100 121 144 169 196 225 256 289 324 361 400
## End(Not run)
## and also for tc1, an object of a class that extends "track"
tc1

showMethods

Show all the methods for the specified function(s) or class

Description

Show a summary of the methods for one or more generic functions, possibly restricted to those involving specified classes.

Usage

showMethods(f = character(), where = topenv(parent.frame()),
   classes = NULL, includeDefs = FALSE,
   inherited = !includeDefs,
   showEmpty, printTo = stdout(), fdef)
   .S4methods(generic.function, class)

Arguments

f

one or more function names. If omitted, all functions will be shown that match the other arguments.

The argument can also be an expression that evaluates to a single generic function, in which case argument fdef is ignored. Providing an expression for the function allows examination of hidden or anonymous functions; see the example for isDiagonal().

where

Where to find the generic function, if not supplied as an argument. When f is missing, or length 0, this also determines which generic functions to examine. If where is supplied, only the generic functions returned by getGenerics(where) are eligible for printing. If where is also missing, all the cached generic functions are considered.

classes

If argument classes is supplied, it is a vector of class names that restricts the displayed results to those methods whose signatures include one or more of those classes.

includeDefs

If includeDefs is TRUE, include the definitions of the individual methods in the printout.

inherited

logical indicating if methods that have been found by inheritance, so far in the session, will be included and marked as inherited. Note that an inherited method will not usually appear until it has been used in this session. See selectMethod if you want to know what method would be dispatched for particular classes of arguments.

showEmpty

logical indicating whether methods with no defined methods matching the other criteria should be shown at all. By default, TRUE if and only if argument f is not missing.
printTo The connection on which the information will be shown; by default, on standard
output.

def Optional, the generic function definition to use; if missing, one is found, look-
ing in where if that is specified. See also comment in ‘Details’.

generic.function, class
See methods.

Details
See methods for a description of .S4methods.

The name and package of the generic are followed by the list of signatures for which methods
are currently defined, according to the criteria determined by the various arguments. Note that
the package refers to the source of the generic function. Individual methods for that generic can come
from other packages as well.

When more than one generic function is involved, either as specified or because f was missing, the
functions are found and showMethods is recalled for each, including the generic as the argument
fdef. In complicated situations, this can avoid some anomalous results.

Value
If printTo is FALSE, the character vector that would have been printed is returned; otherwise the
value is the connection or filename, via invisible.

References
version.)
Chambers, John M. (1998) Programming with Data Springer (For the original S4 version.)

See Also
setMethod, and GenericFunctions for other tools involving methods; selectMethod will show
you the method dispatched for a particular function and signature of classes for the arguments.
methods provides method discovery tools for light-weight interactive use.

Examples

require(graphics)

## Assuming the methods for plot
## are set up as in the example of help(setMethod),
## print (without definitions) the methods that involve class "track":
showMethods("plot", classes = "track")

## Not run:
# Function "plot":
# x = ANY, y = track
# x = track, y = missing
# x = track, y = ANY

require("Matrix")
showMethods("%^%")# many!
methods(class = "Matrix")# nothing
showMethods(class = "Matrix")# everything
signature-class

showMethods(Matrix:::isDiagonal) # a non-exported generic
## End(Not run)

if(no4 <- is.na(match("stats4", loadedNamespaces())))
  loadNamespace("stats4")
showMethods(classes = "mle") # -> a method for show()
if(no4) unloadNamespace("stats4")

signature-class

Class "signature" For Method Definitions

Description

This class represents the mapping of some of the formal arguments of a function onto the corresponding classes. It is used for two slots in the MethodDefinition class.

Objects from the Class

Objects can be created by calls of the form new("signature", functionDef,...). The functionDef argument, if it is supplied as a function object, defines the formal names. The other arguments define the classes. More typically, the objects are created as side effects of defining methods. Either way, note that the classes are expected to be well defined, usually because the corresponding class definitions exist. See the comment on the package slot.

Slots

.Data: Object of class "character" the class names.
names: Object of class "character" the corresponding argument names.
package: Object of class "character" the names of the packages corresponding to the class names. The combination of class name and package uniquely defines the class. In principle, the same class name could appear in more than one package, in which case the package information is required for the signature to be well defined.

Extends

Class "character", from data part. Class "vector", by class "character".

Methods

initialize signature(object = "signature"): see the discussion of objects from the class, above.

See Also

class MethodDefinition for the use of this class.
The Slots in an Object from a Formal Class

Description

These functions return or set information about the individual slots in an object.

Usage

object@name
object@name <- value

slot(object, name)
slot(object, name, check = TRUE) <- value
.hasSlot(object, name)

slotNames(x)
getSlots(x)

Arguments

object       An object from a formally defined class.
name         The name of the slot. The operator takes a fixed name, which can be unquoted if it is syntactically a name in the language. A slot name can be any non-empty string, but if the name is not made up of letters, numbers, and ., it needs to be quoted (by backticks or single or double quotes). In the case of the slot function, name can be any expression that evaluates to a valid slot in the class definition. Generally, the only reason to use the functional form rather than the simpler operator is because the slot name has to be computed.
value        A new value for the named slot. The value must be valid for this slot in this object’s class.
check        In the replacement version of slot, a flag. If TRUE, check the assigned value for validity as the value of this slot. User’s code should not set this to FALSE in normal use, since the resulting object can be invalid.
x            either the name of a class (as character string), or a class definition. If given an argument that is neither a character string nor a class definition, slotNames (only) uses class(x) instead.

Details

The definition of the class specifies all slots directly and indirectly defined for that class. Each slot has a name and an associated class. Extracting a slot returns an object from that class. Setting a slot first coerces the value to the specified slot and then stores it.

Unlike general attributes, slots are not partially matched, and asking for (or trying to set) a slot with an invalid name for that class generates an error.

The @ extraction operator and slot function themselves do no checking against the class definition, simply matching the name in the object itself. The replacement forms do check (except for slot in the case check=FALSE). So long as slots are set without cheating, the extracted slots will be valid.
Be aware that there are two ways to cheat, both to be avoided but with no guarantees. The obvious way is to assign a slot with `check=FALSE`. Also, slots in R are implemented as attributes, for the sake of some back compatibility. The current implementation does not prevent attributes being assigned, via `attr<-`, and such assignments are not checked for legitimate slot names.

Note that the "@" operators for extraction and replacement are primitive and actually reside in the `base` package.

The replacement versions of "@" and `slot()` differ in the computations done to coerce the right side of the assignment to the declared class of the slot. Both verify that the value provided is from a subclass of the declared slot class. The `slot()` version will go on to call the coerce method if there is one, in effect doing the computation `as(value, slotClass, strict = FALSE)`. The "@" version just verifies the relation, leaving any coerce to be done later (e.g., when a relevant method is dispatched).

In most uses the result is equivalent, and the "@" version saves an extra function call, but if empirical evidence shows that a conversion is needed, either call `as()` before the replacement or use the replacement version of `slot()`.

**Value**

The "@" operator and the `slot` function extract or replace the formally defined slots for the object.

Functions `slotNames` and `getSlots` return respectively the names of the slots and the classes associated with the slots in the specified class definition. Except for its extended interpretation of `x` (above), `slotNames(x)` is just `names(getSlots(x))`.

**References**


Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

**See Also**

`@`, `Classes_Details`, `Methods_Details`, `getClass`, `names`.

**Examples**

```r
setClass("track", slots = c(x="numeric", y="numeric"))
myTrack <- new("track", x = -4:4, y = exp(-4:4))
slot(myTrack, "x")
slot(myTrack, "y") <- log(slot(myTrack, "y"))
utils::str(myTrack)
getSlots("track") # or
getSlots(getClass("track"))
slotNames(class(myTrack)) # is the same as
slotNames(myTrack)
```
StructureClasses

**Description**

The virtual class `structure` and classes that extend it are formal classes analogous to S language structures such as arrays and time-series.

**Usage**

```
## The following class names can appear in method signatures,
## as the class in as() and is() expressions, and, except for
## the classes commented as VIRTUAL, in calls to new()

"matrix"
"array"
"ts"

"structure" ## VIRTUAL
```

**Objects from the Classes**

Objects can be created by calls of the form `new(Class, ...)`, where `Class` is the quoted name of the specific class (e.g., "matrix"), and the other arguments, if any, are interpreted as arguments to the corresponding function, e.g., to function `matrix()`. There is no particular advantage over calling those functions directly, unless you are writing software designed to work for multiple classes, perhaps with the class name and the arguments passed in.

Objects created from the classes "matrix" and "array" are unusual, to put it mildly, and have been for some time. Although they may appear to be objects from these classes, they do not have the internal structure of either an S3 or S4 class object. In particular, they have no "class" attribute and are not recognized as objects with classes (that is, both `is.object` and `isS4` will return `FALSE` for such objects). However, methods (both S4 and S3) can be defined for these pseudo-classes and new classes (both S4 and S3) can inherit from them.

That the objects still behave as if they came from the corresponding class (most of the time, anyway) results from special code recognizing such objects being built into the base code of R. For most purposes, treating the classes in the usual way will work, fortunately. One consequence of the special treatment is that these two classes may be used as the data part of an S4 class; for example, you can get away with `contains = "matrix"` in a call to `setGeneric` to create an S4 class that is a subclass of "matrix". There is no guarantee that everything will work perfectly, but a number of classes have been written in this form successfully.

Note that a class containing "matrix" or "array" will have a `.Data` slot with that class. This is the only use of `.Data` other than as a pseudo-class indicating the type of the object. In this case the type of the object will be the type of the contained matrix or array. See `Classes_Details` for a general discussion.

The class "ts" is basically an S3 class that has been registered with S4, using the `setOldClass` mechanism. Versions of R through 2.7.0 treated this class as a pure S4 class, which was in principal a good idea, but in practice did not allow subclasses to be defined and had other intrinsic problems. (For example, setting the "tsp" parameters as a slot often fails because the built-in implementation does not allow the slot to be temporarily inconsistent with the length of the data. Also, the S4 class prevented the correct specification of the S3 inheritance for class "mts".)
StructureClasses

Time-series objects, in contrast to matrices and arrays, have a valid S3 class, "ts", registered using an S4-style definition (see the documentation for setOldClass in the examples section for an abbreviated listing of how this is done). The S3 inheritance of "mts" in package stats is also registered. These classes, as well as "matrix" and "array" should be valid in most examples as superclasses for new S4 class definitions.

All of these classes have special S4 methods for initialize that accept the same arguments as the basic generator functions, matrix, array, and ts, in so far as possible. The limitation is that a class that has more than one non-virtual superclass must accept objects from that superclass in the call to new; therefore, a such a class (what is called a “mixin” in some languages) uses the default method for initialize, with no special arguments.

Extends

The specific classes all extend class "structure", directly, and class "vector", by class "structure".

Methods

coerce  Methods are defined to coerce arbitrary objects to these classes, by calling the corresponding basic function, for example, as(x, "matrix") calls as.matrix(x). If strict = TRUE in the call to as(), the method goes on to delete all other slots and attributes other than the dim and dimnames.

Ops  Group methods (see, e.g., S4groupGeneric) are defined for combinations of structures and vectors (including special cases for array and matrix), implementing the concept of vector structures as in the reference. Essentially, structures combined with vectors retain the structure as long as the resulting object has the same length. Structures combined with other structures remove the structure, since there is no automatic way to determine what should happen to the slots defining the structure.

Note that these methods will be activated when a package is loaded containing a class that inherits from any of the structure classes or class "vector".

References


Chambers, John M. (1998) Programming with Data Springer (For the original S4 version.)


See Also

Class nonStructure, which enforces the alternative model, in which all slots are dropped if any math transformation or operation is applied to an object from a class extending one of the basic classes.

Examples

showClass("structure")

## explore a bit :
showClass("ts")
(ts0 <- new("ts"))
str(ts0)
Description

A set of distinct inherited signatures is generated to test inheritance for all the methods of a specified generic function. If method selection is ambiguous for some of these, a summary of the ambiguities is attached to the returned object. This test should be performed by package authors before releasing a package.

Usage

testInheritedMethods(f, signatures, test = TRUE, virtual = FALSE, groupMethods = TRUE, where = .GlobalEnv)

Arguments

- **f**: a generic function or the character string name of one. By default, all currently defined subclasses of all the method signatures for this generic will be examined. The other arguments are mainly options to modify which inheritance patterns will be examined.
- **signatures**: An optional set of subclass signatures to use instead of the relevant subclasses computed by testInheritedMethods. See the Details for how this is done. This argument might be supplied after a call with test = FALSE, to test selection in batches.
- **test**: optional flag to control whether method selection is actually tested. If FALSE, returns just the list of relevant signatures for subclasses, without calling selectMethod for each signature. If there are a very large number of signatures, you may want to collect the full list and then test them in batches.
- **virtual**: should virtual classes be included in the relevant subclasses. Normally not, since only the classes of actual arguments will trigger the inheritance calculation in a call to the generic function. Including virtual classes may be useful if the class has no current non-virtual subclasses but you anticipate your users may define such classes in the future.
- **groupMethods**: should methods for the group generic function be included?
- **where**: the environment in which to look for class definitions. Nearly always, use the default global environment after attaching all the packages with relevant methods and/or class definitions.

Details

The following description applies when the optional arguments are omitted, the usual case. First, the defining signatures for all methods are computed by calls to findMethodSignatures. From these all the known non-virtual subclasses are found for each class that appears in the signature of some method. These subclasses are split into groups according to which class they inherit from, and only one subclass from each group is retained (for each argument in the generic signature). So if a method was defined with class "vector" for some argument, one actual vector class is chosen arbitrarily. The case of "ANY" is dealt with specially, since all classes extend it. A dummy,
nonvirtual class, ".Other", is used to correspond to all classes that have no superclasses among those being tested.

All combinations of retained subclasses for the arguments in the generic signature are then computed. Each row of the resulting matrix is a signature to be tested by a call to `selectMethod`. To collect information on ambiguous selections, `testInheritedMethods` establishes a calling handler for the special signal "ambiguousMethodSelection", by setting the corresponding option.

**Value**

An object of class "methodSelectionReport". The details of this class are currently subject to change. It has slots "target", "selected", "candidates", and "note", all referring to the ambiguous cases (and so of length 0 if there were none). These slots are intended to be examined by the programmer to detect and preferably fix ambiguous method selections. The object contains in addition slots "generic", the name of the generic function, and "allSelections", giving the vector of labels for all the signatures tested.

**References**


**Examples**

```r
## if no other attached packages have methods for `+` or its group
## generic functions, this returns a 16 by 2 matrix of selection
## patterns (in R 2.9.0)
##
testInheritedMethods("+")
```

---

**TraceClasses** Classes Used Internally to Control Tracing

**Description**

The classes described here are used by the R function `trace` to create versions of functions and methods including browser calls, etc., and also to `untrace` the same objects.

**Usage**

```r
### Objects from the following classes are generated
### by calling trace() on an object from the corresponding
### class without the "WithTrace" in the name.

"functionWithTrace"
"MethodDefinitionWithTrace"
"MethodWithNextWithTrace"
"genericFunctionWithTrace"
"groupGenericFunctionWithTrace"

### the following is a virtual class extended by each of the
```
### classes above

"traceable"

**Objects from the Class**

Objects will be created from these classes by calls to `trace`. (There is an `initialize` method for class "traceable", but you are unlikely to need it directly.)

**Slots**

- `.Data`: The data part, which will be "function" for class "functionWithTrace", and similarly for the other classes.
- `original`: Object of the original class; e.g., "function" for class "functionWithTrace".

**Extends**

Each of the classes extends the corresponding untraced class, from the data part; e.g., "functionWithTrace" extends "function". Each of the specific classes extends "traceable", directly, and class "VIRTUAL", by class "traceable".

**Methods**

The point of the specific classes is that objects generated from them, by function `trace()`, remain callable or dispatchable, in addition to their new trace information.

**See Also**

- function `trace`

---

**validObject**

*Test the Validity of an Object*

**Description**

`validObject()` tests the validity of object related to its class definition; specifically, it checks that all slots specified in the class definition are present and that the object in the slot is from the required class or a subclass of that class.

If the object is valid, `TRUE` is returned; otherwise, an error is generated, reporting all the validity failures encountered. If argument `test` is `TRUE`, the errors are returned as a character vector rather than generating an error.

When an object from a class is initialized, the default method for `initialize()` calls `validObject`.

A class definition may have a validity method, set by a call to the function `setValidity`, in the package or environment that defines the class (or via the validity argument to `setClass`). The method should be a function of one object that returns `TRUE` or a character-string description of the non-validity. If such a method exists, it will be called from `validObject` and any strings from failure will be included in the result or the error message. Any validity methods defined for superclasses (from the `contains=` argument to `setClass`), will also be called.
validObject

Usage

validObject(object, test = FALSE, complete = FALSE)

setValidity(Class, method, where = topenv(parent.frame()) )

getValidity(ClassDef)

Arguments

object any object, but not much will happen unless the object’s class has a formal definition.
test logical; if TRUE and validity fails, the function returns a vector of strings describing the problems. If test is FALSE (the default) validity failure generates an error.
complete logical; if TRUE, validObject is called recursively for each of the slots. The default is FALSE.
Class the name or class definition of the class whose validity method is to be set.
ClassDef a class definition object, as from getClassDef.
method a validity method; that is, either NULL or a function of one argument (object). Like validObject, the function should return TRUE if the object is valid, and one or more descriptive strings if any problems are found. Unlike validObject, it should never generate an error.
where an environment to store the modified class definition. Should be omitted, specifically for calls from a package that defines the class. The definition will be stored in the namespace of the package.

Details

Validity testing takes place ‘bottom up’, checking the slots, then the superclasses, then the object’s own validity method, if there is one.

For each slot and superclass, the existence of the specified class is checked. For each slot, the object in the slot is tested for inheritance from the corresponding class. If complete is TRUE, validObject is called recursively for the object in the slot.

Then, for each of the classes that this class extends (the ‘superclasses’), the explicit validity method of that class is called, if one exists. Finally, the validity method of object’s class is called, if there is one.

Value

validObject returns TRUE if the object is valid. Otherwise a vector of strings describing problems found, except that if test is FALSE, validity failure generates an error, with the corresponding strings in the error message.

Validity methods

A validity method must be a function of one argument; formally, that argument should be named object. If the argument has a different name, setValidity makes the substitution but in obscure cases that might fail, so it’s wiser to name the argument object.

A good method checks all the possible errors and returns a character vector citing all the exceptions found, rather than returning after the first one. validObject will accumulate these errors in its error message or its return value.
Note that validity methods do not have to check validity of superclasses: validObject calls such methods explicitly.

References


See Also

`setClass`, `class`, `classRepresentation`.

Examples

```r
setCode("track",
   slots = c(x="numeric", y = "numeric"))
t1 <- new("track", x=1:10, y=sort(stats::rnorm(10)))
## A valid "track" object has the same number of x, y values
validTrackObject <- function(object) {
   if(length(object@x) == length(object@y)) TRUE
   else paste("Unequal x,y lengths: ", length(object@x), ", ",
              length(object@y), sep="")
}
## assign the function as the validity method for the class
setValidity("track", validTrackObject)
## t1 should be a valid "track" object
validObject(t1)
## Now we do something bad

## This should generate an error
## Not run: try(validObject(t2))

setClass("trackCurve", contains = "track",
   slots = c(smooth = "numeric"))
## all superclass validity methods are used when validObject
## is called from initialize() with arguments, so this fails
## Not run: trynew("trackCurve", t2)

setClass("twoTrack", slots = c(tr1 = "track", tr2 ="track"))
## validity tests are not applied recursively by default,
## so this object is created (invalidly)
tT <- new("twoTrack", tr2 = t2)
## A stricter test detects the problem
## Not run: try(validObject(tT, complete = TRUE))
```
Chapter 8

The parallel package

parallel-package  Support for Parallel Computation

Description

Support for parallel computation, including random-number generation.

Details

This package was first included with R 2.14.0 in 2011.

There is support for multiple RNG streams with the ‘"L’Ecuyer-CMRG’’ RNG: see nextRNGStream.

It contains functionality derived from and pretty much equivalent to that contained in packages multicore (formerly on CRAN, with some low-level functions renamed and not exported) and snow (for socket clusters only, but MPI clusters generated by snow are also supported). There have been many enhancements and bug fixes since 2011.

This package also provides makeForkCluster to create socket clusters by forking (not Windows). For a complete list of exported functions, use library(help = "parallel").

Author(s)

Brian Ripley, Luke Tierney and Simon Urbanek

Maintainer: R Core Team <R-core@r-project.org>

See Also

Parallel computation involves launching worker processes: functions psnice and pskill in package tools provide means to manage such processes.
clusterApply  
Apply Operations using Clusters

Description

These functions provide several ways to parallelize computations using a cluster.

Usage

clusterCall(cl = NULL, fun, ...)
clusterApply(cl = NULL, x, fun, ...)
clusterApplyLB(cl = NULL, x, fun, ...)
clusterEvalQ(cl = NULL, expr)
clusterExport(cl = NULL, varlist, envir = .GlobalEnv)
clusterMap(cl = NULL, Fun, ..., MoreArgs = NULL, RECYCLE = TRUE,
          SIMPLIFY = FALSE, USE.NAMES = TRUE,
          .scheduling = c("static", "dynamic"))
clusterSplit(cl = NULL, seq)
parLapply(cl = NULL, X, fun, ..., chunk.size = NULL)
parSapply(cl = NULL, X, FUN, ..., simplify = TRUE,
          USE.NAMES = TRUE, chunk.size = NULL)
parApply(cl = NULL, X, MARGIN, FUN, ..., chunk.size = NULL)
parCapply(cl = NULL, x, FUN, ..., chunk.size = NULL)
parLapplyLB(cl = NULL, X, fun, ..., chunk.size = NULL)
parSapplyLB(cl = NULL, X, FUN, ..., simplify = TRUE,
            USE.NAMES = TRUE, chunk.size = NULL)

Arguments

cl a cluster object, created by this package or by package snow. If NULL, use the
     registered default cluster.
fun, FUN function or character string naming a function.
expr expression to evaluate.
seq vector to split.
varlist character vector of names of objects to export.
envir environment from which to export variables
x a vector for clusterApply and clusterApplyLB, a matrix for parRapply and
    parCapply.
... additional arguments to pass to fun or FUN: beware of partial matching to earlier
     arguments.
MoreArgs additional arguments for fun.
RECYCLE logical; if true shorter arguments are recycled.
X A vector (atomic or list) for parLapply and parSapply, an array for parApply.
chunk.size scalar number; number of invocations of fun or FUN in one chunk; a chunk is a
     unit for scheduling.
clusterApply

MARGIN vector specifying the dimensions to use.
simplify, USE.NAMES logical; see sapply.
SIMPLIFY logical; see mapply.
.scheduling should tasks be statically allocated to nodes or dynamic load-balancing used?

Details

clusterCall calls a function Fun with identical arguments ... on each node.
clusterEvalQ evaluates a literal expression on each cluster node. It is a parallel version of evalq, and is a convenience function invoking clusterCall.
clusterApply calls fun on the first node with arguments x[[1]] and ..., on the second node with x[[2]] and ..., and so on, recycling nodes as needed.
clusterApplyLB is a load balancing version of clusterApply. If the length n of x is not greater than the number of nodes p, then a job is sent to n nodes. Otherwise the first p jobs are placed in order on the p nodes. When the first job completes, the next job is placed on the node that has become free; this continues until all jobs are complete. Using clusterApplyLB can result in better cluster utilization than using clusterApply, but increased communication can reduce performance. Furthermore, the node that executes a particular job is non-deterministic. This means that simulations that assign RNG streams to nodes will not be reproducible.
clusterMap is a multi-argument version of clusterApply, analogous to mapply and Map. If RECYCLE is true shorter arguments are recycled (and either none or all must be of length zero); otherwise, the result length is the length of the shortest argument. Nodes are recycled if the length of the result is greater than the number of nodes. (mapply always uses RECYCLE = TRUE, and has argument SIMPLIFY = TRUE. Map always uses RECYCLE = TRUE.)
clusterExport assigns the values on the master R process of the variables named in varlist to variables of the same names in the global environment (aka 'workspace') of each node. The environment on the master from which variables are exported defaults to the global environment.
clusterSplit splits seq into a consecutive piece for each cluster and returns the result as a list with length equal to the number of nodes. Currently the pieces are chosen to be close to equal in length: the computation is done on the master.
parLapply, parSapply, and parApply are parallel versions of lapply, sapply and apply. Chunks of computation are statically allocated to nodes using clusterApply. By default, the number of chunks is the same as the number of nodes. parLapplyLB, parSapplyLB are load-balancing versions, intended for use when applying FUN to different elements of X takes quite variable amounts of time, and either the function is deterministic or reproducible results are not required. Chunks of computation are allocated dynamically to nodes using clusterApplyLB. From R 3.5.0, the default number of chunks is twice the number of nodes. Before R 3.5.0, the (fixed) number of chunks was the same as the number of nodes. As for clusterApplyLB, with load balancing the node that executes a particular job is non-deterministic and simulations that assign RNG streams to nodes will not be reproducible.
parRapply and parCapply are parallel row and column apply functions for a matrix x; they may be slightly more efficient than parApply but do less post-processing of the result.
A chunk size of 0 with static scheduling uses the default (one chunk per node). With dynamic scheduling, chunk size of 0 has the same effect as 1 (one invocation of FUN/fun per chunk).

Value

For clusterCall, clusterEvalQ and clusterSplit, a list with one element per node.
For `clusterApply` and `clusterApplyLB`, a list the same length as \( x \).

`clusterMap` follows `mapply`.

`clusterExport` returns nothing.

`parLapply` returns a list the length of \( X \).

`parSapply` and `parApply` follow `sapply` and `apply` respectively.

`parRapply` and `parCapply` always return a vector. If \( \text{FUN} \) always returns a scalar result this will be of length the number of rows or columns; otherwise it will be the concatenation of the returned values.

An error is signalled on the master if any of the workers produces an error.

**Note**

These functions are almost identical to those in package `snow`.

Two exceptions: `parLapply` has argument \( X \) not \( x \) for consistency with `lapply`, and `parSapply` has been updated to match `sapply`.

**Author(s)**

Luke Tierney and R Core.

Derived from the `snow` package.

**Examples**

```r
## Use option cl.cores to choose an appropriate cluster size.
cl <- makeCluster(getOption("cl.cores", 2))

clusterApply(cl, 1:2, get("+"), 3)
xx <- 1
clusterExport(cl, "xx")
clusterCall(cl, function(y) xx + y, 2)

## Use clusterMap like an mapply example
clusterMap(cl, function(x, y) seq_len(x) + y,
    c(a = 1, b = 2, c = 3), c(A = 10, B = 0, C = -10))

parSapply(cl, 1:20, get("+"), 3)
## A bootstrapping example, which can be done in many ways:
clusterEvalQ(cl, {
    ## set up each worker. Could also use clusterExport()
    library(boot)
    cd4.rg <- function(data, mle) MASS::mvrnorm(nrow(data), mle$m, mle$v)
    cd4.mle <- list(m = colMeans(cd4), v = var(cd4))
    NULL
  })
res <- clusterEvalQ(cl, boot(cd4, corr, R = 100,
    sim = "parametric", ran.gen = cd4.rg, mle = cd4.mle))
library(boot)
cd4.boot <- do.call(c, res)
boot.ci(cd4.boot, type = c("norm", "basic", "perc"),
    conf = 0.9, h = atanh, hinv = tanh)
stopCluster(cl)
```
## or
library(boot)
run1 <- function(...) {
  library(boot)
  cd4.rg <- function(data, mle) MASS::mvrnorm(nrow(data), mle$m, mle$v)
  cd4.mle <- list(m = colMeans(cd4), v = var(cd4))
  boot(cd4, corr, R = 500, sim = "parametric",
       ran.gen = cd4.rg, mle = cd4.mle)
}
cl <- makeCluster(mc <- getOption("cl.cores", 2))
## to make this reproducible
clusterSetRNGStream(cl, 123)
cd4.boot <- do.call(c, parLapply(cl, seq_len(mc), run1))
boot.ci(cd4.boot, type = c("norm", "basic", "perc"),
        conf = 0.9, h = atanh, hinv = tanh)
stopCluster(cl)

### detectCores

Detect the Number of CPU Cores

detectCores

**Description**

Attempt to detect the number of CPU cores on the current host.

**Usage**

detectCores(all.tests = FALSE, logical = TRUE)

**Arguments**

- `all.tests` Logical: if true apply all known tests.
- `logical` Logical: if possible, use the number of physical CPUs/cores (if FALSE) or logical CPUs (if TRUE). Currently this is honoured only on macOS, Solaris and Windows.

**Details**

This attempts to detect the number of available CPU cores.

It has methods to do so for Linux, macOS, FreeBSD, OpenBSD, Solaris and Windows. `detectCores(TRUE)` could be tried on other Unix-alike systems.

**Value**

An integer, NA if the answer is unknown.

Exactly what this represents is OS-dependent: where possible by default it counts logical (e.g., hyperthreaded) CPUs and not physical cores or packages.

Under macOS there is a further distinction between ‘available in the current power management mode’ and ‘could be available this boot’, and this function returns the first.

On Sparc Solaris `logical = FALSE` returns the number of physical cores and `logical = TRUE` returns the number of available hardware threads. (Some Sparc CPUs have multiple cores per CPU,
others have multiple threads per core and some have both.) For example, the UltraSparc T2 CPU in the former CRAN check server was a single physical CPU with 8 cores, and each core supports 8 hardware threads. So `detectCores(logical = FALSE)` returns 8, and `detectCores(logical = TRUE)` returns 64.

Where virtual machines are in use, one would hope that the result for `logical = TRUE` represents the number of CPUs available (or potentially available) to that particular VM.

Note

This is not suitable for use directly for the `mc.cores` argument of `mclapply` nor specifying the number of cores in `makeCluster`. First because it may return `NA`, second because it does not give the number of allowed cores, and third because on Sparc Solaris and some Windows boxes it is not reasonable to try to use all the logical CPUs at once.

Author(s)

Simon Urbanek and Brian Ripley

Examples

detectCores()

detectCores(logical = FALSE)

makeCluster

Create a Parallel Socket Cluster

Description

Creates a set of copies of \texttt{R} running in parallel and communicating over sockets.

Usage

```r
makeCluster(spec, type, ...)
makePSOCKcluster(names, ...)
makeForkCluster(nnodes = getOption("mc.cores", 2L), ...)
stopCluster(cl = NULL)
setDefaultCluster(cl = NULL)
getDefaultCluster()
```

Arguments

- `spec` A specification appropriate to the type of cluster.
- `names` Either a character vector of host names on which to run the worker copies of \texttt{R}, or a positive integer (in which case that number of copies is run on ‘localhost’).
- `nnodes` The number of nodes to be forked.
- `type` One of the supported types: see ‘Details’.
- `...` Options to be passed to the function spawning the workers. See ‘Details’.
- `cl` an object of class "cluster".
Details

makeCluster creates a cluster of one of the supported types. The default type, "PSOCK", calls makePSOCKcluster. Type "FORK" calls makeForkCluster. Other types are passed to package snow.

makePSOCKcluster is an enhanced version of makeSOCKcluster in package snow. It runs Rscript on the specified host(s) to set up a worker process which listens on a socket for expressions to evaluate, and returns the results (as serialized objects).

makeForkCluster is merely a stub on Windows. On Unix-alike platforms it creates the worker process by forking.

The workers are most often running on the same host as the master, when no options need be set. Several options are supported (mainly for makePSOCKcluster):

- **master** The host name of the master, as known to the workers. This may not be the same as it is known to the master, and on private subnets it may be necessary to specify this as a numeric IP address. For example, macOS is likely to detect a machine as ‘somename.local’, a name known only to itself.

- **port** The port number for the socket connection, default taken from the environment variable R_PARALLEL_PORT, then a randomly chosen port in the range 11000:11999.

- **timeout** The timeout in seconds for that port. This is the maximum time of zero communication between master and worker before failing. Default is 30 days (and the POSIX standard only requires values up to 31 days to be supported).

- **setup_timeout** The maximum number of seconds a worker attempts to connect to master before failing. Default is 2 minutes. The waiting time before the next attempt starts at 0.1 seconds and is incremented 50% after each retry.

- **outfile** Where to direct the stdout and stderr connection output from the workers. "" indicates no redirection (which may only be useful for workers on the local machine). Defaults to ‘/dev/null’ (‘nul:’ on Windows). The other possibility is a file path on the worker’s host. Files will be opened in append mode, as all workers log to the same file.

- **homogeneous** Logical, default true. See ‘Note’.

- **rscript** Character vector of additional arguments for Rscript such as ‘--no-environ’.

- **renice** A numerical ‘niceness’ to set for the worker processes, e.g. 15 for a low priority. OS-dependent: see psnice for details.

- **rshcmd** The command to be run on the master to launch a process on another host. Defaults to ssh.

- **user** The user name to be used when communicating with another host.

- **manual** Logical. If true the workers will need to be run manually.

- **methods** Logical. If true (default) the workers will load the methods package: not loading it saves ca 30% of the startup CPU time of the cluster.

- **useXDR** Logical. If true (default) serialization will use XDR: where large amounts of data are to be transferred and all the nodes are little-endian, communication may be substantially faster if this is set to false.

- **setup_strategy** Character. If "parallel" (default) workers will be started in parallel during cluster setup when this is possible, which is now for homogeneous "PSOCK" clusters with all workers started automatically (manual = FALSE) on the local machine. Workers will be started sequentially on other clusters, on all clusters with setup_strategy = "sequential" and on R 3.6.0 and older. This option is for expert use only (e.g. debugging) and may be removed in future versions of R.
Function `makeForkCluster` creates a socket cluster by forking (and hence is not available on Windows). It supports options `port`, `timeout` and `outfile`, and always uses `useXDR = FALSE`. It is strongly discouraged to use the "FORK" cluster with GUI front-ends or multi-threaded libraries. See `mcfork` for details.

It is good practice to shut down the workers by calling `stopCluster`: however the workers will terminate themselves once the socket on which they are listening for commands becomes unavailable, which it should if the master R session is completed (or its process dies).

Function `setDefaultCluster` registers a cluster as the default one for the current session. Using `setDefaultCluster(NULL)` removes the registered cluster, as does stopping that cluster.

**Value**

For the cluster creators, an object of class c("SOCKcluster", "cluster").

For the default cluster setter and getter, the registered default cluster or NULL if there is no such cluster.

**Note**

Option `homogeneous = TRUE` was for years documented as ‘Are all the hosts running identical set-ups?’, but this was apparently more restrictive than its author intended and not required by the code.

The current interpretation of `homogeneous = TRUE` is that `Rscript` can be launched using the same path on each worker. That path is given by the option `rscript` and defaults to the full path to `Rscript` on the master. (The workers are not required to be running the same version of R as the master, nor even as each other.)

For `homogeneous = FALSE`, `Rscript` on the workers is found on their default shell’s path.

For the very common usage of running both master and worker on a single multi-core host, the default settings are the appropriate ones.

**Author(s)**

Luke Tierney and R Core.

Derived from the `snow` package.
mcchildren

Details

mcaffinity can be used to obtain (affinity = NULL) or set the CPU affinity mask of the current process. The affinity mask is a list of integer CPU identifiers (starting from 1) that this process is allowed to run on. Not all systems provide user access to the process CPU affinity, in cases where no support is present at all mcaffinity() will return NULL. Some systems may take into account only the number of CPUs present in the mask.

Typically, it is legal to specify larger set than the number of logical CPUs (but at most as many as the OS can handle) and the system will return back the actually present set.

Value

NULL if CPU affinity is not supported by the system or an integer vector with the set of CPUs in the active affinity mask for this process (this may be different than affinity).

Author(s)

Simon Urbanek.

See Also

mcparallel

Low-level Functions for Management of Forked Processes

Description

These are low-level support functions for the forking approach.

They are not available on Windows, and not exported from the namespace.

Usage

children(select)
readChild(child)
readChildren(timeout = 0)
selectChildren(children = NULL, timeout = 0)
sendTime(child, what)
sendMaster(what, raw.asis = TRUE)
mckill(process, signal = 2L)

mcchildren

Arguments

select if omitted, all active children are returned, otherwise select should be a list of processes and only those from the list that are active will be returned.

child child process (object of the class "childProcess") or a process ID (pid). See also ‘Details’.

timeout timeout (in seconds, fractions supported) to wait for a response before giving up.
**children**

A list of child processes or a single child process object or a vector of process IDs or NULL. If NULL behaves as if all currently known children were supplied.

**what**

For `sendChildStdin`:
- Character or raw vector. In the former case elements are collapsed using the newline character. (But no trailing newline is added at the end!)
- For `sendMaster`:
  - Data to send to the master process. If what is not a raw vector, it will be serialized into a raw vector. Do NOT send an empty raw vector – that is reserved for internal use.

**raw.asis**

Logical, if TRUE and what is a raw vector then it is sent directly as-is to the master (default, suitable for arbitrary payload passing), otherwise raw vectors are serialized before sending just as any other objects (suitable for passing evaluation results).

**process**

Process (object of the class `process`) or a process ID (pid)

**signal**

integer: signal to send. Values of 2 (SIGINT), 9 (SIGKILL) and 15 (SIGTERM) are pretty much portable, but for maximal portability use `tools::SIGTERM` and so on.

**Details**

- `children` returns currently active children.
- `readChild` reads data (sent by `sendMaster`) from a given child process.
- `selectChildren` checks children for available data.
- `readChildren` checks all children for available data and reads from the first child that has available data.
- `sendChildStdin` sends a string (or data) to one or more child’s standard input. Note that if the master session was interactive, it will also be echoed on the standard output of the master process (unless disabled). The function is vector-compatible, so you can specify `child` as a list or a vector of process IDs.
- `sendMaster` sends data from the child to the master process.
- `mckill` sends a signal to a child process: it is equivalent to `pskill` in package `tools`.

**Value**

- `children` returns a (possibly empty) list of objects of class "process", the process ID.
- `readChild` and `readChildren` return a raw vector with a "pid" attribute if data were available, an integer vector of length one with the process ID if a child terminated or NULL if the child no longer exists (no children at all for `readChildren`).
- `selectChildren` returns TRUE is the timeout was reached, FALSE if an error occurred (e.g., if the master process was interrupted) or an integer vector of process IDs with children that have data available, or NULL if there are no children.
- `sendChildStdin` returns a vector of TRUE values (one for each member of `child`) or throws an error.
- `sendMaster` returns TRUE or throws an error.
- `mckill` returns TRUE.
Warning

This is a very low-level interface for expert use only: it not regarded as part of the \texttt{R} API and subject to change without notice.

\texttt{sendMaster}, \texttt{readChild} and \texttt{sendChildStdin} did not support long vectors prior to \texttt{R} 3.4.0 and so were limited to \(2^{31} - 1\) bytes (and still are on 32-bit platforms).

Author(s)

Simon Urbanek and R Core.

Derived from the \texttt{multicore} package formerly on CRAN.

See Also

\texttt{mcfork, sendMaster, mcparallel}

Examples

\begin{verbatim}
## Not run:
  p <- mcparallel(scan(n = 1, quiet = TRUE))
  sendChildStdin(p, "17.4\n")
  mccollect(p)[[1]]

## End(Not run)
\end{verbatim}

\emph{mcfork} \hspace{1cm} \textit{Fork a Copy of the Current R Process}

Description

These are low-level functions, not available on Windows, and not exported from the namespace. \texttt{mcfork} creates a new child process as a copy of the current \texttt{R} process. \texttt{mcexit} closes the current child process, informing the master process as necessary.

Usage

\begin{verbatim}
mcfork(estranged = FALSE)
mcexit(exit.code = 0L, send = NULL)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{estranged} logical, if \texttt{TRUE} then the new process has no ties to the parent process, will not show in the list of children and will not be killed on exit.
  \item \texttt{exit.code} process exit code. By convention \texttt{0L} signifies a clean exit, \texttt{1L} an error.
  \item \texttt{send} if not \texttt{NULL} send this data before exiting (equivalent to using \texttt{sendMaster}).
\end{itemize}
Details

The `mcfork` function provides an interface to the `fork` system call. In addition it sets up a pipe between the master and child process that can be used to send data from the child process to the master (see `sendMaster`) and child's 'stdin' is re-mapped to another pipe held by the master process (see `sendChildStdin`).

If you are not familiar with the `fork` system call, do not use this function directly as it leads to very complex inter-process interactions amongst the R processes involved.

In a nutshell `fork` spawns a copy (child) of the current process, that can work in parallel to the master (parent) process. At the point of forking both processes share exactly the same state including the workspace, global options, loaded packages etc. Forking is relatively cheap in modern operating systems and no real copy of the used memory is created, instead both processes share the same memory and only modified parts are copied. This makes `mcfork` an ideal tool for parallel processing since there is no need to setup the parallel working environment, data and code is shared automatically from the start.

`mcexit` is to be run in the child process. It sends `send` to the master (unless `NULL`) and then shuts down the child process. The child can also be shut down by sending it the signal `SIGUSR1`, as is done by the unexported function `parallel::rmChild`.

Value

`mcfork` returns an object of the class "childProcess" to the master and of class "masterProcess" to the child: both the classes inherit from class "process". If `estranged` is set to `TRUE` then the child process will be of the class "estrangedProcess" and cannot communicate with the master process nor will it show up on the list of children. These are lists with components `pid` (the process id of the other process) and a vector `fd` of the two file descriptor numbers for ends in the current process of the inter-process pipes.

`mcexit` never returns.

GUI/embedded environments

It is strongly discouraged to use `mcfork` and the higher-level functions which rely on it (e.g., `mcparallel`, `mclapply` and `pvec`) in GUI or embedded environments, because it leads to several processes sharing the same GUI which will likely cause chaos (and possibly crashes). Child processes should never use on-screen graphics devices. Some precautions have been taken to make this usable in R.app on macOS, but users of third-party front-ends should consult their documentation.

This can also apply to other connections (e.g., to an X server) created before forking, and to files opened by e.g. graphics devices.

Note that `tktk` counts as a GUI for these purposes since Tk1 runs an event loop. That event loop is inhibited in a child process but there could still be problems with Tk graphical connections.

It is strongly discouraged to use `mcfork` and the higher-level functions in any multi-threaded R process (with additional threads created by a third-party library or package). Such use can lead to deadlocks or crashes, because the child process created by `mcfork` may not be able to access resources locked in the parent or may see an inconsistent version of global data (`mcfork` runs system call `fork` without `exec`).

If in doubt, it is safer to use a non-FORK cluster (see `makeCluster`, `clusterApply`).

Warning

This is a very low-level API for expert use only.
mclapply

Description

mclapply is a parallelized version of lapply, it returns a list of the same length as X, each element of which is the result of applying FUN to the corresponding element of X.

It relies on forking and hence is not available on Windows unless mc.cores = 1.

mcmapply is a parallelized version of mapply, and mcMap corresponds to Map.

Usage

mclapply(X, FUN, ..., mc.preschedule = TRUE, mc.set.seed = TRUE, mc.silent = FALSE, mc.cores = getOption("mc.cores", 2L), mc.cleanup = TRUE, mc.allow.recursive = TRUE, affinity.list = NULL)
mcmapply(FUN, ..., MoreArgs = NULL, SIMPLIFY = TRUE, USE.NAMES = TRUE, mc.preschedule = TRUE, mc.set.seed = TRUE, mc.silent = FALSE, mc.cores = getOption("mc.cores", 2L), mc.cleanup = TRUE, affinity.list = NULL)
mcMap(f, ...)

Arguments

X a vector (atomic or list) or an expressions vector. Other objects (including classed objects) will be coerced by as.list.

FUN the function to be applied to (mclapply) each element of X or (mcmapply) in parallel to ....
the function to be applied in parallel to...

For mclapply, optional arguments to FUN. For mcapply and mcMap, vector or list inputs: see mapply.

MoreArgs, SIMPLIFY, USE.NAMES see mapply.

mc.preschedule if set to TRUE then the computation is first divided to (at most) as many jobs are there are cores and then the jobs are started, each job possibly covering more than one value. If set to FALSE then one job is for each value of X. The former is better for short computations or large number of values in X, the latter is better for jobs that have high variance of completion time and not too many values of X compared to mc.cores.

mc.set.seed See mcparallel.

mc.silent if set to TRUE then all output on 'stdout' will be suppressed for all parallel processes forked ('stderr' is not affected).

mc.cores The number of cores to use, i.e. at most how many child processes will be run simultaneously. The option is initialized from environment variable MC_CORES if set. Must be at least one, and parallelization requires at least two cores.

mc.cleanup if set to TRUE then all children that have been forked by this function will be killed (by sending SIGTERM) before this function returns. Under normal circumstances mclapply waits for the children to deliver results, so this option usually has only effect when mclapply is interrupted. If set to FALSE then child processes are collected, but not forcefully terminated. As a special case this argument can be set to the number of the signal that should be used to kill the children instead of SIGTERM.

mc.allow.recursive Unless true, calling mclapply in a child process will use the child and not fork again.

affinity.list a vector (atomic or list) containing the CPU affinity mask for each element of X. The CPU affinity mask describes on which CPU (core or hyperthread unit) a given item is allowed to run, see mcaffinity. To use this parameter prescheduling has to be deactivated (mc.preschedule = FALSE).

Details

mclapply is a parallelized version of lapply, provided mc.cores > 1: for mc.cores == 1 (and the affinity.list is NULL) it simply calls lapply.

By default (mc.preschedule = TRUE) the input X is split into as many parts as there are cores (currently the values are spread across the cores sequentially, i.e. first value to core 1, second to core 2, ...(core + 1)-th value to core 1 etc.) and then one process is for each core and the results are collected.

Without prescheduling, a separate job is for each value of X. To ensure that no more than mc.cores jobs are running at once, once that number has been forked the master process waits for a child to complete before the next fork.

Due to the parallel nature of the execution random numbers are not sequential (in the random number sequence) as they would be when using lapply. They are sequential for each forked process, but not all jobs as a whole. See mcparallel or the package’s vignette for ways to make the results reproducible with mc.preschedule = TRUE.

Note: the number of file descriptors (and processes) is usually limited by the operating system, so you may have trouble using more than 100 cores or so (see ulimit -n or similar in your OS
documentation) unless you raise the limit of permissible open file descriptors (fork will fail with error "unable to create a pipe").

Prior to R 3.4.0 and on a 32-bit platform, the serialized result from each forked process is limited to $2^{31} - 1$ bytes. (Returning very large results via serialization is inefficient and should be avoided.)

affinity.list can be used to run elements of X on specific CPUs. This can be helpful, if elements of X have a high variance of completion time or if the hardware architecture is heterogeneous. It also enables the development of scheduling strategies for optimizing the overall runtime of parallel jobs. If affinity.list is set, the mc.core parameter is replaced with the number of CPU ids used in the affinity masks.

Value

For mclapply, a list of the same length as X and named by X.

For mcmapply, a list, vector or array: see mapply.

For mcMap, a list.

Each forked process runs its job inside try(..., silent = TRUE) so if errors occur they will be stored as class "try-error" objects in the return value and a warning will be given. Note that the job will typically involve more than one value of X and hence a "try-error" object will be returned for all the values involved in the failure, even if not all of them failed. If any forked process is killed or fails to deliver a result for any reason, values involved in the failure will be NULL. To allow detection of such errors, FUN should not return NULL. As of R 4.0, the return value of mcmapply is always a list when it needs to contain "try-error" objects (SIMPLIFY is overridden to FALSE).

Warning

It is strongly discouraged to use these functions in GUI or embedded environments, because it leads to several processes sharing the same GUI which will likely cause chaos (and possibly crashes). Child processes should never use on-screen graphics devices.

Some precautions have been taken to make this usable in R.app on macOS, but users of third-party front-ends should consult their documentation.

Note that tcltk counts as a GUI for these purposes since Tcl runs an event loop. That event loop is inhibited in a child process but there could still be problems with Tk graphical connections.

It is strongly discouraged to use these functions with multi-threaded libraries or packages (see mcfork for more details). If in doubt, it is safer to use a non-FORK cluster (see makeCluster, clusterApply).

Author(s)

Simon Urbanek and R Core. The affinity.list feature by Helena Kotthaus and Andreas Lang, TU Dortmund. Derived from the multicore package formerly on CRAN.

See Also

mcparallel, pvec, parLapply, clusterMap.

simplify2array for results like sapply.
Examples

```r
simplify2array(mclapply(rep(4, 5), rnorm))
# use the same random numbers for all values
set.seed(1)

simplify2array(mclapply(rep(4, 5), rnorm, mc.preschedule = FALSE,
                         mc.set.seed = FALSE))

## Contrast this with the examples for clusterCall
library(boot)

cd4.rg <- function(data, mle) MASS::mvrnorm(nrow(data), mle$m, mle$v)
cd4.mle <- list(m = colMeans(cd4), v = var(cd4))
mc <- getOption("mc.cores", 2)
run1 <- function(...) boot(cd4, corr, R = 500, sim = "parametric",
                          ran.gen = cd4.rg, mle = cd4.mle)

## To make this reproducible:
set.seed(123, "L'Ecuyer")

cd4.boot <- do.call(c, res)

boot.ci(cd4.boot, type = c("norm", "basic", "perc"),
        conf = 0.9, h = atanh, hinv = tanh)
```

```r
## Usage of the affinity.list parameter
A <- runif(2500000, 0, 100)
B <- runif(2500000, 0, 100)
C <- runif(5000000, 0, 100)
first <- function(i) head(sort(i), n = 1)

# Restrict all elements of X to run on CPU 1 and 2
affL <- list(c(1,2), c(1,2), c(1,2))
mclapply(list(A, A, A), first, mc.preschedule = FALSE, affinity.list = affL)

# Completion times are assumed to have a high variance
# To optimize the overall execution time elements of X are scheduled to suitable CPUs
# Assuming that the runtime for C is as long as the runtime of A plus B
# mapping: A to 1, B to 1, C to 2
X <- list(A, B, C)
affL <- c(1, 1, 2)
mclapply(X, first, mc.preschedule = FALSE, affinity.list = affL)
```

**mcp**arelle

Evaluate an \texttt{R} Expression Asynchronously in a Separate Process

**Description**

These functions are based on forking and so are not available on Windows.

\texttt{mcp}arallel starts a parallel \texttt{R} process which evaluates the given expression.

\texttt{mcc}ollect collects results from one or more parallel processes.
Usage

mcparallel(expr, name, mc.set.seed = TRUE, silent = FALSE,
mc.affinity = NULL, mc.interactive = FALSE,
detached = FALSE)

mccollect(jobs, wait = TRUE, timeout = 0, intermediate = FALSE)

Arguments

expr  expression to evaluate (do not use any on-screen devices or GUI elements in this code, see mcfork for the inadvisability of using mcparallel with GUI front-ends and multi-threaded libraries). Raw vectors are reserved for internal use and cannot be returned, but the expression may evaluate e.g. to a list holding a raw vector. NULL should not be returned because it is used by mccollect to signal an error.

name  an optional name (character vector of length one) that can be associated with the job.

mc.set.seed  logical: see section ‘Random numbers’.

silent  if set to TRUE then all output on stdout will be suppressed (stderr is not affected).

mc.affinity  either a numeric vector specifying CPUs to restrict the child process to (1-based) or NULL to not modify the CPU affinity

mc.interactive  logical, if TRUE or FALSE then the child process will be set as interactive or non-interactive respectively. If NA then the child process will inherit the interactive flag from the parent.

detached  logical, if TRUE then the job is detached from the current session and cannot deliver any results back - it is used for the code side-effect only.

jobs  list of jobs (or a single job) to collect results for. Alternatively jobs can also be an integer vector of process IDs. If omitted collect will wait for all currently existing children.

wait  if set to FALSE it checks for any results that are available within timeout seconds from now, otherwise it waits for all specified jobs to finish.

timeout  timeout (in seconds) to check for job results – applies only if wait is FALSE.

intermediate  FALSE or a function which will be called while collect waits for results. The function will be called with one parameter which is the list of results received so far.

Details

mcparallel evaluates the expr expression in parallel to the current R process. Everything is shared read-only (or in fact copy-on-write) between the parallel process and the current process, i.e. no side-effects of the expression affect the main process. The result of the parallel execution can be collected using mccollect function.

mccollect function collects any available results from parallel jobs (or in fact any child process). If wait is TRUE then collect waits for all specified jobs to finish before returning a list containing the last reported result for each job. If wait is FALSE then mccollect merely checks for any results available at the moment and will not wait for jobs to finish. If jobs is specified, jobs not listed there will not be affected or acted upon.

Note: If expr uses low-level multicore functions such as sendMaster a single job can deliver results multiple times and it is the responsibility of the user to interpret them correctly. mccollect will
return NULL for a terminating job that has sent its results already after which the job is no longer available.

Jobs are identified by process IDs (even when referred to as job objects), which are reused by the operating system. Detached jobs created by mcparallel can thus never be safely referred to by their process IDs nor job objects. Non-detached jobs are guaranteed to exist until collected by mccollect, even if crashed or terminated by a signal. Once collected by mccollect, a job is regarded as detached, and thus must no longer be referred to by its process ID nor its job object. With wait = TRUE, all jobs passed to mccollect are collected. With wait = FALSE, the collected jobs are given as names of the result vector, and thus in subsequent calls to mccollect these jobs must be excluded. Job objects should be used in preference of process IDs whenever accepted by the API.

The mc.affinity parameter can be used to try to restrict the child process to specific CPUs. The availability and the extent of this feature is system-dependent (e.g., some systems will only consider the CPU count, others will ignore it completely).

Value

mcparallel returns an object of the class "parallelJob" which inherits from "childProcess" (see the ‘Value’ section of the help for mcfork). If argument name was supplied this will have an additional component name.

mccollect returns any results that are available in a list. The results will have the same order as the specified jobs. If there are multiple jobs and a job has a name it will be used to name the result, otherwise its process ID will be used. If none of the specified children are still running, it returns NULL.

Random numbers

If mc.set.seed = FALSE, the child process has the same initial random number generator (RNG) state as the current R session. If the RNG has been used (or .Random.seed was restored from a saved workspace), the child will start drawing random numbers at the same point as the current session. If the RNG has not yet been used, the child will set a seed based on the time and process ID when it first uses the RNG: this is pretty much guaranteed to give a different random-number stream from the current session and any other child process.

The behaviour with mc.set.seed = TRUE is different only if RNGkind("L'Ecuyer-CMRG") has been selected. Then each time a child is forked it is given the next stream (see nextRNGStream). So if you select that generator, set a seed and call mc.reset.stream just before the first use of mcparallel the results of simulations will be reproducible provided the same tasks are given to the first, second, ...forked process.

Note

Prior to R 3.4.0 and on a 32-bit platform, the serialized result from each forked process is limited to $2^{31} - 1$ bytes. (Returning very large results via serialization is inefficient and should be avoided.)

Author(s)

Simon Urbanek and R Core.

Derived from the multicore package formerly on CRAN. (but with different handling of the RNG stream).

See Also

pvec, mclapply
Examples

```r
p <- mcparallel(1:10)
q <- mcparallel(1:20)
# wait for both jobs to finish and collect all results
res <- mccollect(list(p, q))
```

## IGNORE_RDIFF_BEGIN
## reports process ids, so not reproducible
```
p <- mcparallel(1:10)
mccollect(p, wait = FALSE, 10) # will retrieve the result (since it's fast)
mccollect(p, wait = FALSE) # will signal the job as terminating
mccollect(p, wait = FALSE) # there is no longer such a job
## IGNORE_RDIFF_END
```

# a naive parallel lapply can be created using mcparallel alone:
```r
jobs <- lapply(1:10, function(x) mcparallel(rnorm(x), name = x))
mccollect(jobs)
```

---

**pvec**

*Parallelize a Vector Map Function using Forking*

**Description**

*pvec* parallelizes the execution of a function on vector elements by splitting the vector and submitting each part to one core. The function must be a vectorized map, i.e. it takes a vector input and creates a vector output of exactly the same length as the input which doesn’t depend on the partition of the vector.

It relies on forking and hence is not available on Windows unless `mc.cores = 1`.

**Usage**

```r
pvec(v, FUN, ..., mc.set.seed = TRUE, mc.silent = FALSE,
     mc.cores = getOption("mc.cores", 2L), mc.cleanup = TRUE)
```

**Arguments**

- `v` vector to operate on
- `FUN` function to call on each part of the vector
- `...` any further arguments passed to `FUN` after the vector
- `mc.set.seed` See `mcparallel`.
- `mc.silent` if set to `TRUE` then all output on ‘stdout’ will be suppressed for all parallel processes forked (‘stderr’ is not affected).
- `mc.cores` The number of cores to use, i.e. at most how many child processes will be run simultaneously. Must be at least one, and at least two for parallel operation. The option is initialized from environment variable `MC_CORES` if set.
- `mc.cleanup` See the description of this argument in `mclapply`. 
Details

`pvec` parallelizes `FUN(x, ...)` where `FUN` is a function that returns a vector of the same length as `x`. `FUN` must also be pure (i.e., without side-effects) since side-effects are not collected from the parallel processes. The vector is split into nearly identically sized subvectors on which `FUN` is run. Although it is in principle possible to use functions that are not necessarily maps, the interpretation would be case-specific as the splitting is in theory arbitrary (a warning is given in such cases).

The major difference between `pvec` and `mclapply` is that `mclapply` will run `FUN` on each element separately whereas `pvec` assumes that `c(FUN(x[1]), FUN(x[2]))` is equivalent to `FUN(x[1:2])` and thus will split into as many calls to `FUN` as there are cores (or elements, if fewer), each handling a subset vector. This makes it more efficient than `mclapply` but requires the above assumption on `FUN`.

If `mc.cores == 1` this evaluates `FUN(v, ...)` in the current process.

Value

The result of the computation – in a successful case it should be of the same length as `v`. If an error occurred or the function was not a map the result may be shorter or longer, and a warning is given.

Note

Due to the nature of the parallelization, error handling does not follow the usual rules since errors will be returned as strings and results from killed child processes will show up simply as non-existent data. Therefore it is the responsibility of the user to check the length of the result to make sure it is of the correct size. `pvec` raises a warning if that is the case since it does not know whether such an outcome is intentional or not.

See `mcfork` for the inadvisability of using this with GUI front-ends and multi-threaded libraries.

Author(s)

Simon Urbanek and R Core.

Derived from the `multicore` package formerly on CRAN.

See Also

`mcparallel, mclapply, parLapply, clusterMap`.

Examples

```r
x <- pvec(1:1000, sqrt)
stopifnot(all(x == sqrt(1:1000)))
```

# One use is to convert date strings to unix time in large datasets
# as that is a relatively slow operation.
# So let's get some random dates first
# (A small test only with 2 cores: set options("mc.cores")
# and increase N for a larger-scale test.)
N <- 1e5
dates <- sprintf('%04d-%02d-%02d', as.integer(2000+runif(N)),
                 as.integer(runif(N, 1, 12)), as.integer(runif(N, 1, 28)))

system.time(a <- as.POSIXct(dates))
```
<p># But specifying the format is faster
system.time(a <- as.POSIXct(dates, format = "%Y-%m-%d"))
</p>

<p># pvec ought to be faster, but system overhead can be high
system.time(b <- pvec(dates, as.POSIXct, format = "%Y-%m-%d"))
stopifnot(all(a == b))
</p>

<p># using mclapply for this would much slower because each value
# will require a separate call to as.POSIXct()
# as lapply(dates, as.POSIXct) does
system.time(c <- unlist(mclapply(dates, as.POSIXct, format = "%Y-%m-%d")))
stopifnot(all(a == c))
</p>

---

### RNGstreams

**Implementation of Pierre L'Ecuyer's RngStreams**

#### Description

This is an R re-implementation of Pierre L'Ecuyer's 'RngStreams' multiple streams of pseudo-random numbers.

#### Usage

- `nextRNGStream(seed)`
- `nextRNGSubStream(seed)`
- `clusterSetRNGStream(cl = NULL, iseed)`
- `mc.reset.stream()`

#### Arguments

- **seed**: An integer vector of length 7 as given by `.Random.seed` when the "L'Ecuyer-CMRG" RNG is in use. See `RNG` for the valid values.
- **cl**: A cluster from this package or package `snow`, or (if `NULL`) the registered cluster.
- **iseed**: An integer to be supplied to `set.seed`, or `NULL` not to set reproducible seeds.

#### Details

The 'RngStream' interface works with (potentially) multiple streams of pseudo-random numbers: this is particularly suitable for working with parallel computations since each task can be assigned a separate RNG stream.

This uses as its underlying generator `RNGkind("L 'Ecuyer-CMRG")`, of L'Ecuyer (1999), which has a seed vector of 6 (signed) integers and a period of around $2^{191}$. Each 'stream' is a subsequence of the period of length $2^{127}$ which is in turn divided into 'substreams' of length $2^{76}$.

The idea of L'Ecuyer <i>et al</i> (2002) is to use a separate stream for each of the parallel computations (which ensures that the random numbers generated never get into sync) and the parallel computations can themselves use substreams if required. The original interface stores the original seed of the first stream, the original seed of the current stream and the current seed: this could be implemented in R, but it is as easy to work by saving the relevant values of `.Random.seed`: see the examples.
clusterSetRNGStream selects the "L'Ecuyer-CMRG" RNG and then distributes streams to the members of a cluster, optionally setting the seed of the streams by set.seed(iseed) (otherwise they are set from the current seed of the master process: after selecting the L'Ecuyer generator).

When not on Windows, Calling mc.reset.stream() after setting the L'Ecuyer random number generator and seed makes runs from mcparallel(mc.set.seed = TRUE) reproducible. This is done internally in mclapply and pvec. (Note that it does not set the seed in the master process, so does not affect the fallback-to-serial versions of these functions.)

Value

For nextRNGStream and nextRNGSubStream, a value which can be assigned to .Random.seed.

Note

Interfaces to L'Ecuyer's C code are available in CRAN packages rlecuyer and rstream.

Author(s)

Brian Ripley

References


See Also

RNG for fuller details of R's built-in random number generators.

The vignette for package parallel.

Examples

RNGkind("L'Ecuyer-CMRG")
set.seed(123)
(s <- .Random.seed)
## do some work involving random numbers.
nextRNGStream(s)
nextRNGSubStream(s)

splitIndices  Divide Tasks for Distribution in a Cluster

Description

This divides up 1:nx into nc1 lists of approximately equal size, as a way to allocate tasks to nodes in a cluster.

It is mainly for internal use, but some package authors have found it useful.
Usage

splitIndices(nx, ncl)

Arguments

nx Number of tasks.
ncl Number of cluster nodes.

Value

A list of length ncl, each element being an integer vector.

Examples

splitIndices(20, 3)
Chapter 9

The splines package

splines-package Regression Spline Functions and Classes

Description

Regression spline functions and classes.

Details

This package provides functions for working with regression splines using the B-spline basis, \texttt{bs}, and the natural cubic spline basis, \texttt{ns}.

For a complete list of functions, use \texttt{library(help = "splines")}.

Author(s)

Douglas M. Bates <bates@stat.wisc.edu> and William N. Venables <Bill.Venables@csiro.au>

Maintainer: R Core Team <R-core@r-project.org>

asVector Coerce an Object to a Vector

Description

This is a generic function. Methods for this function coerce objects of given classes to vectors.

Usage

\texttt{asVector(object)}

Arguments

\begin{itemize}
  \item \texttt{object} An object.
\end{itemize}
Details

Methods for vector coercion in new classes must be created for the `asVector` generic instead of `as.vector`. The `as.vector` function is internal and not easily extended. Currently the only class with an `asVector` method is the `xyVector` class.

Value

a vector

Author(s)

Douglas Bates and Bill Venables

See Also

`xyVector`

Examples

```r
require(stats)
ispl <- interpSpline( weight ~ height, women )
pred <- predict(ispl)
class(pred)
utils::str(pred)
asVector(pred)
```

---

**backSpline**

*Monotone Inverse Spline*

Description

Create a monotone inverse of a monotone natural spline.

Usage

`backSpline(object)`

Arguments

- `object` an object that inherits from class `nbSpline` or `npolySpline`. That is, the object must represent a natural interpolation spline but it can be either in the B-spline representation or the piecewise polynomial one. The spline is checked to see if it represents a monotone function.

Value

An object of class `polySpline` that contains the piecewise polynomial representation of a function that has the appropriate values and derivatives at the knot positions to be an inverse of the spline represented by `object`. Technically this object is not a spline because the second derivative is not constrained to be continuous at the knot positions. However, it is often a much better approximation to the inverse than fitting an interpolation spline to the y/x pairs.
bs

Author(s)
Douglas Bates and Bill Venables

See Also
interpSpline

Examples

```r
require(graphics)
ispl <- interpSpline( women$height, women$weight )
bspl <- backSpline( ispl )
plot( bspl )  # plots over the range of the knots
points( women$weight, women$height )
```

bs  

B-Spline Basis for Polynomial Splines

Description
Generate the B-spline basis matrix for a polynomial spline.

Usage

```r
bs(x, df = NULL, knots = NULL, degree = 3, intercept = FALSE,
    Boundary.knots = range(x), warn.outside = TRUE)
```

Arguments

- `x` the predictor variable. Missing values are allowed.
- `df` degrees of freedom; one can specify `df` rather than `knots`; `bs()` then chooses `df-degree` (minus one if there is an intercept) knots at suitable quantiles of `x` (which will ignore missing values). The default, `NULL`, takes the number of inner knots as `length(knots)`. If that is zero as per default, that corresponds to `df = degree - intercept`.
- `knots` the internal breakpoints that define the spline. The default is `NULL`, which results in a basis for ordinary polynomial regression. Typical values are the mean or median for one knot, quantiles for more knots. See also `Boundary.knots`.
- `degree` degree of the piecewise polynomial—default is 3 for cubic splines.
- `intercept` if `TRUE`, an intercept is included in the basis; default is `FALSE`.
- `Boundary.knots` boundary points at which to anchor the B-spline basis (default the range of the non-NA data). If both `knots` and `Boundary.knots` are supplied, the basis parameters do not depend on `x`. Data can extend beyond `Boundary.knots`.
- `warn.outside` logical indicating if a `warning` should be signalled in case some `x` values are outside the boundary knots.
**Details**

bs is based on the function `splineDesign`. It generates a basis matrix for representing the family of piecewise polynomials with the specified interior knots and degree, evaluated at the values of x. A primary use is in modeling formulas to directly specify a piecewise polynomial term in a model. When Boundary.knots are set inside range(x), bs() now uses a 'pivot' inside the respective boundary knot which is important for derivative evaluation. In R versions ≤ 3.2.2, the boundary knot itself had been used as pivot, which lead to somewhat wrong extrapolations.

**Value**

A matrix of dimension c(length(x), df), where either df was supplied or if knots were supplied, df = length(knots) + degree plus one if there is an intercept. Attributes are returned that correspond to the arguments to bs, and explicitly give the knots, Boundary.knots etc for use by predict.bs().

**Author(s)**

Douglas Bates and Bill Venables. Tweaks by R Core, and a patch fixing extrapolation “outside” Boundary.knots by Trevor Hastie.

**References**


**See Also**

`ns`, `poly`, `smooth.spline`, `predict.bs`, `SafePrediction`

**Examples**

```r
require(stats); require(graphics)
bs(women$height, df = 5)
summary(fm1 <- lm(weight ~ bs(height, df = 5), data = women))
## example of safe prediction
plot(women, xlab = "Height (in)", ylab = "Weight (lb)"
ht <- seq(57, 73, length.out = 200)
lines(ht, predict(fm1, data.frame(height = ht)))
```

**interpSpline**

Create an Interpolation Spline

**Description**

Create an interpolation spline, either from x and y vectors (default method), or from a formula / data.frame combination (formula method).

**Usage**

```r
interpSpline(obj1, obj2, bSpline = FALSE, period = NULL,
ord = 4L,
na.action = na.fail, sparse = FALSE)
```
Arguments

obj1 either a numeric vector of x values or a formula.

obj2 if obj1 is numeric this should be a numeric vector of the same length. If obj1 is a formula this can be an optional data frame in which to evaluate the names in the formula.

bSpline if TRUE the b-spline representation is returned, otherwise the piecewise polynomial representation is returned. Defaults to FALSE.

period an optional positive numeric value giving a period for a periodic interpolation spline.

ord an integer specifying the spline order, the number of coefficients per interval. \( ord = d + 1 \) where \( d \) is the degree polynomial degree. Currently, only cubic splines (\( ord = 4 \)) are implemented.

na.action a optional function which indicates what should happen when the data contain NAs. The default action (na.omit) is to omit any incomplete observations. The alternative action na.fail causes interpSpline to print an error message and terminate if there are any incomplete observations.

sparse logical passed to the underlying splineDesign. If true, saves memory and is faster when there are more than a few hundred points.

Value

An object that inherits from (S3) class spline. The object can be in the B-spline representation, in which case it will be of class nbSpline for natural B-spline, or in the piecewise polynomial representation, in which case it will be of class npolySpline.

Author(s)

Douglas Bates and Bill Venables

See Also

splineKnots, splineOrder, periodicSpline.

Examples

```r
require(graphics); require(stats)
ispl <- interpSpline( women$height, women$weight )
ispl2 <- interpSpline( weight ~ height, women )
# ispl and ispl2 should be the same
plot( predict( ispl, seq( 55, 75, length.out = 51 ) ), type = "l" )
points( women$height, women$weight )
plot( ispl )  # plots over the range of the knots
points( women$height, women$weight )
splineKnots( ispl )
```
Generate a Basis Matrix for Natural Cubic Splines

Description

Generate the B-spline basis matrix for a natural cubic spline.

Usage

```r
ns(x, df = NULL, knots = NULL, intercept = FALSE,
    Boundary.knots = range(x))
```

Arguments

- `x` the predictor variable. Missing values are allowed.
- `df` degrees of freedom. One can supply `df` rather than `knots`; `ns()` then chooses `df - 1 - intercept` knots at suitably chosen quantiles of `x` (which will ignore missing values). The default, `df = NULL`, sets the number of inner knots as `length(knots)`.
- `knots` breakpoints that define the spline. The default is no knots; together with the natural boundary conditions this results in a basis for linear regression on `x`. Typical values are the mean or median for one knot, quantiles for more knots. See also `Boundary.knots`.
- `intercept` if `TRUE`, an intercept is included in the basis; default is `FALSE`.
- `Boundary.knots` boundary points at which to impose the natural boundary conditions and anchor the B-spline basis (default the range of the data). If both `knots` and `Boundary.knots` are supplied, the basis parameters do not depend on `x`. Data can extend beyond `Boundary.knots`.

Details

`ns` is based on the function `splineDesign`. It generates a basis matrix for representing the family of piecewise-cubic splines with the specified sequence of interior knots, and the natural boundary conditions. These enforce the constraint that the function is linear beyond the boundary knots, which can either be supplied or default to the extremes of the data.

A primary use is in modeling formula to directly specify a natural spline term in a model: see the examples.

Value

A matrix of dimension `length(x) * df` where either `df` was supplied or if `knots` were supplied, `df = length(knots) + 1 + intercept`. Attributes are returned that correspond to the arguments to `ns`, and explicitly give the knots, `Boundary.knots` etc for use by `predict.ns()`.

References

periodicSpline

Create a Periodic Interpolation Spline

Description

Create a periodic interpolation spline, either from x and y vectors, or from a formula/data.frame combination.

Usage

periodicSpline(obj1, obj2, knots, period = 2*pi, ord = 4L)

Arguments

- **obj1**: either a numeric vector of x values or a formula.
- **obj2**: if obj1 is numeric this should be a numeric vector of the same length. If obj1 is a formula this can be an optional data frame in which to evaluate the names in the formula.
- **knots**: optional numeric vector of knot positions.
- **period**: positive numeric value giving the period for the periodic spline. Defaults to 2 * pi.
- **ord**: integer giving the order of the spline, at least 2. Defaults to 4. See splineOrder for a definition of the order of a spline.

Value

An object that inherits from class spline. The object can be in the B-spline representation, in which case it will be a pbSpline object, or in the piecewise polynomial representation (a ppolySpline object).

See Also

bs, predict.ns, SafePrediction

Examples

```r
require(stats); require(graphics)
ns(women$height, df = 5)
summary(fm1 <- lm(weight ~ ns(height, df = 5), data = women))

## To see what knots were selected
attr(terms(fm1), "predvars")

## example of safe prediction
plot(women, xlab = "Height (in)", ylab = "Weight (lb)")
ht <- seq(57, 73, length.out = 200) ; nD <- data.frame(height = ht)
lines(ht, p1 <- predict(fm1, nD))
stopifnot(all.equal(p1, predict(update(fm1, . ~ splines::ns(height, df=5)), nD)))

# not true in R < 3.5.0
```
polySpline

Piecewise Polynomial Spline Representation

Description

Create the piecewise polynomial representation of a spline object.

Usage

polySpline(object, ...) as.polySpline(object, ...)

Arguments

object  An object that inherits from class spline.

...  Optional additional arguments. At present no additional arguments are used.

Value

An object that inherits from class polySpline. This is the piecewise polynomial representation of a univariate spline function. It is defined by a set of distinct numeric values called knots. The spline function is a polynomial function between each successive pair of knots. At each interior knot the polynomial segments on each side are constrained to have the same value of the function and some of its derivatives.

Author(s)

Douglas Bates and Bill Venables
**predict.bs**

Evaluate a predefined spline basis at given values.

### Description

Evaluate a pre-defined spline basis at given values.

### Usage

```r
## S3 method for class 'bs'
predict(object, newx, ...)

## S3 method for class 'ns'
predict(object, newx, ...)
```

### Arguments

- `object` - the result of a call to `bs` or `ns` having attributes describing knots, degree, etc.
- `newx` - the x values at which evaluations are required.
- `...` - Optional additional arguments. At present no additional arguments are used.

### Value

An object just like `object`, except evaluated at the new values of `x`.

These are methods for the generic function `predict` for objects inheriting from classes "bs" or "ns". See `predict` for the general behavior of this function.

### See Also

`bs`, `ns`, `poly`.

### Examples

```r
require(stats)
basis <- ns(women$height, df = 5)
newX <- seq(58, 72, length.out = 51)
# evaluate the basis at the new data
predict(basis, newX)
```
predict.bSpline  Evaluate a Spline at New Values of x

Description
The `predict` methods for the classes that inherit from the virtual classes `bSpline` and `polySpline` are used to evaluate the spline or its derivatives. The `plot` method for a spline object first evaluates `predict` with the `x` argument missing, then plots the resulting `xyVector` with `type = "l"`.

Usage
```r
## S3 method for class 'bSpline'
predict(object, x, nseg = 50, deriv = 0, ...)  
## S3 method for class 'nbSpline'
predict(object, x, nseg = 50, deriv = 0, ...)  
## S3 method for class 'pbSpline'
predict(object, x, nseg = 50, deriv = 0, ...)  
## S3 method for class 'npolySpline'
predict(object, x, nseg = 50, deriv = 0, ...)  
## S3 method for class 'ppolySpline'
predict(object, x, nseg = 50, deriv = 0, ...)
```

Arguments
- `object`: An object that inherits from the `bSpline` or the `polySpline` class.
- `x`: A numeric vector of `x` values at which to evaluate the spline. If this argument is missing a suitable set of `x` values is generated as a sequence of `nseg` segments spanning the range of the knots.
- `nseg`: A positive integer giving the number of segments in a set of equally-spaced `x` values spanning the range of the knots in `object`. This value is only used if `x` is missing.
- `deriv`: An integer between 0 and `splineOrder(object) - 1` specifying the derivative to evaluate.
- `...`: further arguments passed to or from other methods.

Value
an `xyVector` with components
- `x`: the supplied or inferred numeric vector of `x` values
- `y`: the value of the spline (or its `deriv`'th derivative) at the `x` vector

Author(s)
Douglas Bates and Bill Venables

See Also
`xyVector`, `interpSpline`, `periodicSpline`
Examples

```r
require(graphics); require(stats)
ispl <- interpSpline(weight ~ height, women)
opar <- par(mfrow = c(2, 2), las = 1)
plot(predict(ispl, nseg = 201), # plots over the range of the knots
     main = "Original data with interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
points(women$height, women$weight, col = 4)
plot(predict(ispl, nseg = 201, deriv = 1),
     main = "First derivative of interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
plot(predict(ispl, nseg = 201, deriv = 2),
     main = "Second derivative of interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
plot(predict(ispl, nseg = 401, deriv = 3),
     main = "Third derivative of interpolating spline", type = "l",
     xlab = "height", ylab = "weight")
par(opar)
```

`splineDesign`  
*Design Matrix for B-splines*

**Description**

Evaluate the design matrix for the B-splines defined by knots at the values in x.

**Usage**

```r
splineDesign(knots, x, ord = 4, derivs, outer.ok = FALSE, sparse = FALSE)
spline.des (knots, x, ord = 4, derivs, outer.ok = FALSE, sparse = FALSE)
```

**Arguments**

- **knots**  
  a numeric vector of knot positions (which will be sorted increasingly if needed).

- **x**  
  a numeric vector of values at which to evaluate the B-spline functions or derivatives. Unless outer.ok is true, the values in x must be between the “inner” knots knots[ord] and knots[length(knots) - (ord-1)].

- **ord**  
  a positive integer giving the order of the spline function. This is the number of coefficients in each piecewise polynomial segment, thus a cubic spline has order 4. Defaults to 4.

- **derivs**  
  an integer vector with values between 0 and ord - 1, conceptually recycled to the length of x. The derivative of the given order is evaluated at the x positions. Defaults to zero (or a vector of zeroes of the same length as x).

- **outer.ok**  
  logical indicating if x should be allowed outside the inner knots, see the x argument.

- **sparse**  
  logical indicating if the result should inherit from class "sparseMatrix" (from package Matrix).
splineKnots

Knot Vector from a Spline

Description

Return the knot vector corresponding to a spline object.

Usage

splineKnots(object)

Arguments

object an object that inherits from class "spline".

Value

A non-decreasing numeric vector of knot positions.
splineOrder

Author(s)
Douglas Bates and Bill Venables

Examples
ispl <- interpSpline( weight ~ height, women )
splineKnots( ispl )

splineOrder  Determine the Order of a Spline

Description
Return the order of a spline object.

Usage
splineOrder(object)

Arguments
object  An object that inherits from class "spline".

Details
The order of a spline is the number of coefficients in each piece of the piecewise polynomial representation. Thus a cubic spline has order 4.

Value
A positive integer.

Author(s)
Douglas Bates and Bill Venables

See Also
splineKnots, interpSpline, periodicSpline

Examples
splineOrder( interpSpline( weight ~ height, women ) )
Construct an *xyVector* Object

Description

Create an object to represent a set of x-y pairs. The resulting object can be treated as a matrix or as a data frame or as a vector. When treated as a vector it reduces to the y component only.

The result of functions such as `predict.spline` is returned as an *xyVector* object so the x-values used to generate the y-positions are retained, say for purposes of generating plots.

Usage

```r
xyVector(x, y)
```

Arguments

- `x` a numeric vector
- `y` a numeric vector of the same length as `x`

Value

An object of class *xyVector* with components

- `x` a numeric vector
- `y` a numeric vector of the same length as `x`

Author(s)

Douglas Bates and Bill Venables

Examples

```r
require(stats); require(graphics)
ispl <- interpSpline( weight ~ height, women )
weights <- predict( ispl, seq( 55, 75, length.out = 51 ))
class( weights )
plot( weights, type = "l", xlab = "height", ylab = "weight" )
points( women$height, women$weight )
weights
```
Chapter 10

The stats package

---

stats-package  The R Stats Package

Description
R statistical functions

Details
This package contains functions for statistical calculations and random number generation. For a complete list of functions, use `library(help = "stats")`.

Author(s)
R Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

---

.checkMFClasses  Functions to Check the Type of Variables passed to Model Frames

Description
.checkMFClasses checks if the variables used in a predict method agree in type with those used for fitting.
.MFclass categorizes variables for this purpose.
getXlevels() extracts factor levels from factor or character variables.

Usage
.checkMFClasses(cl, m, ordNotOK = FALSE)
.MFclass(x)
.getXlevels(Terms, m)

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Arguments

- **cl**: a character vector of class descriptions to match.
- **m**: a model frame (model.frame() result).
- **x**: any R object.
- **ordNotOK**: logical: are ordered factors different?
- **Terms**: a terms object (terms.object).

Details

For applications involving model.matrix() such as linear models we do not need to differentiate between ordered factors and factors as although these affect the coding, the coding used in the fit is already recorded and imposed during prediction. However, other applications may treat ordered factors differently: rpart does, for example.

Value

-.checkMFClasses() checks and either signals an error calling stop() or returns NULL invisibly.
-.MFclass() returns a character string, one of "logical", "ordered", "factor", "numeric", "nmatrix.*" (a numeric matrix with a number of columns appended) or "other".
-.getXlevels returns a named list of character vectors, possibly empty, or NULL.

Examples

```r
sapply(warpbreaks, .MFclass) # "numeric" plus 2 x "factor"
sapply(iris, .MFclass) # 4 x "numeric" plus "factor"

mf <- model.frame(Sepal.Width ~ Species, iris)
mc <- model.frame(Sepal.Width ~ Sepal.Length, iris)

.checkMFClasses("numeric", mc) # nothing else
.checkMFClasses(c("numeric", "factor"), mf)

## simple .getXlevels() cases:
(xl <- .getXlevels(terms(mf), mf)) # a list with one entry "$ Species" with 3 levels:
stopifnot(exprs = {identical(xl$Species, levels(iris$Species))})
identical(.getXlevels(terms(mc), mc), xl[0]) # a empty named list, as no factors
is.null(.getXlevels(terms(x~x), list(x=1)))
```

acf

Auto- and Cross-Covariance and -Correlation Function Estimation

Description

The function acf computes (and by default plots) estimates of the autocovariance or autocorrelation function. Function pacf is the function used for the partial autocorrelations. Function ccf computes the cross-correlation or cross-covariance of two univariate series.
acf

Usage

acf(x, lag.max = NULL,
    type = c("correlation", "covariance", "partial"),
    plot = TRUE, na.action = na.fail, demean = TRUE, ...)

pacf(x, lag.max, plot, na.action, ...)

## Default S3 method:
pacf(x, lag.max = NULL, plot = TRUE, na.action = na.fail, ...

ccf(x, y, lag.max = NULL, type = c("correlation", "covariance"),
    plot = TRUE, na.action = na.fail, ...)

## S3 method for class 'acf'
x[i, j]

Arguments

x, y
a univariate or multivariate (not ccf) numeric time series object or a numeric
vector or matrix, or an "acf" object.

lag.max
maximum lag at which to calculate the acf. Default is \(10 \log_{10}(N/m)\) where \(N\)
is the number of observations and \(m\) the number of series. Will be automatically
limited to one less than the number of observations in the series.

type
character string giving the type of acf to be computed. Allowed values are
"correlation" (the default), "covariance" or "partial". Will be partially
matched.

plot
logical. If TRUE (the default) the acf is plotted.

na.action
function to be called to handle missing values. na.pass can be used.

demean
logical. Should the covariances be about the sample means?

... further arguments to be passed to plot.acf.

i
a set of lags (time differences) to retain.

j
a set of series (names or numbers) to retain.

details

For type = "correlation" and "covariance", the estimates are based on the sample covariance.
(The lag 0 autocorrelation is fixed at 1 by convention.)

By default, no missing values are allowed. If the na.action function passes through missing
values (as na.pass does), the covariances are computed from the complete cases. This means that
the estimate computed may well not be a valid autocorrelation sequence, and may contain missing
values. Missing values are not allowed when computing the PACF of a multivariate time series.

The partial correlation coefficient is estimated by fitting autoregressive models of successively
higher orders up to lag.max.

The generic function plot has a method for objects of class "acf".

The lag is returned and plotted in units of time, and not numbers of observations.

There are print and subsetting methods for objects of class "acf".
Value

An object of class "acf", which is a list with the following elements:

- **lag**: A three dimensional array containing the lags at which the acf is estimated.
- **acf**: An array with the same dimensions as `lag` containing the estimated acf.
- **type**: The type of correlation (same as the `type` argument).
- **n.used**: The number of observations in the time series.
- **series**: The name of the series `x`.
- **snames**: The series names for a multivariate time series.

The lag k value returned by `ccf(x, y)` estimates the correlation between `x[t+k]` and `y[t]`.

The result is returned invisibly if `plot` is `TRUE`.

Author(s)


References


(This contains the exact definitions used.)

See Also

`plot.acf`, `ARMAacf` for the exact autocorrelations of a given ARMA process.

Examples

```r
require(graphics)

## Examples from Venables & Ripley
acf(lh)
acf(lh, type = "covariance")
pacf(lh)

acf(ldeaths)
acf(ldeaths, ci.type = "ma")
acf(ts.union(mdeaths, fdeaths))
ccf(mdeaths, fdeaths, ylab = "cross-correlation")
# (just the cross-correlations)

presidents # contains missing values
acf(presidents, na.action = na.pass)
pacf(presidents, na.action = na.pass)
```
acf2AR

Compute an AR Process Exactly Fitting an ACF

Description

Compute an AR process exactly fitting an autocorrelation function.

Usage

acf2AR(acf)

Arguments

acf

An autocorrelation or autocovariance sequence.

Value

A matrix, with one row for the computed AR(p) coefficients for 1 <= p <= length(acf).

See Also

ARMAacf, ar.yw which does this from an empirical ACF.

Examples

(Acf <- ARMAacf(c(0.6, 0.3, -0.2)))
acf2AR(Acf)

add1

Add or Drop All Possible Single Terms to a Model

Description

Compute all the single terms in the scope argument that can be added to or dropped from the model, fit those models and compute a table of the changes in fit.

Usage

add1(object, scope, ...)  
## Default S3 method:
add1(object, scope, scale = 0, test = c("none", "Chisq"),
    k = 2, trace = FALSE, ...)

## S3 method for class 'lm'
add1(object, scope, scale = 0, test = c("none", "Chisq", "F"),
    x = NULL, k = 2, ...)

## S3 method for class 'glm'
add1(object, scope, scale = 0,
drop1(object, scope, ...)  

## Default S3 method: 
drop1(object, scope, scale = 0, test = c("none", "Chisq"),  
      k = 2, trace = FALSE, ...)  

## S3 method for class 'lm' 
drop1(object, scope, scale = 0, all.cols = TRUE,  
      test = c("none", "Chisq", "F"), k = 2, ...)  

## S3 method for class 'glm' 
drop1(object, scope, scale = 0,  
      test = c("none", "Rao", "LRT", "Chisq", "F"),  
      k = 2, ...)  

Arguments

object  a fitted model object.
scope  a formula giving the terms to be considered for adding or dropping.
scale  an estimate of the residual mean square to be used in computing $C_p$. Ignored if 0 or NULL.
test  should the results include a test statistic relative to the original model? The F test is only appropriate for lm and aov models or perhaps for glm fits with estimated dispersion. The $\chi^2$ test can be an exact test (lm models with known scale) or a likelihood-ratio test or a test of the reduction in scaled deviance depending on the method. For glm fits, you can also choose "LRT" and "Rao" for likelihood ratio tests and Rao’s efficient score test. The former is synonymous with "Chisq" (although both have an asymptotic chi-square distribution). Values can be abbreviated.
k  the penalty constant in AIC / $C_p$.
trace  if TRUE, print out progress reports.
x  a model matrix containing columns for the fitted model and all terms in the upper scope. Useful if add1 is to be called repeatedly. Warning: no checks are done on its validity.
all.cols  (Provided for compatibility with S.) Logical to specify whether all columns of the design matrix should be used. If FALSE then non-estimable columns are dropped, but the result is not usually statistically meaningful.
...  further arguments passed to or from other methods.

details

For drop1 methods, a missing scope is taken to be all terms in the model. The hierarchy is respected when considering terms to be added or dropped: all main effects contained in a second-order interaction must remain, and so on.
In a scope formula . means ‘what is already there’.
The methods for lm and glm are more efficient in that they do not recompute the model matrix and call the fit methods directly.
The default output table gives AIC, defined as minus twice log likelihood plus 2\(p\) where \(p\) is the rank of the model (the number of effective parameters). This is only defined up to an additive constant (like log-likelihoods). For linear Gaussian models with fixed scale, the constant is chosen to give Mallows' \(C_p\), \(RSS/scale + 2p - n\). Where \(C_p\) is used, the column is labelled as \(C_p\) rather than AIC.

The F tests for the "glm" methods are based on analysis of deviance tests, so if the dispersion is estimated it is based on the residual deviance, unlike the F tests of \texttt{anova.glm}.

Value

An object of class "anova" summarizing the differences in fit between the models.

Warning

The model fitting must apply the models to the same dataset. Most methods will attempt to use a subset of the data with no missing values for any of the variables if \texttt{na.action = na.omit}, but this may give biased results. Only use these functions with data containing missing values with great care.

The default methods make calls to the function \texttt{nobs} to check that the number of observations involved in the fitting process remained unchanged.

Note

These are not fully equivalent to the functions in S. There is no keep argument, and the methods used are not quite so computationally efficient.

Their authors’ definitions of Mallows' \(C_p\) and Akaike’s AIC are used, not those of the authors of the models chapter of S.

Author(s)

The design was inspired by the S functions of the same names described in Chambers (1992).

References


See Also

\texttt{step, aov, lm, extractAIC, anova}

Examples

```r
require(graphics); require(utils)
## following example(swiss)
lm1 <- lm(Fertility ~ ., data = swiss)
add1(lm1, ~ I(Education^2) + .^2)
drop1(lm1, test = "F")  # So called 'type II' anova

## following example(glm)
drop1(glm.D93, test = "Chisq")
drop1(glm.D93, test = "F")
add1(glm.D93, scope = "outcome*treatment, test = "Rao")  # Pearson Chi-square
```
addmargins

Puts Arbitrary Margins on Multidimensional Tables or Arrays

Description

For a given table one can specify which of the classifying factors to expand by one or more levels to hold margins to be calculated. One may for example form sums and means over the first dimension and medians over the second. The resulting table will then have two extra levels for the first dimension and one extra level for the second. The default is to sum over all margins in the table. Other possibilities may give results that depend on the order in which the margins are computed. This is flagged in the printed output from the function.

Usage

```
addmargins(A, margin = seq_along(dim(A)), FUN = sum, quiet = FALSE)
```

Arguments

- **A**: table or array. The function uses the presence of the "dim" and "dimnames" attributes of A.
- **margin**: vector of dimensions over which to form margins. Margins are formed in the order in which dimensions are specified in margin.
- **FUN**: list of the same length as margin, each element of the list being either a function or a list of functions. In the length-1 case, can be a function instead of a list of one. Names of the list elements will appear as levels in dimnames of the result. Unnamed list elements will have names constructed: the name of a function or a constructed name based on the position in the table.
- **quiet**: logical which suppresses the message telling the order in which the margins were computed.

Details

If the functions used to form margins are not commutative, the result depends on the order in which margins are computed. Annotation of margins is done naming the FUN list.

Value

A table or array with the same number of dimensions as A, but with extra levels of the dimensions mentioned in margin. The number of levels added to each dimension is the length of the entries in FUN. A message with the order of computation of margins is printed.

Author(s)

Bendix Carstensen, Steno Diabetes Center & Department of Biostatistics, University of Copenhagen, [https://BendixCarstensen.com](https://BendixCarstensen.com), autumn 2003. Margin naming enhanced by Duncan Murdoch.

See Also

table, ftable, margin.table.
Examples

Aye <- sample(c("Yes", "Si", "Oui"), 177, replace = TRUE)
Bee <- sample(c("Hum", "Buzz"), 177, replace = TRUE)
Sea <- sample(c("White", "Black", "Red", "Dead"), 177, replace = TRUE)
(A <- table(Aye, Bee, Sea))
(aA <- addmargins(A))

ftable(A)
ftable(aA)

# Non-commutative functions - note differences between resulting tables:
ftable( addmargins(A, c(3, 1),
   FUN = list(list(Min = min, Max = max),
              Sum = sum)))
ftable( addmargins(A, c(1, 3),
   FUN = list(Sum = sum,
              list(Min = min, Max = max))))

# Weird function needed to return the N when computing percentages
sqsm <- function(x) sum(x)^2/100
B <- table(Sea, Bee)
round(sweep(addmargins(B, 1, list(list(All = sum, N = sqsm))), 2,
   apply(B, 2, sum)/100, `/`), 1)
round(sweep(addmargins(B, 2, list(list(All = sum, N = sqsm))), 1,
   apply(B, 1, sum)/100, `/`), 1)

# A total over Bee requires formation of the Bee-margin first:
mB <- addmargins(B, 2, FUN = list(list(Total = sum)))
round(ftable(sweep(addmargins(mB, 1, list(list(All = sum, N = sqsm))), 2,
   apply(mB, 2, sum)/100, `/`)), 1)

## Zero.Printing table+margins:
set.seed(1)
x <- sample(1:7, 20, replace = TRUE)
y <- sample(1:7, 20, replace = TRUE)
(tx <- addmargins( table(x, y) )
print(tx, zero.print = ".")

aggregate

Compute Summary Statistics of Data Subsets

Description

Splits the data into subsets, computes summary statistics for each, and returns the result in a convenient form.

Usage

aggregate(x, ...)

## Default S3 method:
aggregate(x, ...)
## S3 method for class 'data.frame'
aggregate(x, by, FUN, ..., simplify = TRUE, drop = TRUE)

## S3 method for class 'formula'
aggregate(x, data, FUN, ..., subset, na.action = na.omit)

## S3 method for class 'ts'
aggregate(x, nfrequency = 1, FUN = sum, ndeltat = 1,
          ts.eps = getOption("ts.eps"), ...)

Arguments

x
  an R object. For the formula method a formula, such as y ~ x or
  cbind(y1, y2) ~ x1 + x2, where the y variables are numeric data to
  be split into groups according to the grouping x variables (usually
  factors).

by
  a list of grouping elements, each as long as the variables in the
data frame x, or
  a formula. The elements are coerced to factors before use.

FUN
  a function to compute the summary statistics which can be applied to
  all data subsets.

simplify
  a logical indicating whether results should be simplified to a vector
  or matrix if possible.

drop
  a logical indicating whether to drop unused combinations of
  grouping values. The non-default case drop=FALSE has been amended
  for R 3.5.0 to drop unused combinations.

data
  a data frame (or list) from which the variables in the formula
  should be taken.

subset
  an optional vector specifying a subset of observations to be used.

na.action
  a function which indicates what should happen when the data contain
  NA values. The default is to only consider complete cases with respect
  to the given variables.

nfrequency
  new number of observations per unit of time; must be a divisor of the
  frequency of x.

ndeltat
  new fraction of the sampling period between successive observations;
  must be a divisor of the sampling interval of x.

ts.eps
  tolerance used to decide if nfrequency is a sub-multiple of the original
  frequency.

... further arguments passed to or used by methods.

Details

aggregate is a generic function with methods for data frames and time series.

The default method, aggregate.default, uses the time series method if x is a time
series, and otherwise coerces x to a data frame and calls the data frame method.

aggregate.data.frame is the data frame method. If x is not a data frame, it is coerced to one,
which must have a non-zero number of rows. Then, each of the variables (columns) in x is split
into subsets of cases (rows) of identical combinations of the components of by, and FUN is applied
to each such subset with further arguments in ... passed to it. The result is reformatted into a
data frame containing the variables in by and x. The ones arising from by contain the unique
combinations of grouping values used for determining the subsets, and the ones arising from x
the corresponding summaries for the subset of the respective variables in \( x \). If simplify is true, summaries are simplified to vectors or matrices if they have a common length of one or greater than one, respectively; otherwise, lists of summary results according to subsets are obtained. Rows with missing values in any of the by variables will be omitted from the result. (Note that versions of R prior to 2.11.0 required \( \text{FUN} \) to be a scalar function.)

The formula method provides a standard formula interface to \( \text{aggregate.data.frame} \). The latter invokes the formula method if by is a formula, in which case \( \text{aggregate}(x, \text{by}, \text{FUN}) \) is the same as \( \text{aggregate(by, x, FUN)} \) for a data frame \( x \).

\( \text{aggregate.ts} \) is the time series method, and requires \( \text{FUN} \) to be a scalar function. If \( x \) is not a time series, it is coerced to one. Then, the variables in \( x \) are split into appropriate blocks of length \( \text{frequency}(x) / \text{nfrequency} \), and \( \text{FUN} \) is applied to each such block, with further (named) arguments in \( \ldots \) passed to it. The result returned is a time series with frequency \( \text{nfrequency} \) holding the aggregated values. Note that this make most sense for a quarterly or yearly result when the original series covers a whole number of quarters or years: in particular aggregating a monthly series to quarters starting in February does not give a conventional quarterly series.

\( \text{FUN} \) is passed to \( \text{match.fun} \), and hence it can be a function or a symbol or character string naming a function.

### Value

For the time series method, a time series of class \"ts\" or class \text{c("mts", "ts")}.

For the data frame method, a data frame with columns corresponding to the grouping variables in by followed by aggregated columns from \( x \). If the by has names, the non-empty times are used to label the columns in the results, with unnamed grouping variables being named \text{Group.}i for \text{by[[}i\text{]}].

### Warning

The first argument of the \"formula\" method was named \text{formula} rather than \text{x} prior to R 4.2.0. Portable uses should not name that argument.

### Author(s)

Kurt Hornik, with contributions by Arni Magnusson.

### References


### See Also

\texttt{apply}, \texttt{lapply}, \texttt{tapply}.

### Examples

```r
## Compute the averages for the variables in \'state.x77\', grouped
## according to the region (Northeast, South, North Central, West) that
## each state belongs to.
aggregate(state.x77, list(Region = state.region), mean)

## Compute the averages according to region and the occurrence of more
## than 130 days of frost.
aggregate(state.x77,
list(Region = state.region,
    Cold = state.x77[,"Frost"] > 130),
    mean)
## (Note that no state in 'South' is THAT cold.)

## example with character variables and NAs

```
testDF <- data.frame(v1 = c(1,3,5,7,8,3,5,NA,4,5,7,9),
    v2 = c(11,33,55,77,88,33,55,NA,44,55,77,99) )
by1 <- c("red", "blue", 1, 2, NA, "big", 1, 2, "red", 1, NA, 12)
by2 <- c("wet", "dry", 99, 95, NA, "damp", 95, 99, "red", 99, NA, NA)
aggregate(x = testDF, by = list(by1, by2), FUN = "mean")
```

# and if you want to treat NAs as a group

```
fb1 <- factor(by1, exclude = "")
fb2 <- factor(by2, exclude = "")
aggregate(x = testDF, by = list(fb1, fb2), FUN = "mean")
```

## Formulas, one ~ one, one ~ many, many ~ one, and many ~ many:

```
aggregate(weight ~ feed, data = chickwts, mean)
aggregate(breaks ~ wool + tension, data = warpbreaks, mean)
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, mean)
aggregate(cbind(ncases, ncontrols) ~ alcgp + tobgp, data = esoph, sum)
```

## "complete cases" vs. "available cases"

```
colSums(is.na(airquality)) # NAs in Ozone but not Temp
## the default is to summarize *complete cases*:
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, FUN = mean)
## to handle missing values *per variable*:
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, FUN = mean,
    na.action = na.pass, na.rm = TRUE)
```

## Dot notation:

```
aggregate(. ~ Species, data = iris, mean)
aggregate(len ~ ., data = ToothGrowth, mean)
```

## Often followed by xtabs():

```
ag <- aggregate(len ~ ., data = ToothGrowth, mean)
xtabs(len ~ ., data = ag)
```

## Formula interface via 'by' (for pipe operations)

```
ToothGrowth |> aggregate(len ~ ., FUN = mean)
```

## Compute the average annual approval ratings for American presidents.

```
aggregate(presidents, nfrequency = 1, FUN = mean)
## Give the summer less weight.
aggregate(presidents, nfrequency = 1,
    FUN = weighted.mean, w = c(1, 1, 0.5, 1))
```
Description

Generic function calculating Akaike's 'An Information Criterion' for one or several fitted model objects for which a log-likelihood value can be obtained, according to the formula $\text{AIC} = -2\text{log-likelihood} + k n_{par}$, where $n_{par}$ represents the number of parameters in the fitted model, and $k = 2$ for the usual AIC, or $k = \log(n)$ ($n$ being the number of observations) for the so-called BIC or SBC (Schwarz's Bayesian criterion).

Usage

AIC(object, ..., k = 2)
BIC(object, ...)

Arguments

object
  a fitted model object for which there exists a logLik method to extract the corresponding log-likelihood, or an object inheriting from class logLik.

...  optionally more fitted model objects.

k
  numeric, the penalty per parameter to be used; the default $k = 2$ is the classical AIC.

Details

When comparing models fitted by maximum likelihood to the same data, the smaller the AIC or BIC, the better the fit.

The theory of AIC requires that the log-likelihood has been maximized: whereas AIC can be computed for models not fitted by maximum likelihood, their AIC values should not be compared.

Examples of models not 'fitted to the same data' are where the response is transformed (accelerated-life models are fitted to log-times) and where contingency tables have been used to summarize data.

These are generic functions (with S4 generics defined in package stats4): however methods should be defined for the log-likelihood function logLik rather than these functions: the action of their default methods is to call logLik on all the supplied objects and assemble the results. Note that in several common cases logLik does not return the value at the MLE: see its help page.

The log-likelihood and hence the AIC/BIC is only defined up to an additive constant. Different constants have conventionally been used for different purposes and so extractAIC and AIC may give different values (and do for models of class "lm": see the help for extractAIC). Particular care is needed when comparing fits of different classes (with, for example, a comparison of a Poisson and gamma GLM being meaningless since one has a discrete response, the other continuous).

BIC is defined as $\text{BIC} = \text{AIC}(object, ..., k = \log(nobs(object)))$. This needs the number of observations to be known: the default method looks first for a "nobs" attribute on the return value from the logLik method, then tries the nobs generic, and if neither succeed returns BIC as NA.

Value

If just one object is provided, a numeric value with the corresponding AIC (or BIC, or ..., depending on $k$).

If multiple objects are provided, a data.frame with rows corresponding to the objects and columns representing the number of parameters in the model (df) and the AIC or BIC.
Alias

Find Aliases (Dependencies) in a Model

Description

Find aliases (linearly dependent terms) in a linear model specified by a formula.

Usage

alias(object, ...)

## S3 method for class 'formula'
alias(object, data, ...)

## S3 method for class 'lm'
alias(object, complete = TRUE, partial = FALSE,
partial.pattern = FALSE, ...)

Arguments

object A fitted model object, for example from `lm` or `aov`, or a formula for alias.formula.
data Optionally, a data frame to search for the objects in the formula.
complete Should information on complete aliasing be included?
partial Should information on partial aliasing be included?
Should partial aliasing be presented in a schematic way? If this is done, the results are presented in a more compact way, usually giving the deciles of the coefficients.

... further arguments passed to or from other methods.

Details

Although the main method is for class "lm", alias is most useful for experimental designs and so is used with fits from aov. Complete aliasing refers to effects in linear models that cannot be estimated independently of the terms which occur earlier in the model and so have their coefficients omitted from the fit. Partial aliasing refers to effects that can be estimated less precisely because of correlations induced by the design.

Some parts of the "lm" method require recommended package MASS to be installed.

Value

A list (of class "listof") containing components

- Model: Description of the model; usually the formula.
- Complete: A matrix with columns corresponding to effects that are linearly dependent on the rows.
- Partial: The correlations of the estimable effects, with a zero diagonal. An object of class "mtable" which has its own print method.

Note

The aliasing pattern may depend on the contrasts in use: Helmert contrasts are probably most useful. The defaults are different from those in S.

Author(s)

The design was inspired by the S function of the same name described in Chambers et al (1992).

References


Examples

```r
op <- options(contrasts = c("contr.helmert", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
alias(npk.aov)
options(op)  # reset
```
### anova

#### Description

Compute analysis of variance (or deviance) tables for one or more fitted model objects.

#### Usage

```r
anova(object, ...)"```

#### Arguments

- `object`: an object containing the results returned by a model fitting function (e.g., `lm` or `glm`).
- `...`: additional objects of the same type.

#### Value

This (generic) function returns an object of class `anova`. These objects represent analysis-of-variance and analysis-of-deviance tables. When given a single argument it produces a table which tests whether the model terms are significant.

When given a sequence of objects, `anova` tests the models against one another in the order specified. The print method for `anova` objects prints tables in a 'pretty' form.

#### Warning

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R’s default of `na.action = na.omit` is used.

#### References


#### See Also

- `coefficients`, `effects`, `fitted.values`, `residuals`, `summary`, `drop1`, `add1`.

### anova.glm

#### Description

Compute an analysis of deviance table for one or more generalized linear model fits.

#### Usage

```r
## S3 method for class 'glm'
anova(object, ..., dispersion = NULL, test = NULL)"
```
Arguments

object, ... objects of class glm, typically the result of a call to glm, or a list of objects for the "glmlist" method.
dispersion the dispersion parameter for the fitting family. By default it is obtained from the object(s).
test a character string, (partially) matching one of "Chisq", "LRT", "Rao", "F" or "Cp". See stat.anova.

Details

Specifying a single object gives a sequential analysis of deviance table for that fit. That is, the reductions in the residual deviance as each term of the formula is added in turn are given in as the rows of a table, plus the residual deviances themselves.

If more than one object is specified, the table has a row for the residual degrees of freedom and deviance for each model. For all but the first model, the change in degrees of freedom and deviance is also given. (This only makes statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain test statistics (and P values) comparing the reduction in deviance for the row to the residuals. For models with known dispersion (e.g., binomial and Poisson fits) the chi-squared test is most appropriate, and for those with dispersion estimated by moments (e.g., gaussian, quasibinomial and quasipoisson fits) the F test is most appropriate. Mallows' $C_p$ statistic is the residual deviance plus twice the estimate of $\sigma^2$ times the residual degrees of freedom, which is closely related to AIC (and a multiple of it if the dispersion is known). You can also choose "LRT" and "Rao" for likelihood ratio tests and Rao's efficient score test. The former is synonymous with "Chisq" (although both have an asymptotic chi-square distribution).

The dispersion estimate will be taken from the largest model, using the value returned by summary.glm. As this will in most cases use a Chisquared-based estimate, the F tests are not based on the residual deviance in the analysis of deviance table shown.

Value

An object of class "anova" inheriting from class "data.frame".

Warning

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of na.action = na.omit is used, and anova will detect this with an error.

References


See Also

glm, anova.
drop1 for so-called ‘type II’ anova where each term is dropped one at a time respecting their hierarchy.
Examples

```r
## --- Continuing the Example from '?glm':

anova(glm.D93)
anova(glm.D93, test = "Cp")
anova(glm.D93, test = "Chisq")
glm.D93a <-
  update(glm.D93, ~treatment*outcome) # equivalent to Pearson Chi-square
anova(glm.D93, glm.D93a, test = "Rao")
```

Description

Compute an analysis of variance table for one or more linear model fits.

Usage

```r
## S3 method for class 'lm'
aanova(object, ...)

## S3 method for class 'lm_list'
aanova(object, ..., scale = 0, test = "F")
```

Arguments

- `object, ...`: objects of class `lm`, usually, a result of a call to `lm`.
- `test`: a character string specifying the test statistic to be used. Can be one of "F", "Chisq" or "Cp", with partial matching allowed, or NULL for no test.
- `scale`: numeric. An estimate of the noise variance $\sigma^2$. If zero this will be estimated from the largest model considered.

Details

Specifying a single object gives a sequential analysis of variance table for that fit. That is, the reductions in the residual sum of squares as each term of the formula is added in turn are given in the rows of a table, plus the residual sum of squares.

The table will contain F statistics (and P values) comparing the mean square for the row to the residual mean square.

If more than one object is specified, the table has a row for the residual degrees of freedom and sum of squares for each model. For all but the first model, the change in degrees of freedom and sum of squares is also given. (This only make statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

Optionally the table can include test statistics. Normally the F statistic is most appropriate, which compares the mean square for a row to the residual sum of squares for the largest model considered. If `scale` is specified chi-squared tests can be used. Mallows' $C_p$ statistic is the residual sum of squares plus twice the estimate of $\sigma^2$ times the residual degrees of freedom.
Value
An object of class "anova" inheriting from class "data.frame".

Warning
The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R’s default of na.action = na.omit is used, and anova.lmlist will detect this with an error.

References

See Also
The model fitting function lm, anova.
drop1 for so-called ‘type II’ anova where each term is dropped one at a time respecting their hierarchy.

Examples
## sequential table
fit <- lm(sr ~ ., data = LifeCycleSavings)
anova(fit)

## same effect via separate models
fit0 <- lm(sr ~ 1, data = LifeCycleSavings)
fit1 <- update(fit0, . ~ . + pop15)
fit2 <- update(fit1, . ~ . + pop75)
fit3 <- update(fit2, . ~ . + dpi)
fit4 <- update(fit3, . ~ . + ddpi)
anova(fit0, fit1, fit2, fit3, fit4, test = "F")
anova(fit4, fit2, fit0, test = "F") # unconventional order
Arguments

object  an object of class "mlm".
...  further objects of class "mlm".

test  choice of test statistic (see below). Can be abbreviated.

Sigma  (only relevant if test == "Spherical"). Covariance matrix assumed proportional to Sigma.

T  transformation matrix. By default computed from M and X.

M  formula or matrix describing the outer projection (see below).

X  formula or matrix describing the inner projection (see below).

idata  data frame describing intra-block design.

tol  tolerance to be used in deciding if the residuals are rank-deficient: see qr.

Details

The anova.mlm method uses either a multivariate test statistic for the summary table, or a test based on sphericity assumptions (i.e. that the covariance is proportional to a given matrix).

For the multivariate test, Wilks’ statistic is most popular in the literature, but the default Pillai–Bartlett statistic is recommended by Hand and Taylor (1987). See summary.manova for further details.

For the "Spherical" test, proportionality is usually with the identity matrix but a different matrix can be specified using Sigma. Corrections for asphericity known as the Greenhouse–Geisser, respectively Huynh–Feldt, epsilons are given and adjusted F tests are performed.

It is common to transform the observations prior to testing. This typically involves transformation to intra-block differences, but more complicated within-block designs can be encountered, making more elaborate transformations necessary. A transformation matrix T can be given directly or specified as the difference between two projections onto the spaces spanned by M and X, which in turn can be given as matrices or as model formulas with respect to idata (the tests will be invariant to parametrization of the quotient space M/X).

As with anova.lm, all test statistics use the SSD matrix from the largest model considered as the (generalized) denominator.

Contrary to other anova methods, the intercept is not excluded from the display in the single-model case. When contrast transformations are involved, it often makes good sense to test for a zero intercept.

Value

An object of class "anova" inheriting from class "data.frame"

Note

The Huynh–Feldt epsilon differs from that calculated by SAS (as of v. 8.2) except when the DF is equal to the number of observations minus one. This is believed to be a bug in SAS, not in R.

References

Examples

require(graphics)
utils::example(SSD) # Brings in the mlmfit and reacttime objects

mlmfit0 <- update(mlmfit, ~0)

### Traditional tests of intrasubj. contrasts
## Using MANOVA techniques on contrasts:
anova(mlmfit, mlmfit0, X = ~1)

## Assuming sphericity
anova(mlmfit, mlmfit0, X = ~1, test = "Spherical")

### tests using intra-subject 3x2 design
idata <- data.frame(deg = gl(3, 1, 6, labels = c(0, 4, 8)),
noise = gl(2, 3, 6, labels = c("A", "P")))

anova(mlmfit, mlmfit0, X = ~ deg + noise,
idata = idata, test = "Spherical")
anova(mlmfit, mlmfit0, M = ~ deg + noise, X = ~ noise,
idata = idata, test = "Spherical")
anova(mlmfit, mlmfit0, M = ~ deg + noise, X = ~ deg,
idata = idata, test = "Spherical")

f <- factor(rep(1:2, 5)) # bogus, just for illustration
mlmfit2 <- update(mlmfit, ~f)
anova(mlmfit2, mlmfit, mlmfit0, X = ~1, test = "Spherical")
anova(mlmfit2, X = ~1, test = "Spherical")

# one-model form, equiv. to previous

### There seems to be a strong interaction in these data
plot(colMeans(reacttime))

---

ansari.test  Ansari-Bradley Test

Description

Performs the Ansari-Bradley two-sample test for a difference in scale parameters.

Usage

ansari.test(x, ...)

## Default S3 method:
ansari.test(x, y,
alternative = c("two.sided", "less", "greater"),
exact = NULL, conf.int = FALSE, conf.level = 0.95,
## S3 method for class 'formula'
ansari.test(formula, data, subset, na.action, ...)

**Arguments**

- **x**: numeric vector of data values.
- **y**: numeric vector of data values.
- **alternative**: indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter.
- **exact**: a logical indicating whether an exact p-value should be computed.
- **conf.int**: a logical, indicating whether a confidence interval should be computed.
- **conf.level**: confidence level of the interval.
- **formula**: a formula of the form `lhs ~ rhs` where `lhs` is a numeric variable giving the data values and `rhs` a factor with two levels giving the corresponding groups.
- **data**: an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
- **subset**: an optional vector specifying a subset of observations to be used.
- **na.action**: a function which indicates what should happen when the data contain NAs. Defaults to `getOption("na.action")`.
- **...**: further arguments to be passed to or from methods.

**Details**

Suppose that `x` and `y` are independent samples from distributions with densities \( f((t - m)/s)/s \) and \( f(t - m) \), respectively, where \( m \) is an unknown nuisance parameter and \( s \), the ratio of scales, is the parameter of interest. The Ansari-Bradley test is used for testing the null that \( s = 1 \), the two-sided alternative being that \( s \neq 1 \) (the distributions differ only in variance), and the one-sided alternatives being \( s > 1 \) (the distribution underlying `x` has a larger variance, "greater") or \( s < 1 \) ("less").

By default (if `exact` is not specified), an exact p-value is computed if both samples contain less than 50 finite values and there are no ties. Otherwise, a normal approximation is used.

Optionally, a nonparametric confidence interval and an estimator for `s` are computed. If exact p-values are available, an exact confidence interval is obtained by the algorithm described in Bauer (1972), and the Hodges-Lehmann estimator is employed. Otherwise, the returned confidence interval and point estimate are based on normal approximations.

Note that mid-ranks are used in the case of ties rather than average scores as employed in Hollander & Wolfe (1973). See, e.g., Hajek, Sidak and Sen (1999), pages 131ff, for more information.

**Value**

A list with class "htest" containing the following components:

- **statistic**: the value of the Ansari-Bradley test statistic.
- **p.value**: the p-value of the test.
- **null.value**: the ratio of scales `s` under the null, 1.
- **alternative**: a character string describing the alternative hypothesis.
method the string "Ansari-Bradley test".
data.name a character string giving the names of the data.
conf.int a confidence interval for the scale parameter. (Only present if argument
conf.int = TRUE.)
estimate an estimate of the ratio of scales. (Only present if argument conf.int = TRUE.)

Note
To compare results of the Ansari-Bradley test to those of the F test to compare two variances (under the assumption of normality), observe that $s$ is the ratio of scales and hence $s^2$ is the ratio of variances (provided they exist), whereas for the F test the ratio of variances itself is the parameter of interest. In particular, confidence intervals are for $s$ in the Ansari-Bradley test but for $s^2$ in the F test.

References

See Also
`fligner.test` for a rank-based (nonparametric) k-sample test for homogeneity of variances; `mood.test` for another rank-based two-sample test for a difference in scale parameters; `var.test` and `bartlett.test` for parametric tests for the homogeneity in variance.
`ansari.test` in package `coin` for exact and approximate conditional p-values for the Ansari-Bradley test, as well as different methods for handling ties.

Examples
```r
## Hollander & Wolfe (1973, p. 86f):
## Serum iron determination using Hyland control sera
ansari.test(ramsay, jung.parekh)

ansari.test(rnorm(10), rnorm(10, 0, 2), conf.int = TRUE)
## try more points - failed in 2.4.1
ansari.test(rnorm(100), rnorm(100, 0, 2), conf.int = TRUE)
```
**Description**

Fit an analysis of variance model by a call to `lm` (for each stratum if an `Error(.)` is used).

**Usage**

```r
aov(formula, data = NULL, projections = FALSE, qr = TRUE,
     contrasts = NULL, ...)
```

**Arguments**

- `formula` A formula specifying the model.
- `data` A data frame in which the variables specified in the formula will be found. If missing, the variables are searched for in the standard way.
- `projections` Logical flag: should the projections be returned?
- `qr` Logical flag: should the QR decomposition be returned?
- `contrasts` A list of contrasts to be used for some of the factors in the formula. These are not used for any `Error` term, and supplying contrasts for factors only in the `Error` term will give a warning.
- `...` Arguments to be passed to `lm`, such as `subset` or `na.action`. See ‘Details’ about `weights`.

**Details**

This provides a wrapper to `lm` for fitting linear models to balanced or unbalanced experimental designs.

The main difference from `lm` is in the way `print`, `summary` and so on handle the fit: this is expressed in the traditional language of the analysis of variance rather than that of linear models.

If the formula contains a single `Error` term, this is used to specify error strata, and appropriate models are fitted within each error stratum.

The formula can specify multiple responses.

Weights can be specified by a `weights` argument, but should not be used with an `Error` term, and are incompletely supported (e.g., not by `model.tables`).

**Value**

An object of class `c("aov", "lm")` or for multiple responses of class `c("maov", "aov", "mlm", "lm")` or for multiple error strata of class `c("aovlist", "listof")`. There are `print` and `summary` methods available for these.
 approxfun

Description

Return a list of points which linearly interpolate given data points, or a function performing the linear (or constant) interpolation.
approx

approx (x, y = NULL, xout, method = "linear", n = 50, 
yleft, yright, rule = 1, f = 0, ties = mean, na.rm = TRUE)

approxfun(x, y = NULL, method = "linear", 
yleft, yright, rule = 1, f = 0, ties = mean, na.rm = TRUE)

Arguments

x, y numeric vectors giving the coordinates of the points to be interpolated. Alternatively a single plotting structure can be specified: see xy.coords.
xout an optional set of numeric values specifying where interpolation is to take place.
method specifies the interpolation method to be used. Choices are "linear" or "constant".
n If xout is not specified, interpolation takes place at n equally spaced points spanning the interval [min(x), max(x)].
yleft the value to be returned when input x values are less than min(x). The default is defined by the value of rule given below.
yright the value to be returned when input x values are greater than max(x). The default is defined by the value of rule given below.
rule an integer (of length 1 or 2) describing how interpolation is to take place outside the interval [min(x), max(x)]. If rule is 1 then NAs are returned for such points and if it is 2, the value at the closest data extreme is used. Use, e.g., rule = 2:1, if the left and right side extrapolation should differ.
f for method = "constant" a number between 0 and 1 inclusive, indicating a compromise between left- and right-continuous step functions. If y0 and y1 are the values to the left and right of the point then the value is y0 if f == 0, y1 if f == 1, and y0*(1-f)+y1*f for intermediate values. In this way the result is right-continuous for f == 0 and left-continuous for f == 1, even for non-finite y values.
ties handling of tied x values. The string "ordered" or a function (or the name of a function) taking a single vector argument and returning a single number or a list of both, e.g., list("ordered", mean), see 'Details'.
na.rm logical specifying how missing values (NA's) should be handled. Setting na.rm=FALSE will propagate NA's in y to the interpolated values, also depending on the rule set. Note that in this case, NA's in x are invalid, see also the examples.

details

The inputs can contain missing values which are deleted (if na.rm is true, i.e., by default), so at least two complete (x, y) pairs are required (for method = "linear", one otherwise). If there are duplicated (tied) x values and ties contains a function it is applied to the y values for each distinct x value to produce (x,y) pairs with unique x. Useful functions in this context include mean, min, and max.

If ties = "ordered" the x values are assumed to be already ordered (and unique) and ties are not checked but kept if present. This is the fastest option for large length(x).

If ties is a list of length two, ties[[2]] must be a function to be applied to ties, see above, but if ties[[1]] is identical to "ordered", the x values are assumed to be sorted and are only checked
for ties. Consequently, ties = list("ordered", mean) will be slightly more efficient than the
default ties = mean in such a case.
The first y value will be used for interpolation to the left and the last one for interpolation to the
right.

Value
approx returns a list with components x and y, containing n coordinates which interpolate the given
data points according to the method (and rule) desired.
The function approxfun returns a function performing (linear or constant) interpolation of the given
data points. For a given set of x values, this function will return the corresponding interpolated
values. It uses data stored in its environment when it was created, the details of which are subject
to change.

Warning
The value returned by approxfun contains references to the code in the current version of R: it is
not intended to be saved and loaded into a different R session. This is safer for R >= 3.0.0.

References
Brooks/Cole.

See Also
spline and splinefun for spline interpolation.

Examples
```
require(graphics)
x <- 1:10
y <- rnorm(10)
par(mfrow = c(2,1))
plot(x, y, main = "approx(.) and approxfun(.)")
points(approx(x, y), col = 2, pch = "*")
points(approx(x, y, method = "constant"), col = 4, pch = "*")
f <- approxfun(x, y)
curve(f(x), 0, 11, col = "green2")
points(x, y)
is.function(fc <- approxfun(x, y, method = "const")) # TRUE
curve(fc(x), 0, 10, col = "darkblue", add = TRUE)
## different extrapolation on left and right side :
plot(approxfun(x, y, rule = 2:1), 0, 11,
    col = "tomato", add = TRUE, lty = 3, lwd = 2)
### Treatment of 'NA's -- are kept if na.rm=FALSE :
xn <- 1:4
yn <- c(1,NA,3:4)
xout <- (1:9)/2
## Default behavior (na.rm = TRUE): NA's omitted; extrapolation gives NA
data.frame(approx(xn,yn, xout))
```
data.frame(approx(xn,yn, xout, rule = 2))# -> *constant* extrapolation
## New (2019-2020) na.rm = FALSE: NA's are "kept"
data.frame(approx(xn,yn, xout, na.rm=FALSE, rule = 2))
data.frame(approx(xn,yn, xout, na.rm=FALSE, rule = 2, method="constant"))

## NA's in x[] are not allowed:
stopifnot(inherits( try( approx(yn,yn, na.rm=FALSE) ), "try-error"))

## Give a nice overview of all possibilities rule * method * na.rm :
### --------------------------------- ------ ------ =====
## extrapolations "N":= NA; "C":= Constant :
rules <- list(N=1, C=2, NC=1:2, CN=2:1)
methods <- c("constant", "linear")
ry <- sapply(rules, function(R) {
sapply(methods, function(M)
sapply(setNames(,c(TRUE,FALSE)), function(na.)
  approx(xn, yn, xout=xout, method=M, rule=R, na.rm=na.)$y),
  simplify="array")
}, simplify="array")
names(dimnames(ry)) <- c("x = ", "na.rm", "method", "rule")
dimnames(ry)[[1]] <- format(xout)
ftable(aperm(ry, 4:1)) # --> (4 * 2 * 2) x length(xout) = 16 x 9 matrix

## Show treatment of 'ties' :
x <- c(2,2:4,4,4,5,5,7,7)
y <- c(1:6, 5:4, 3:1)
(amy <- approx(x, y, xout = x)$y) # warning, can be avoided by specifying 'ties=':
op <- options(warn=2) # warnings would be error
stopifnot(identical(amy, approx(x, y, xout = x, ties=mean)$y))
(ay <- approx(x, y, xout = x, ties = "ordered")$y)
stopifnot(amy == c(1.5,1.5, 3, 5,5,5, 4.5,4.5, 2,2,2),
  ay == c(2, 2, 3, 6,6,6, 4, 4, 1,1,1))
approx(x, y, xout = x, ties = min)$y
approx(x, y, xout = x, ties = max)$y
options(op) # revert 'warn'ing level

---

**ar**

*Fit Autoregressive Models to Time Series*

**Description**

Fit an autoregressive time series model to the data, by default selecting the complexity by AIC.

**Usage**

```r
ar(x, aic = TRUE, order.max = NULL,
   method = c("yule-walker", "burg", "ols", "mle", "yw"),
   na.action, series, ...)
ar.burg(x, ...)
```

## Default S3 method:
ar.burg(x, aic = TRUE, order.max = NULL,
ar

na.action = na.fail, demean = TRUE, series, var.method = 1, ...)
## S3 method for class 'mts'
ar.burg(x, aic = TRUE, order.max = NULL, na.action = na.fail, demean = TRUE, series, var.method = 1, ...)

ar.yw(x, ...)
## Default S3 method:
ar.yw(x, aic = TRUE, order.max = NULL, na.action = na.fail, demean = TRUE, series, ...)
## S3 method for class 'mts'
ar.yw(x, aic = TRUE, order.max = NULL, na.action = na.fail, demean = TRUE, series, var.method = 1, ...)
ar.mle(x, aic = TRUE, order.max = NULL, na.action = na.fail, demean = TRUE, series, ...)
## S3 method for class 'ar'
predict(object, newdata, n.ahead = 1, se.fit = TRUE, ...)

Arguments

x

a univariate or multivariate time series.

aic

logical. If TRUE then the Akaike Information Criterion is used to choose the order of the autoregressive model. If FALSE, the model of order order.max is fitted.

order.max

maximum order (or order) of model to fit. Defaults to the smaller of \( N - 1 \) and \( 10 \log_{10}(N) \) where \( N \) is the number of non-missing observations except for method = "mle" where it is the minimum of this quantity and 12.

method

character string specifying the method to fit the model. Must be one of the strings in the default argument (the first few characters are sufficient). Defaults to "yule-walker".

na.action

function to be called to handle missing values. Currently, via na.action = na.pass, only Yule-Walker method can handle missing values which must be consistent within a time point: either all variables must be missing or none.

demean

should a mean be estimated during fitting?

series

names for the series. Defaults to deparse1(substitute(x)).

var.method

the method to estimate the innovations variance (see ‘Details’).

... additional arguments for specific methods.

object

a fit from ar().

newdata

data to which to apply the prediction.

n.ahead

number of steps ahead at which to predict.

se.fit

logical: return estimated standard errors of the prediction error?

Details

For definiteness, note that the AR coefficients have the sign in
\[ x_t - \mu = a_1(x_{t-1} - \mu) + \cdots + a_p(x_{t-p} - \mu) + e_t \]

`ar` is just a wrapper for the functions `ar.yw`, `ar.burg`, `ar.ols` and `ar.mle`.

Order selection is done by AIC if `aic` is true. This is problematic, as of the methods here only `ar.mle` performs true maximum likelihood estimation. The AIC is computed as if the variance estimate were the MLE, omitting the determinant term from the likelihood. Note that this is not the same as the Gaussian likelihood evaluated at the estimated parameter values. In `ar.yw` the variance matrix of the innovations is computed from the fitted coefficients and the autocovariance of \(x\).

`ar.burg` allows two methods to estimate the innovations variance and hence AIC. Method 1 is to use the update given by the Levinson-Durbin recursion (Brockwell and Davis, 1991, (8.2.6) on page 242), and follows S-PLUS. Method 2 is the mean of the sum of squares of the forward and backward prediction errors (as in Brockwell and Davis, 1996, page 145). Percival and Walden (1998) discuss both. In the multivariate case the estimated coefficients will depend (slightly) on the variance estimation method.

Remember that `ar` includes by default a constant in the model, by removing the overall mean of \(x\) before fitting the AR model, or (`ar.mle`) estimating a constant to subtract.

**Value**

For `ar` and its methods a list of class "ar" with the following elements:

- `order`: The order of the fitted model. This is chosen by minimizing the AIC if `aic = TRUE`, otherwise it is `order.max`.
- `ar`: Estimated autoregression coefficients for the fitted model.
- `var.pred`: The prediction variance: an estimate of the portion of the variance of the time series that is not explained by the autoregressive model.
- `x.mean`: The estimated mean of the series used in fitting and for use in prediction.
- `x.intercept` (ar.ols only) The intercept in the model for \(x - x.mean\).
- `aic`: The differences in AIC between each model and the best-fitting model. Note that the latter can have an AIC of \(-\infty\).
- `n.used`: The number of observations in the time series, including missing.
- `n.obs`: The number of non-missing observations in the time series.
- `order.max`: The value of the `order.max` argument.
- `partialacf`: The estimate of the partial autocorrelation function up to lag `order.max`.
- `resid`: Residuals from the fitted model, conditioning on the first `order` observations. The first `order` residuals are set to NA. If `x` is a time series, so is `resid`.
- `method`: The value of the `method` argument.
- `series`: The name(s) of the time series.
- `frequency`: The frequency of the time series.
- `call`: The matched call.
- `asy.var.coef`: (univariate case, `order > 0`) The asymptotic-theory variance matrix of the coefficient estimates.

For `predict.ar`, a time series of predictions, or if `se.fit = TRUE`, a list with components `pred`, the predictions, and `se`, the estimated standard errors. Both components are time series.
**Note**

Only the univariate case of `ar.mle` is implemented.
Fitting by method="mle" to long series can be very slow.
If x contains missing values, see NA, also consider using `arima()`, possibly with method = "ML".

**Author(s)**

Martyn Plummer. Univariate case of `ar.yw`, `ar.mle` and C code for univariate case of `ar.burg` by B. D. Ripley.

**References**


**See Also**

`ar.ols`, `arima` for ARMA models; `acf2AR`, for AR construction from the ACF.

`arima.sim` for simulation of AR processes.

**Examples**

```r
ar(1h)
ar(1h, method = "burg")
ar(1h, method = "ols")
ar(1h, FALSE, 4) # fit ar(4)

(sunspot.ar <- ar(sunspot.year))
predict(sunspot.ar, n.ahead = 25)
## try the other methods too

ar(ts.union(BJsales, BJsales.lead))
## Burg is quite different here, as is OLS (see ar.ols)
ar(ts.union(BJsales, BJsales.lead), method = "burg")
```

---

**ar.ols**  
*Fit Autoregressive Models to Time Series by OLS*

**Description**

Fit an autoregressive time series model to the data by ordinary least squares, by default selecting the complexity by AIC.
Usage

```r
ar.ols(x, aic = TRUE, order.max = NULL, na.action = na.fail,
           demean = TRUE, intercept = demean, series, ...)
```

Arguments

- `x` A univariate or multivariate time series.
- `aic` Logical flag. If `TRUE` then the Akaike Information Criterion is used to choose the order of the autoregressive model. If `FALSE`, the model of order `order.max` is fitted.
- `order.max` Maximum order (or order) of model to fit. Defaults to $10 \log_{10}(N)$ where $N$ is the number of observations.
- `na.action` function to be called to handle missing values.
- `demean` should the AR model be for `x` minus its mean?
- `intercept` should a separate intercept term be fitted?
- `series` names for the series. Defaults to `deparse1(substitute(x))`.
- `...` further arguments to be passed to or from methods.

Details

`ar.ols` fits the general AR model to a possibly non-stationary and/or multivariate system of series `x`. The resulting unconstrained least squares estimates are consistent, even if some of the series are non-stationary and/or co-integrated. For definiteness, note that the AR coefficients have the sign in

$$x_t - \mu = a_0 + a_1(x_{t-1} - \mu) + \cdots + a_p(x_{t-p} - \mu) + e_t$$

where $a_0$ is zero unless `intercept` is true, and $\mu$ is the sample mean if `demean` is true, zero otherwise.

Order selection is done by AIC if `aic` is true. This is problematic, as `ar.ols` does not perform true maximum likelihood estimation. The AIC is computed as if the variance estimate (computed from the variance matrix of the residuals) were the MLE, omitting the determinant term from the likelihood. Note that this is not the same as the Gaussian likelihood evaluated at the estimated parameter values.

Some care is needed if `intercept` is true and `demean` is false. Only use this if the series are roughly centred on zero. Otherwise the computations may be inaccurate or fail entirely.

Value

A list of class "ar" with the following elements:

- `order` The order of the fitted model. This is chosen by minimizing the AIC if `aic = TRUE`, otherwise it is `order.max`.
- `ar` Estimated autoregression coefficients for the fitted model.
- `var.pred` The prediction variance: an estimate of the portion of the variance of the time series that is not explained by the autoregressive model.
- `x.mean` The estimated mean (or zero if `demean` is false) of the series used in fitting and for use in prediction.
- `x.intercept` The intercept in the model for `x - x.mean`, or zero if `intercept` is false.
arima

The differences in AIC between each model and the best-fitting model. Note that the latter can have an AIC of -Inf.

n.used The number of observations in the time series.

order.max The value of the order.max argument.

partialacf NULL. For compatibility with ar.

resid residuals from the fitted model, conditioning on the first order observations. The first order residuals are set to NA. If x is a time series, so is resid.

method The character string "Unconstrained LS".

series The name(s) of the time series.

frequency The frequency of the time series.

call The matched call.

asy.se.coef The asymptotic-theory standard errors of the coefficient estimates.

Author(s)

Adrian Trapletti, Brian Ripley.

References


See Also

ar

Examples

ar(lh, method = "burg")
ar.ols(lh)
ar.ols(lh, FALSE, 4) # fit ar(4)
ar.ols(ts.union(BJsales, BJsales.lead))
x <- diff(log(EuStockMarkets))
ar.ols(x, order.max = 6, demean = FALSE, intercept = TRUE)

arima ARIMA Modelling of Time Series

Description

Fit an ARIMA model to a univariate time series.
Usage

```r
arima(x, order = c(0L, 0L, 0L),
    seasonal = list(order = c(0L, 0L, 0L), period = NA),
    xreg = NULL, include.mean = TRUE,
    transform.pars = TRUE,
    fixed = NULL, init = NULL,
    method = c("CSS-ML", "ML", "CSS"), n.cond,
    SSinit = c("Gardner1980", "Rossignol2011"),
    optim.method = "BFGS",
    optim.control = list(), kappa = 1e6)
```

Arguments

- **x**: a univariate time series
- **order**: A specification of the non-seasonal part of the ARIMA model: the three integer components \((p, d, q)\) are the AR order, the degree of differencing, and the MA order.
- **seasonal**: A specification of the seasonal part of the ARIMA model, plus the period (which defaults to `frequency(x)`). This may be a list with components `order` and `period`, or just a numeric vector of length 3 which specifies the seasonal order. In the latter case the default period is used.
- **xreg**: Optionally, a vector or matrix of external regressors, which must have the same number of rows as `x`.
- **include.mean**: Should the ARMA model include a mean/intercept term? The default is `TRUE` for undifferenced series, and it is ignored for ARIMA models with differencing.
- **transform.pars**: logical; if true, the AR parameters are transformed to ensure that they remain in the region of stationarity. Not used for `method = "CSS"`. For `method = "ML"`, it has been advantageous to set `transform.pars = FALSE` in some cases, see also `fixed`.
- **fixed**: optional numeric vector of the same length as the total number of coefficients to be estimated. It should be of the form 

  \[
  (\phi_1, \ldots, \phi_p, \theta_1, \ldots, \theta_q, \Phi_1, \ldots, \Phi_P, \Theta_1, \ldots, \Theta_Q, \mu),
  \]

  where \(\phi_i\) are the AR coefficients, \(\theta_i\) are the MA coefficients, \(\Phi_i\) are the seasonal AR coefficients, \(\Theta_i\) are the seasonal MA coefficients and \(\mu\) is the intercept term. Note that the \(\mu\) entry is required if and only if `include.mean` is `TRUE`. In particular it should not be present if the model is an ARIMA model with differencing. The entries of the `fixed` vector should consist of the values at which the user wishes to “fix” the corresponding coefficient, or `NA` if that coefficient should not be fixed, but estimated.

  The argument `transform.pars` will be set to `FALSE` if any AR parameters are fixed. A warning will be given if `transform.pars` is set to (or left at its default) `TRUE`. It may be wise to set `transform.pars = FALSE` even when fixing MA parameters, especially at values that cause the model to be nearly non-invertible.

- **init**: optional numeric vector of initial parameter values. Missing values will be filled in, by zeroes except for regression coefficients. Values already specified in `fixed` will be ignored.
- **method**: fitting method: maximum likelihood or minimize conditional sum-of-squares. The default (unless there are missing values) is to use conditional-sum-of-squares to find starting values, then maximum likelihood. Can be abbreviated.
**arima**

- **n.cond** only used if fitting by conditional-sum-of-squares: the number of initial observations to ignore. It will be ignored if less than the maximum lag of an AR term.

- **SSinit** a string specifying the algorithm to compute the state-space initialization of the likelihood; see KalmanLike for details. Can be abbreviated.

- **optim.method** The value passed as the method argument to optim.

- **optim.control** List of control parameters for optim.

- **kappa** the prior variance (as a multiple of the innovations variance) for the past observations in a differenced model. Do not reduce this.

**Details**

Different definitions of ARMA models have different signs for the AR and/or MA coefficients. The definition used here has

\[
X_t = a_1 X_{t-1} + \cdots + a_p X_{t-p} + e_t + b_1 e_{t-1} + \cdots + b_q e_{t-q}
\]

and so the MA coefficients differ in sign from those of S-PLUS. Further, if include.mean is true (the default for an ARMA model), this formula applies to \( X - m \) rather than \( X \). For ARIMA models with differencing, the differenced series follows a zero-mean ARMA model. If an xreg term is included, a linear regression (with a constant term if include.mean is true and there is no differencing) is fitted with an ARMA model for the error term.

The variance matrix of the estimates is found from the Hessian of the log-likelihood, and so may only be a rough guide.

Optimization is done by optim. It will work best if the columns in xreg are roughly scaled to zero mean and unit variance, but does attempt to estimate suitable scalings.

**Value**

A list of class "Arima" with components:

- **coef** a vector of AR, MA and regression coefficients, which can be extracted by the coef method.
- **sigma2** the MLE of the innovations variance.
- **var.coef** the estimated variance matrix of the coefficients coef, which can be extracted by the vcov method.
- **loglik** the maximized log-likelihood (of the differenced data), or the approximation to it used.
- **arma** A compact form of the specification, as a vector giving the number of AR, MA, seasonal AR and seasonal MA coefficients, plus the period and the number of non-seasonal and seasonal differences.
- **aic** the AIC value corresponding to the log-likelihood. Only valid for method = "ML" fits.
- **residuals** the fitted innovations.
- **call** the matched call.
- **series** the name of the series x.
- **code** the convergence value returned by optim.
- **n.cond** the number of initial observations not used in the fitting.
nobs the number of “used” observations for the fitting, can also be extracted via `nobs()` and is used by `BIC`.

model A list representing the Kalman Filter used in the fitting. See `KalmanLike`.

Fitting methods

The exact likelihood is computed via a state-space representation of the ARIMA process, and the innovations and their variance found by a Kalman filter. The initialization of the differenced ARMA process uses stationarity and is based on Gardner et al (1980). For a differenced process the non-stationary components are given a diffuse prior (controlled by `kappa`). Observations which are still controlled by the diffuse prior (determined by having a Kalman gain of at least 1e4) are excluded from the likelihood calculations. (This gives comparable results to `arima0` in the absence of missing values, when the observations excluded are precisely those dropped by the differencing.)

Missing values are allowed, and are handled exactly in method "ML".

If `transform.pars` is true, the optimization is done using an alternative parametrization which is a variation on that suggested by Jones (1980) and ensures that the model is stationary. For an AR(p) model the parametrization is via the inverse tanh of the partial autocorrelations: the same procedure is applied (separately) to the AR and seasonal AR terms. The MA terms are not constrained to be invertible during optimization, but they will be converted to invertible form after optimization if `transform.pars` is true.

Conditional sum-of-squares is provided mainly for expositional purposes. This computes the sum of squares of the fitted innovations from observation `n.cond` on, (where `n.cond` is at least the maximum lag of an AR term), treating all earlier innovations to be zero. Argument `n.cond` can be used to allow comparability between different fits. The ‘part log-likelihood’ is the first term, half the log of the estimated mean square. Missing values are allowed, but will cause many of the innovations to be missing.

When regressors are specified, they are orthogonalized prior to fitting unless any of the coefficients is fixed. It can be helpful to roughly scale the regressors to zero mean and unit variance.

Note

The results are likely to be different from S-PLUS’s `arima.mle`, which computes a conditional likelihood and does not include a mean in the model. Further, the convention used by `arima.mle` reverses the signs of the MA coefficients.

`arima` is very similar to `arima0` for ARMA models or for differenced models without missing values, but handles differenced models with missing values exactly. It is somewhat slower than `arima0`, particularly for seasonally differenced models.

References


Simulate from an ARIMA Model

Description

Simulate from an ARIMA model.
Usage

arima.sim(model, n, rand.gen = rnorm, innov = rand.gen(n, ...),
          n.start = NA, start.innov = rand.gen(n.start, ...),
          ...)

Arguments

model A list with component ar and/or ma giving the AR and MA coefficients respectively. Optionally a component order can be used. An empty list gives an ARIMA(0, 0, 0) model, that is white noise.
n length of output series, before un-differencing. A strictly positive integer.
rand.gen optional: a function to generate the innovations.
innov an optional times series of innovations. If not provided, rand.gen is used.
n.start length of ‘burn-in’ period. If NA, the default, a reasonable value is computed.
start.innov an optional times series of innovations to be used for the burn-in period. If supplied there must be at least n.start values (and n.start is by default computed inside the function).
... additional arguments for rand.gen. Most usefully, the standard deviation of the innovations generated by rnorm can be specified by sd.

Details

See arima for the precise definition of an ARIMA model.
The ARMA model is checked for stationarity.
ARIMA models are specified via the order component of model, in the same way as for arima. Other aspects of the order component are ignored, but inconsistent specifications of the MA and AR orders are detected. The un-differencing assumes previous values of zero, and to remind the user of this, those values are returned.
Random inputs for the ‘burn-in’ period are generated by calling rand.gen.

Value

A time-series object of class "ts".

See Also

arima

Examples

require(graphics)
arima.sim(n = 63, list(ar = c(0.8897, -0.4858), ma = c(-0.2279, 0.2488)),
          sd = sqrt(0.1796))
# mildly long-tailed
arima.sim(n = 63, list(ar = c(0.8897, -0.4858), ma = c(-0.2279, 0.2488)),
          rand.gen = function(n, ...) sqrt(0.1796) * rt(n, df = 5))
# An ARIMA simulation
ts.sim <- arima.sim(list(order = c(1,1,0), ar = 0.7), n = 200)
ts.plot(ts.sim)
**arima0**  

**Description**  
Fit an ARIMA model to a univariate time series, and forecast from the fitted model.

**Usage**

```r
arima0(x, order = c(0, 0, 0),
seasonal = list(order = c(0, 0, 0), period = NA),
xreg = NULL, include.mean = TRUE, delta = 0.01,
transform.pars = TRUE, fixed = NULL, init = NULL,
method = c("ML", "CSS"), n.cond, optim.control = list())
```

```r
## S3 method for class 'arima0'
predict(object, n.ahead = 1, newxreg, se.fit = TRUE, ...)
```

**Arguments**

- `x` a univariate time series
- `order` A specification of the non-seasonal part of the ARIMA model: the three components \((p, d, q)\) are the AR order, the degree of differencing, and the MA order.
- `seasonal` A specification of the seasonal part of the ARIMA model, plus the period (which defaults to `frequency(x)`). This should be a list with components `order` and `period`, but a specification of just a numeric vector of length 3 will be turned into a suitable list with the specification as the order.
- `xreg` Optionally, a vector or matrix of external regressors, which must have the same number of rows as `x`.
- `include.mean` Should the ARIMA model include a mean term? The default is `TRUE` for undifferenced series, `FALSE` for differenced ones (where a mean would not affect the fit nor predictions).
- `delta` A value to indicate at which point ‘fast recursions’ should be used. See the ‘Details’ section.
- `transform.pars` Logical. If true, the AR parameters are transformed to ensure that they remain in the region of stationarity. Not used for `method = "CSS"`.
- `fixed` optional numeric vector of the same length as the total number of parameters. If supplied, only NA entries in `fixed` will be varied. `transform.pars = TRUE` will be overridden (with a warning) if any ARMA parameters are fixed.
- `init` optional numeric vector of initial parameter values. Missing values will be filled in, by zeroes except for regression coefficients. Values already specified in `fixed` will be ignored.
- `method` Fitting method: maximum likelihood or minimize conditional sum-of-squares. Can be abbreviated.
- `n.cond` Only used if fitting by conditional-sum-of-squares: the number of initial observations to ignore. It will be ignored if less than the maximum lag of an AR term.
- `optim.control` List of control parameters for `optim`.

---

**Description**

Fit an ARIMA model to a univariate time series, and forecast from the fitted model.

**Usage**

```r
arima0(x, order = c(0, 0, 0),
seasonal = list(order = c(0, 0, 0), period = NA),
xreg = NULL, include.mean = TRUE, delta = 0.01,
transform.pars = TRUE, fixed = NULL, init = NULL,
method = c("ML", "CSS"), n.cond, optim.control = list())
```

```r
## S3 method for class 'arima0'
predict(object, n.ahead = 1, newxreg, se.fit = TRUE, ...)
```

**Arguments**

- `x` a univariate time series
- `order` A specification of the non-seasonal part of the ARIMA model: the three components \((p, d, q)\) are the AR order, the degree of differencing, and the MA order.
- `seasonal` A specification of the seasonal part of the ARIMA model, plus the period (which defaults to `frequency(x)`). This should be a list with components `order` and `period`, but a specification of just a numeric vector of length 3 will be turned into a suitable list with the specification as the order.
- `xreg` Optionally, a vector or matrix of external regressors, which must have the same number of rows as `x`.
- `include.mean` Should the ARIMA model include a mean term? The default is `TRUE` for undifferenced series, `FALSE` for differenced ones (where a mean would not affect the fit nor predictions).
- `delta` A value to indicate at which point ‘fast recursions’ should be used. See the ‘Details’ section.
- `transform.pars` Logical. If true, the AR parameters are transformed to ensure that they remain in the region of stationarity. Not used for `method = "CSS"`.
- `fixed` optional numeric vector of the same length as the total number of parameters. If supplied, only NA entries in `fixed` will be varied. `transform.pars = TRUE` will be overridden (with a warning) if any ARMA parameters are fixed.
- `init` optional numeric vector of initial parameter values. Missing values will be filled in, by zeroes except for regression coefficients. Values already specified in `fixed` will be ignored.
- `method` Fitting method: maximum likelihood or minimize conditional sum-of-squares. Can be abbreviated.
- `n.cond` Only used if fitting by conditional-sum-of-squares: the number of initial observations to ignore. It will be ignored if less than the maximum lag of an AR term.
- `optim.control` List of control parameters for `optim`. 
object The result of an arima0 fit.
newxreg New values of xreg to be used for prediction. Must have at least n.ahead rows.
n.ahead The number of steps ahead for which prediction is required.
se.fit Logical: should standard errors of prediction be returned?

Details

Different definitions of ARMA models have different signs for the AR and/or MA coefficients. The
definition here has

$$X_t = a_1 X_{t-1} + \cdots + a_p X_{t-p} + \epsilon_t + b_1 \epsilon_{t-1} + \cdots + b_q \epsilon_{t-q}$$

and so the MA coefficients differ in sign from those of S-PLUS. Further, if include.mean is true,
this formula applies to $X - m$ rather than $X$. For ARIMA models with differencing, the differenced
series follows a zero-mean ARMA model.

The variance matrix of the estimates is found from the Hessian of the log-likelihood, and so may
only be a rough guide, especially for fits close to the boundary of invertibility.

Optimization is done by optim. It will work best if the columns in xreg are roughly scaled to zero
mean and unit variance, but does attempt to estimate suitable scalings.

Finite-history prediction is used. This is only statistically efficient if the MA part of the fit is
invertible, so predict.arima0 will give a warning for non-invertible MA models.

Value

For arima0, a list of class "arima0" with components:

coeff a vector of AR, MA and regression coefficients,
sigma2 the MLE of the innovations variance.
var.coef the estimated variance matrix of the coefficients coeff.
loglik the maximized log-likelihood (of the differenced data), or the approximation to
it used.
arma A compact form of the specification, as a vector giving the number of AR, MA,
seasonal AR and seasonal MA coefficients, plus the period and the number of
non-seasonal and seasonal differences.
aic the AIC value corresponding to the log-likelihood. Only valid for method = "ML" fits.
residuals the fitted innovations.
call the matched call.
series the name of the series x.
convergence the value returned by optim.
n.cond the number of initial observations not used in the fitting.

For predict.arima0, a time series of predictions, or if se.fit = TRUE, a list with components
pred, the predictions, and se, the estimated standard errors. Both components are time series.
Fitting methods

The exact likelihood is computed via a state-space representation of the ARMA process, and the innovations and their variance found by a Kalman filter based on Gardner et al (1980). This has the option to switch to ‘fast recursions’ (assume an effectively infinite past) if the innovations variance is close enough to its asymptotic bound. The argument delta sets the tolerance: at its default value the approximation is normally negligible and the speed-up considerable. Exact computations can be ensured by setting delta to a negative value.

If transform.pars is true, the optimization is done using an alternative parametrization which is a variation on that suggested by Jones (1980) and ensures that the model is stationary. For an AR(p) model the parametrization is via the inverse tanh of the partial autocorrelations: the same procedure is applied (separately) to the AR and seasonal AR terms. The MA terms are also constrained to be invertible during optimization by the same transformation if transform.pars is true. Note that the MLE for MA terms does sometimes occur for MA polynomials with unit roots: such models can be fitted by using transform.pars = FALSE and specifying a good set of initial values (often obtainable from a fit with transform.pars = TRUE).

Missing values are allowed, but any missing values will force delta to be ignored and full recursions used. Note that missing values will be propagated by differencing, so the procedure used in this function is not fully efficient in that case.

Conditional sum-of-squares is provided mainly for expositional purposes. This computes the sum of squares of the fitted innovations from observation n.cond on, (where n.cond is at least the maximum lag of an AR term), treating all earlier innovations to be zero. Argument n.cond can be used to allow comparability between different fits. The ‘part log-likelihood’ is the first term, half the log of the estimated mean square. Missing values are allowed, but will cause many of the innovations to be missing.

When regressors are specified, they are orthogonalized prior to fitting unless any of the coefficients is fixed. It can be helpful to roughly scale the regressors to zero mean and unit variance.

Note

This is a preliminary version, and will be replaced by arima.

The standard errors of prediction exclude the uncertainty in the estimation of the ARMA model and the regression coefficients.

The results are likely to be different from S-PLUS’s arima.mle, which computes a conditional likelihood and does not include a mean in the model. Further, the convention used by arima.mle reverses the signs of the MA coefficients.

References


ARMAacf

See Also

arima, ar, tsdiag

Examples

## Not run: arima0(lh, order = c(1,0,0))
arima0(lh, order = c(3,0,0))
arima0(lh, order = c(1,0,1))
predict(arima0(lh, order = c(3,0,0)), n.ahead = 12)
arima0(lh, order = c(3,0,0), method = "CSS")

# for a model with as few years as this, we want full ML
(fit <- arima0(USAccDeaths, order = c(0,1,1),
    seasonal = list(order=c(0,1,1)), delta = -1))
predict(fit, n.ahead = 6)
arima0(LakeHuron, order = c(2,0,0), xreg = time(LakeHuron)-1920)
## Not run:
## presidents contains NAs
## graphs in example(acf) suggest order 1 or 3
(fit1 <- arima0(presidents, c(1, 0, 0), delta = -1)) # avoid warning
   tsdiag(fit1)
(fit3 <- arima0(presidents, c(3, 0, 0), delta = -1)) # smaller AIC
   tsdiag(fit3)
## End(Not run)

ARMAacf

Compute Theoretical ACF for an ARMA Process

Description

Compute the theoretical autocorrelation function or partial autocorrelation function for an ARMA process.

Usage

ARMAacf(ar = numeric(), ma = numeric(), lag.max = r, pacf = FALSE)

Arguments

ar numeric vector of AR coefficients
ma numeric vector of MA coefficients
lag.max integer. Maximum lag required. Defaults to max(p, q+1), where p, q are the numbers of AR and MA terms respectively.
pacf logical. Should the partial autocorrelations be returned?

Details

The methods used follow Brockwell & Davis (1991, section 3.3). Their equations (3.3.8) are solved for the autocovariances at lags 0,..., max(p, q+1), and the remaining autocorrelations are given by a recursive filter.
Value

A vector of (partial) autocorrelations, named by the lags.

References


See Also

`arima`, `ARMAtoMA`, `acf2AR` for inverting part of `ARMAacf`; further `filter`.

Examples

```r
ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10)
## Example from Brockwell & Davis (1991, pp.92-4)
## answer: 2^(-n) * (32/3 + 8 * n) / (32/3)

n <- 1:10
a.n <- 2^(-n) * (32/3 + 8 * n) / (32/3)
(A.n <- ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10))
stopifnot(all.equal(unname(A.n), c(1, a.n)))

ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10, pacf = TRUE)
zapsmall(ARMAacf(c(1.0, -0.25), lag.max = 10, pacf = TRUE))
## Cov-Matrix of length-7 sub-sample of AR(1) example:
toeplitz(ARMAacf(0.8, lag.max = 7))
```

---

**ARMAtoMA**

*Convert ARMA Process to Infinite MA Process*

Description

Convert ARMA process to infinite MA process.

Usage

```r
ARMAtoMA(ar = numeric(), ma = numeric(), lag.max)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ar</code></td>
<td>numeric vector of AR coefficients</td>
</tr>
<tr>
<td><code>ma</code></td>
<td>numeric vector of MA coefficients</td>
</tr>
<tr>
<td><code>lag.max</code></td>
<td>Largest MA(Inf) coefficient required.</td>
</tr>
</tbody>
</table>

Value

A vector of coefficients.
References


See Also

`arima`, `ARMAacf`.

Examples

```r
ARMAtoMA(c(1.0, -0.25), 1.0, 10)
## Example from Brockwell & Davis (1991, p.92)
## answer (1 + 3*n)*2^(-n)
```

n <- 1:10; (1 + 3*n)*2^(-n)

---

**as.hclust**

*Convert Objects to Class hclust*

**Description**

Converts objects from other hierarchical clustering functions to class "hclust".

**Usage**

`as.hclust(x, ...)`

**Arguments**

- `x`  
  Hierarchical clustering object

- `...`  
  Further arguments passed to or from other methods.

**Details**

Currently there is only support for converting objects of class "twins" as produced by the functions `diana` and `agnes` from the package `cluster`. The default method throws an error unless passed an "hclust" object.

**Value**

An object of class "hclust".

**See Also**

`hclust`, and from package `cluster`, `diana` and `agnes`
Examples

```r
x <- matrix(rnorm(30), ncol = 3)
hc <- hclust(dist(x), method = "complete")

if(require("cluster", quietly = TRUE)) { # is a recommended package
  ag <- agnes(x, method = "complete")
hcag <- as.hclust(ag)
  ## The dendrograms order slightly differently:
op <- par(mfrow = c(1,2))
  plot(hc); mtext("hclust", side = 1)
  plot(hcag); mtext("agnes", side = 1)
detach("package:cluster")
}
```

---

asOneSidedFormula  
Convert to One-Sided Formula

Description

Names, calls, expressions (first element), numeric values, and character strings are converted to one-sided formulae associated with the global environment. If the input is a formula, it must be one-sided, in which case it is returned unaltered.

Usage

```r
asOneSidedFormula(object)
```

Arguments

object  
a one-sided formula, name, call, expression, numeric value, or character string.

Value

a one-sided formula representing object

Author(s)

José Pinheiro and Douglas Bates

See Also

`formula`

Examples

```r
(form <- asOneSidedFormula("age"))
stopifnot(exprs = {
  identical(form, asOneSidedFormula(form))
  identical(form, asOneSidedFormula(as.name("age")))
  identical(form, asOneSidedFormula(expression(age)))
})
asOneSidedFormula(quote(log(age)))
asOneSidedFormula(1)
```
Description

Subsets of x[] are averaged, where each subset consist of those observations with the same factor levels.

Usage

ave(x, ..., FUN = mean)

Arguments

x  A numeric.
...
Grouping variables, typically factors, all of the same length as x.
FUN  Function to apply for each factor level combination.

Value

A numeric vector, say y of length length(x). If ... is g1, g2, e.g., y[i] is equal to FUN(x[j]), for all j with g1[j] == g1[i] and g2[j] == g2[i]).

See Also

mean, median.

Examples

require(graphics)
ave(1:3)  # no grouping -> grand mean

attach(warpbreaks)
ave(breaks, wool)
ave(breaks, tension)
ave(breaks, tension, FUN = function(x) mean(x, trim = 0.1))
plot(breaks, main = 
"ave( Warpbreaks ) for wool x tension combinations")
lines(ave(breaks, wool, tension ), type = "s", col = "blue")
lines(ave(breaks, wool, tension, FUN = median), type = "s", col = "green")
legend(40, 70, c("mean", "median"), lty = 1,
       col = c("blue","green"), bg = "gray90")
detach()
Bandwidth selectors for Gaussian kernels in density.

Usage

bw.nrd0(x)
bw.nrd(x)

bw.ucv(x, nb = 1000, lower = 0.1 * hmax, upper = hmax, tol = 0.1 * lower)
bw.bcv(x, nb = 1000, lower = 0.1 * hmax, upper = hmax, tol = 0.1 * lower)
bw.SJ(x, nb = 1000, lower = 0.1 * hmax, upper = hmax, method = c("ste", "dpi"), tol = 0.1 * lower)

Arguments

x numeric vector.

nb number of bins to use.

lower, upper range over which to minimize. The default is almost always satisfactory. hmax is calculated internally from a normal reference bandwidth.

method either "ste" ("solve-the-equation") or "dpi" ("direct plug-in"). Can be abbreviated.

tol for method "ste", the convergence tolerance for unroot. The default leads to bandwidth estimates with only slightly more than one digit accuracy, which is sufficient for practical density estimation, but possibly not for theoretical simulation studies.

Details

bw.nrd0 implements a rule-of-thumb for choosing the bandwidth of a Gaussian kernel density estimator. It defaults to 0.9 times the minimum of the standard deviation and the interquartile range divided by 1.34 times the sample size to the negative one-fifth power (= Silverman’s ‘rule of thumb’, Silverman (1986, page 48, eqn (3.31))) unless the quartiles coincide when a positive result will be guaranteed.

bw.nrd is the more common variation given by Scott (1992), using factor 1.06.

bw.ucv and bw.bcv implement unbiased and biased cross-validation respectively.

bw.SJ implements the methods of Sheather & Jones (1991) to select the bandwidth using pilot estimation of derivatives.

The algorithm for method "ste" solves an equation (via unroot) and because of that, enlarges the interval c(lower, upper) when the boundaries were not user-specified and do not bracket the root.
The last three methods use all pairwise binned distances: they are of complexity $O(n^2)$ up to $n = nb/2$ and $O(n)$ thereafter. Because of the binning, the results differ slightly when $x$ is translated or sign-flipped.

**Value**

A bandwidth on a scale suitable for the `bw` argument of `density`.

**Note**

Long vectors $x$ are not supported, but neither are they by `density` and kernel density estimation and for more than a few thousand points a histogram would be preferred.

**Author(s)**

B. D. Ripley, taken from early versions of package MASS.

**References**


**See Also**

`density`, `bandwidth.nrd`, `ucv`, `bcv` and `width.SJ` in package MASS, which are all scaled to the width argument of `density` and so give answers four times as large.

**Examples**

```
require(graphics)
plot(density(precip, n = 1000))
nrug(precip)
lines(density(precip, bw = "nrd"), col = 2)
lines(density(precip, bw = "ucv"), col = 3)
lines(density(precip, bw = "bcv"), col = 4)
lines(density(precip, bw = "SJ-ste"), col = 5)
lines(density(precip, bw = "SJ-dpi"), col = 6)
legend(55, 0.035,
       legend = c("nrd0", "nrd", "ucv", "bcv", "SJ-ste", "SJ-dpi"),
       col = 1:6, lty = 1)
```
**bartlett.test**  
*Bartlett Test of Homogeneity of Variances*

**Description**

Performs Bartlett’s test of the null that the variances in each of the groups (samples) are the same.

**Usage**

```r
bartlett.test(x, ...)  
```

## Default S3 method:
```
bartlett.test(x, g, ...)  
```

## S3 method for class 'formula'
```
bartlett.test(formula, data, subset, na.action, ...)  
```

**Arguments**

- **x**
  a numeric vector of data values, or a list of numeric data vectors representing the respective samples, or fitted linear model objects (inheriting from class “lm”).
  
- **g**
  a vector or factor object giving the group for the corresponding elements of x.
  Ignored if x is a list.

- **formula**
  a formula of the form `lhs ~ rhs` where `lhs` gives the data values and `rhs` the corresponding groups.

- **data**
  an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.

- **subset**
  an optional vector specifying a subset of observations to be used.

- **na.action**
  a function which indicates what should happen when the data contain NAs. Defaults to `getOption("na.action")`.

- **...**
  further arguments to be passed to or from methods.

**Details**

If x is a list, its elements are taken as the samples or fitted linear models to be compared for homogeneity of variances. In this case, the elements must either all be numeric data vectors or fitted linear model objects, g is ignored, and one can simply use `bartlett.test(x)` to perform the test.

If the samples are not yet contained in a list, use `bartlett.test(list(x, ...))`.

Otherwise, x must be a numeric data vector, and g must be a vector or factor object of the same length as x giving the group for the corresponding elements of x.

**Value**

A list of class "htest" containing the following components:

- **statistic**
  Bartlett’s K-squared test statistic.

- **parameter**
  the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value the p-value of the test.
method the character string "Bartlett test of homogeneity of variances".
data.name a character string giving the names of the data.

References

See Also
var.test for the special case of comparing variances in two samples from normal distributions;
fligner.test for a rank-based (nonparametric) *k*-sample test for homogeneity of variances;
ansari.test and mood.test for two rank based two-sample tests for difference in scale.

Examples
```r
require(graphics)
plot(count ~ spray, data = InsectSprays)
bartlett.test(InsectSprays$count, InsectSprays$spray)
bartlett.test(count ~ spray, data = InsectSprays)
```

---

**Beta**

**The Beta Distribution**

Description
Density, distribution function, quantile function and random generation for the Beta distribution with parameters shape1 and shape2 (and optional non-centrality parameter ncp).

Usage
```r
dbeta(x, shape1, shape2, ncp = 0, log = FALSE)
pbeta(q, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE)
qbeta(p, shape1, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE)
rbeta(n, shape1, shape2, ncp = 0)
```

Arguments
- `x, q` vector of quantiles.
- `p` vector of probabilities.
- `n` number of observations. If length(n) > 1, the length is taken to be the number required.
- `shape1, shape2` non-negative parameters of the Beta distribution.
- `ncp` non-centrality parameter.
- `log, log.p` logical; if TRUE, probabilities p are given as log(p).
- `lower.tail` logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$. 

---
The Beta distribution with parameters $\text{shape1} = a$ and $\text{shape2} = b$ has density

$$f(x) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} x^{a-1}(1-x)^{b-1}$$

for $a > 0$, $b > 0$ and $0 \leq x \leq 1$ where the boundary values at $x = 0$ or $x = 1$ are defined as by continuity (as limits).

The mean is $a/(a+b)$ and the variance is $ab/((a+b)^2(a+b+1))$. If $a, b > 1$, (or one of them $= 1$), the mode is $(a-1)/(a+b-2)$. These and all other distributional properties can be defined as limits (leading to point masses at 0, 1/2, or 1) when $a$ or $b$ are zero or infinite, and the corresponding [dpqr]beta() functions are defined correspondingly.

pbeta is closely related to the incomplete beta function. As defined by Abramowitz and Stegun 6.6.1

$$B_x(a,b) = \int_0^x t^{a-1}(1-t)^{b-1} dt,$$

and 6.6.2 $I_x(a,b) = B_x(a,b)/B(a,b)$ where $B(a,b) = B_1(a,b)$ is the Beta function (beta).

$I_x (a, b)$ is pbeta(x, a, b).

The noncentral Beta distribution (with ncp = $\lambda$) is defined (Johnson et al, 1995, pp. 502) as the distribution of $X/(X+Y)$ where $X \sim \chi^2_{2a}(\lambda)$ and $Y \sim \chi^2_{2b}$. **Value**

dbeta gives the density, pbeta the distribution function, qbeta the quantile function, and rbeta generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

The length of the result is determined by n for rbeta, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

**Note**

Supplying ncp = 0 uses the algorithm for the non-central distribution, which is not the same algorithm as when ncp is omitted. This is to give consistent behaviour in extreme cases with values of ncp very near zero.

**Source**

- The central dbeta is based on a binomial probability, using code contributed by Catherine Loader (see dbinom) if either shape parameter is larger than one, otherwise directly from the definition. The non-central case is based on the derivation as a Poisson mixture of betas (Johnson et al, 1995, pp. 502–3).

We have slightly tweaked the original “TOMS 708” algorithm, and enhanced for log.p = TRUE. For that (log-scale) case, underflow to -Inf (i.e., P = 0) or 0, (i.e., P = 1) still happens because the original algorithm was designed without log-scale considerations. Underflow to -Inf now typically signals a warning.

• The non-central pbeta uses a C translation of
  This computes the lower tail only, so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant.

• The central case of qbeta is based on a C translation of
  Enhancements, notably for starting values and switching to a log-scale Newton search, by R Core.

• The central case of rbeta is based on a C translation of

References


Chapter 6: Gamma and Related Functions.


See Also

*Distributions* for other standard distributions.

`beta` for the Beta function.

Examples

```r
x <- seq(0, 1, length.out = 21)
dbeta(x, 1, 1)
pbeta(x, 1, 1)
```

```r
pl.beta <- function(a,b, asp = if(isLim) 1, ylim = if(isLim) c(0,1.1)) {
  if(isLim <- a == 0 || b == 0 || a == Inf || b == Inf) {
    eps <- 1e-10
    x <- c(0, eps, (1:7)/16, 1/2+c(-eps,0,eps), (9:15)/16, 1-eps, 1)
  } else {
    x <- seq(0, 1, length.out = 1025)
  }
  fx <- cbind(dbeta(x, a,b), pbeta(x, a,b), qbeta(x, a,b))
  f <- fx; f[fx == Inf] <- 1e10
  matplot(x, f, ylab="", type="l", ylim=ylim, asp=asp,
         main = sprintf("[dpq]beta(x, a=%g, b=%g)", a,b))
```
abline(0,1, col="gray", lty=3)
abline(h = 0:1, col="gray", lty=3)
legend("top", paste0(c("d","p","q"), "beta(x, a,b)")
, col=1:3, lty=1:3, bty = "n")
invisible(cbind(x, fx))

pl.beta(3,1)
pl.beta(2, 4)
pl.beta(3, 7)
pl.beta(3, 7, asp=1)

pl.beta(0, 0) ## point masses at {0, 1}
pl.beta(0, 2) ## point mass at 0 ; the same as
pl.beta(1, Inf)

pl.beta(Inf, 2) ## point mass at 1 ; the same as
pl.beta(3, 0)

pl.beta(Inf, Inf)# point mass at 1/2

binom.test 1367

---

**binom.test**

**Exact Binomial Test**

**Description**

Performs an exact test of a simple null hypothesis about the probability of success in a Bernoulli experiment.

**Usage**

```r
cntom.test(x, n, p = 0.5,
alternative = c("two.sided", "less", "greater"),
conf.level = 0.95)
```

**Arguments**

- `x`: number of successes, or a vector of length 2 giving the numbers of successes and failures, respectively.
- `n`: number of trials; ignored if `x` has length 2.
- `p`: hypothesized probability of success.
- `alternative`: indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter.
- `conf.level`: confidence level for the returned confidence interval.

**Details**

Confidence intervals are obtained by a procedure first given in Clopper and Pearson (1934). This guarantees that the confidence level is at least `conf.level`, but in general does not give the shortest-length confidence intervals.
Value

A list with class "htest" containing the following components:

- **statistic**: the number of successes.
- **parameter**: the number of trials.
- **p.value**: the p-value of the test.
- **conf.int**: a confidence interval for the probability of success.
- **estimate**: the estimated probability of success.
- **null.value**: the probability of success under the null, $$p$$.
- **alternative**: a character string describing the alternative hypothesis.
- **method**: the character string "Exact binomial test".
- **data.name**: a character string giving the names of the data.

References


See Also

- `prop.test` for a general (approximate) test for equal or given proportions.

Examples

```r
## Under (the assumption of) simple Mendelian inheritance, a cross
## between plants of two particular genotypes produces progeny 1/4 of
## which are "dwarf" and 3/4 of which are "giant", respectively.
## In an experiment to determine if this assumption is reasonable, a
## cross results in progeny having 243 dwarf and 682 giant plants.
## If "giant" is taken as success, the null hypothesis is that $$p =
## 3/4$$ and the alternative that $$p \neq 3/4$$.
binom.test(c(682, 243), p = 3/4)
binom.test(682, 682 + 243, p = 3/4)  # The same.
## => Data are in agreement with the null hypothesis.
```

Description

Density, distribution function, quantile function and random generation for the binomial distribution with parameters `size` and `prob`.

This is conventionally interpreted as the number of 'successes' in `size` trials.
Binomial

Usage

dbinom(x, size, prob, log = FALSE)
pbinom(q, size, prob, lower.tail = TRUE, log.p = FALSE)
qbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE)
rbinom(n, size, prob)

Arguments

x, q vector of quantiles.
p vector of probabilities.
n number of observations. If length(n) > 1, the length is taken to be the number required.
size number of trials (zero or more).
prob probability of success on each trial.
log, log.p logical; if TRUE, probabilities p are given as log(p).
lower.tail logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).

Details

The binomial distribution with size = \( n \) and prob = \( p \) has density

\[
p(x) = \binom{n}{x} p^x (1 - p)^{n-x}
\]

for \( x = 0, \ldots, n \). Note that binomial coefficients can be computed by choose in R.

If an element of \( x \) is not integer, the result of dbinom is zero, with a warning.

\( p(x) \) is computed using Loader's algorithm, see the reference below.

The quantile is defined as the smallest value \( x \) such that \( F(x) \geq p \), where \( F \) is the distribution function.

Value

dbinom gives the density, pbinom gives the distribution function, qbinom gives the quantile function and rbinom generates random deviates.

If size is not an integer, NaN is returned.

The length of the result is determined by \( n \) for rbinom, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than \( n \) are recycled to the length of the result. Only the first elements of the logical arguments are used.

Source

For dbinom a saddle-point expansion is used: see


pbinom uses pbeta.

qbinom uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.
rbinom (for size < .Machine$integer.max) is based on
For larger values it uses inversion.

See Also
Distributions for other standard distributions, including dnbino for the negative binomial, and dpois for the Poisson distribution.

Examples
require(graphics)
# Compute P(45 < X < 55) for X Binomial(100,0.5)
sum(dbinom(46:54, 100, 0.5))

## Using "log = TRUE" for an extended range :
n <- 2000
k <- seq(0, n, by = 20)
plot (k, dbinom(k, n, pi/10, log = TRUE), type = "l", ylab = "log density",
main = "dbinom(*, log=TRUE) is better than log(dbinom(*))")
lines(k, log(dbinom(k, n, pi/10)), col = "red", lwd = 2)
## extreme points are omitted since dbinom gives 0.
mttext("dbinom(k, log=TRUE)", adj = 0)
mttext("extended range", adj = 0, line = -1, font = 4)
mttext("log(dbinom(k))", col = "red", adj = 1)

biplot Biplot of Multivariate Data

Description
Plot a biplot on the current graphics device.

Usage
biplot(x, ...)

## Default S3 method:
biplot(x, y, var.axes = TRUE, col, cex = rep(par("cex"), 2),
xlabs = NULL, ylabs = NULL, expand = 1,
xlim = NULL, ylim = NULL, arrow.len = 0.1,
main = NULL, sub = NULL, xlab = NULL, ylab = NULL, ...)

Arguments
x The biplot, a fitted object. For biplot.default, the first set of points (a two-
column matrix), usually associated with observations.
y The second set of points (a two-column matrix), usually associated with variables.
var.axes If TRUE the second set of points have arrows representing them as (unscaled) axes.
col
A vector of length 2 giving the colours for the first and second set of points respectively (and the corresponding axes). If a single colour is specified it will be used for both sets. If missing the default colour is looked for in the palette: if there it and the next colour as used, otherwise the first two colours of the palette are used.

cex
The character expansion factor used for labelling the points. The labels can be of different sizes for the two sets by supplying a vector of length two.

xlabs
A vector of character strings to label the first set of points: the default is to use the row dimname of x, or 1:n if the dimname is NULL.

ylabs
A vector of character strings to label the second set of points: the default is to use the row dimname of y, or 1:n if the dimname is NULL.

expand
An expansion factor to apply when plotting the second set of points relative to the first. This can be used to tweak the scaling of the two sets to a physically comparable scale.

arrow.len
The length of the arrow heads on the axes plotted in var.axes is true. The arrow head can be suppressed by arrow.len = 0.

xlim, ylim
Limits for the x and y axes in the units of the first set of variables.

main, sub, xlab, ylab, ...
graphical parameters.

Details
A biplot is plot which aims to represent both the observations and variables of a matrix of multivariate data on the same plot. There are many variations on biplots (see the references) and perhaps the most widely used one is implemented by biplot.princomp. The function biplot.default merely provides the underlying code to plot two sets of variables on the same figure.

Graphical parameters can also be given to biplot: the size of xlabs and ylabs is controlled by cex.

Side Effects
a plot is produced on the current graphics device.

References


See Also
biplot.princomp, also for examples.
Biplot for Principal Components

Description

Produces a biplot (in the strict sense) from the output of `princomp` or `prcomp`.

Usage

```r
## S3 method for class 'prcomp'
biplot(x, choices = 1:2, scale = 1, pc.biplot = FALSE, ...)

## S3 method for class 'princomp'
biplot(x, choices = 1:2, scale = 1, pc.biplot = FALSE, ...)
```

Arguments

- `x`: an object of class "princomp".
- `choices`: length 2 vector specifying the components to plot. Only the default is a biplot in the strict sense.
- `scale`: The variables are scaled by $\lambda^\text{scale}$ and the observations are scaled by $\lambda^\text{1-scale}$ where $\lambda$ are the singular values as computed by `princomp`. Normally $0 \leq \text{scale} \leq 1$, and a warning will be issued if the specified scale is outside this range.
- `pc.biplot`: If true, use what Gabriel (1971) refers to as a "principal component biplot", with $\lambda = 1$ and observations scaled up by $\sqrt{n}$ and variables scaled down by $\sqrt{n}$. Then inner products between variables approximate covariances and distances between observations approximate Mahalanobis distance.
- `...`: optional arguments to be passed to `biplot.default`.

Details

This is a method for the generic function `biplot`. There is considerable confusion over the precise definitions: those of the original paper, Gabriel (1971), are followed here. Gabriel and Odoroff (1990) use the same definitions, but their plots actually correspond to `pc.biplot = TRUE`.

Side Effects

A plot is produced on the current graphics device.

References


See Also

`biplot.princomp`
Examples

```r
require(graphics)
biplot(princomp(USArrests))
```
Examples

require(graphics)

## the standard version
qbirthday() # 23
## probability of > 2 people with the same birthday
qbirthday(23, coincident = 3)

## examples from Diaconis & Mosteller p. 858.
## 'coincidence' is that husband, wife, daughter all born on the 16th
qbirthday(classes = 30, coincident = 3) # approximately 18
qbirthday(coincident = 4) # exact value 187
qbirthday(coincident = 10) # exact value 1181

## same 4-digit PIN number
qbirthday(classes = 10^4)

## 0.9 probability of three or more coincident birthdays
qbirthday(coincident = 3, prob = 0.9)

## Chance of 4 or more coincident birthdays in 150 people
pbirthday(150, coincident = 4)

## 100 or more coincident birthdays in 1000 people: very rare
pbirthday(1000, coincident = 100)

---

Box.test

### Box-Pierce and Ljung-Box Tests

**Description**

Compute the Box–Pierce or Ljung–Box test statistic for examining the null hypothesis of independence in a given time series. These are sometimes known as ‘portmanteau’ tests.

**Usage**

```r
Box.test(x, lag = 1, type = c("Box-Pierce", "Ljung-Box"), fitdf = 0)
```

**Arguments**

- `x` a numeric vector or univariate time series.
- `lag` the statistic will be based on lag autocorrelation coefficients.
- `type` test to be performed: partial matching is used.
- `fitdf` number of degrees of freedom to be subtracted if `x` is a series of residuals.

**Details**

These tests are sometimes applied to the residuals from an ARMA(p, q) fit, in which case the references suggest a better approximation to the null-hypothesis distribution is obtained by setting `fitdf = p+q`, provided of course that `lag > fitdf`. 
Value

A list with class "htest" containing the following components:

- statistic: the value of the test statistic.
- parameter: the degrees of freedom of the approximate chi-squared distribution of the test statistic (taking fitdf into account).
- p.value: the p-value of the test.
- method: a character string indicating which type of test was performed.
- data.name: a character string giving the name of the data.

Note

Missing values are not handled.

Author(s)

A. Trapletti

References


Examples

```r
x <- rnorm(100)
Box.test(x, lag = 1)
Box.test(x, lag = 1, type = "Ljung")
```

C

Sets Contrasts for a Factor

Description

Sets the "contrasts" attribute for the factor.

Usage

`C(object, contr, how.many, ...)`

Arguments

- object: a factor or ordered factor
- contr: which contrasts to use. Can be a matrix with one row for each level of the factor or a suitable function like contr.poly or a character string giving the name of the function
- how.many: the number of contrasts to set, by default one less than nlevels(object).
- ...: additional arguments for the function contr.
Details

For compatibility with S, contr can be treatment, helmert, sum or poly (without quotes) as shorthand for contr.treatment and so on.

Value

The factor object with the "contrasts" attribute set.

References


See Also

characteristics, contr.sum, etc.

Examples

## reset contrasts to defaults
options(contrasts = c("contr.treatment", "contr.poly"))
tens <- with(warpbreaks, C(tension, poly, 1))
attributes(tens)
## tension SHOULD be an ordered factor, but as it is not we can use
aov(breaks ~ wool + tens + tension, data = warpbreaks)
## show the use of ... The default contrast is contr.treatment here
summary(lm(breaks ~ wool + C(tension, base = 2), data = warpbreaks))

# following on from help(esoph)
model3 <- glm(cbind(ncases, ncontrols) ~ agegp + C(tobgp , 1) + 
               C(alcgp, , 1), data = esoph, family = binomial())
summary(model3)

cancor

Canonical Correlations

Description

Compute the canonical correlations between two data matrices.

Usage

cancor(x, y, xcenter = TRUE, ycenter = TRUE)

Arguments

x numeric matrix ($n \times p_1$), containing the x coordinates.
y numeric matrix ($n \times p_2$), containing the y coordinates.
cancor

xcenter logical or numeric vector of length $p_1$, describing any centering to be done on the x values before the analysis. If TRUE (default), subtract the column means. If FALSE, do not adjust the columns. Otherwise, a vector of values to be subtracted from the columns.

ycenter analogous to xcenter, but for the y values.

Details

The canonical correlation analysis seeks linear combinations of the y variables which are well explained by linear combinations of the x variables. The relationship is symmetric as ‘well explained’ is measured by correlations.

Value

A list containing the following components:

- cor correlations.
- xcoef estimated coefficients for the x variables.
- ycoef estimated coefficients for the y variables.
- xcenter the values used to adjust the x variables.
- ycenter the values used to adjust the x variables.

References


See Also

- qr, svd.

Examples

```r
## signs of results are random
pop <- LifeCycleSavings[, 2:3]
oec <- LifeCycleSavings[, -(2:3)]
cancor(pop, oec)

x <- matrix(rnorm(150), 50, 3)
y <- matrix(rnorm(250), 50, 5)
(cxy <- cancor(x, y))
all(abs(cor(x %*% cxy$xcoef, y %*% cxy$ycoef)[,1:3] - diag(cxy $ cor)) < 1e-15)
all(abs(cor(x %*% cxy$xcoef) - diag(3)) < 1e-15)
all(abs(cor(y %*% cxy$ycoef) - diag(5)) < 1e-15)
```
Case and Variable Names of Fitted Models

Description

Simple utilities returning (non-missing) case names, and (non-eliminated) variable names.

Usage

case.names(object, ...)  
## S3 method for class 'lm'  
  case.names(object, full = FALSE, ...)  

variable.names(object, ...)  
## S3 method for class 'lm'  
  variable.names(object, full = FALSE, ...)  

Arguments

object an R object, typically a fitted model.
full logical; if TRUE, all names (including zero weights, ...) are returned.
... further arguments passed to or from other methods.

Value

A character vector.

See Also

lm, further, all.names, all.vars for functions with a similar name but only slightly related purpose.

Examples

```r
x <- 1:20
y <- setNames(x + (x/4 - 2)^3 + rnorm(20, sd = 3),
              paste("O", x, sep = "."))
ww <- rep(1, 20); ww[13] <- 0
summary(lmxy <- lm(y ~ x + I(x^2)+I(x^3) + I((x-10)^2), weights = ww),
         correlation = TRUE)
variable.names(lmxy)
variable.names(lmxy, full = TRUE)  # includes the last
case.names(lmxy)
case.names(lmxy, full = TRUE)  # includes the 0-weight case
```
The Cauchy Distribution

Description

Density, distribution function, quantile function and random generation for the Cauchy distribution with location parameter location and scale parameter scale.

Usage

dcauchy(x, location = 0, scale = 1, log = FALSE)
pcauchy(q, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
qcauchy(p, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
rcauchy(n, location = 0, scale = 1)

Arguments

x, q vector of quantiles.
p vector of probabilities.
n number of observations. If length(n) > 1, the length is taken to be the number required.
location, scale location and scale parameters.
log, log.p logical; if TRUE, probabilities p are given as log(p).
lower.tail logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).

Details

If location or scale are not specified, they assume the default values of 0 and 1 respectively.

The Cauchy distribution with location \( l \) and scale \( s \) has density

\[
f(x) = \frac{1}{\pi s} \left( 1 + \left( \frac{x - l}{s} \right)^2 \right)^{-1}
\]

for all \( x \).

Value

dcauchy, pcauchy, and qcauchy are respectively the density, distribution function and quantile function of the Cauchy distribution. rcauchy generates random deviates from the Cauchy.

The length of the result is determined by \( n \) for rcauchy, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than \( n \) are recycled to the length of the result. Only the first elements of the logical arguments are used.

Source

dcauchy, pcauchy and qcauchy are all calculated from numerically stable versions of the definitions.

rcauchy uses inversion.
chisq.test

References


See Also

*Distributions* for other standard distributions, including *dt* for the t distribution which generalizes *dcauchy(*x*, 1 = 0, s = 1).

Examples

dcauchy(-1:4)

---

chisq.test

*Pearson’s Chi-squared Test for Count Data*

Description

chisq.test performs chi-squared contingency table tests and goodness-of-fit tests.

Usage

```r
chisq.test(x, y = NULL, correct = TRUE, 
p = rep(1/length(x), length(x)), rescale.p = FALSE, 
simulate.p.value = FALSE, B = 2000)
```

Arguments

- **x**: a numeric vector or matrix. *x* and *y* can also both be factors.
- **y**: a numeric vector; ignored if *x* is a matrix. If *x* is a factor, *y* should be a factor of the same length.
- **correct**: a logical indicating whether to apply continuity correction when computing the test statistic for 2 by 2 tables: one half is subtracted from all \(|O - E|\) differences; however, the correction will not be bigger than the differences themselves. No correction is done if `simulate.p.value = TRUE`.
- **p**: a vector of probabilities of the same length as *x*. An error is given if any entry of *p* is negative.
- **rescale.p**: a logical scalar; if TRUE then *p* is rescaled (if necessary) to sum to 1. If `rescale.p` is FALSE, and *p* does not sum to 1, an error is given.
- **simulate.p.value**: a logical indicating whether to compute *p*-values by Monte Carlo simulation.
- **B**: an integer specifying the number of replicates used in the Monte Carlo test.
Details

If \( x \) is a matrix with one row or column, or if \( x \) is a vector and \( y \) is not given, then a goodness-of-fit test is performed (\( x \) is treated as a one-dimensional contingency table). The entries of \( x \) must be non-negative integers. In this case, the hypothesis tested is whether the population probabilities equal those in \( p \), or are all equal if \( p \) is not given.

If \( x \) is a matrix with at least two rows and columns, it is taken as a two-dimensional contingency table: the entries of \( x \) must be non-negative integers. Otherwise, \( x \) and \( y \) must be vectors or factors of the same length; cases with missing values are removed, the objects are coerced to factors, and the contingency table is computed from these. Then Pearson’s chi-squared test is performed of the null hypothesis that the joint distribution of the cell counts in a 2-dimensional contingency table is the product of the row and column marginals.

If \( \text{simulate.p.value} \) is \text{FALSE}, the p-value is computed from the asymptotic chi-squared distribution of the test statistic; continuity correction is only used in the 2-by-2 case (if \( \text{correct} \) is \text{TRUE}, the default). Otherwise the p-value is computed for a Monte Carlo test (Hope, 1968) with \( B \) replicates. The default \( B = 2000 \) implies a minimum p-value of about 0.0005 (\( 1/(B+1) \)).

In the contingency table case, simulation is done by random sampling from the set of all contingency tables with given marginals, and works only if the marginals are strictly positive. Continuity correction is never used, and the statistic is quoted without it. Note that this is not the usual sampling situation assumed for the chi-squared test but rather that for Fisher’s exact test.

In the goodness-of-fit case simulation is done by random sampling from the discrete distribution specified by \( p \), each sample being of size \( n = \text{sum}(x) \). This simulation is done in R and may be slow.

Value

A list with class "htest" containing the following components:

- \text{statistic} \quad \text{the value the chi-squared test statistic.}
- \text{parameter} \quad \text{the degrees of freedom of the approximate chi-squared distribution of the test statistic, NA if the p-value is computed by Monte Carlo simulation.}
- \text{p.value} \quad \text{the p-value for the test.}
- \text{method} \quad \text{a character string indicating the type of test performed, and whether Monte Carlo simulation or continuity correction was used.}
- \text{data.name} \quad \text{a character string giving the name(s) of the data.}
- \text{observed} \quad \text{the observed counts.}
- \text{expected} \quad \text{the expected counts under the null hypothesis.}
- \text{residuals} \quad \text{the Pearson residuals, \((\text{observed} - \text{expected}) / \sqrt{\text{expected}}\).}
- \text{stdres} \quad \text{standardized residuals, \((\text{observed} - \text{expected}) / \sqrt{\text{V}}\), where \( V \) is the residual cell variance (Agresti, 2007, section 2.4.5 for the case where \( x \) is a matrix, \( n \cdot p \cdot (1 - p) \) otherwise).}

Source

The code for Monte Carlo simulation is a C translation of the Fortran algorithm of Patefield (1981).
References


See Also

For goodness-of-fit testing, notably of continuous distributions, *ks.test*.

Examples

```r
## From Agresti(2007) p.39
M <- as.table(rbind(c(762, 327, 468), c(484, 239, 477)))
dimnames(M) <- list(gender = c("F", "M"),
                    party = c("Democrat","Independent","Republican"))
(Xsq <- chisq.test(M)) # Prints test summary
Xsq$observed # observed counts (same as M)
Xsq$expected # expected counts under the null
Xsq$residuals # Pearson residuals
Xsq$stdres # standardized residuals

## Effect of simulating p-values
x <- matrix(c(12, 5, 7, 7), ncol = 2)
chisq.test(x)$p.value # 0.4233
chisq.test(x, simulate.p.value = TRUE, B = 10000)$p.value # around 0.29!

## Testing for population probabilities
## Case A. Tabulated data
x <- c(A = 20, B = 15, C = 25)
chisq.test(x)
chisq.test(as.table(x)) # the same
x <- c(89,37,30,28,2)
p <- c(40,20,20,15,5)
try(
  chisq.test(x, p = p) # gives an error
)
chisq.test(x, p = p, rescale.p = TRUE) # works
p <- c(0.40, 0.20, 0.20, 0.19, 0.01)
# Expected count in category 5
# is 1.86 < 5 ==> chi square approx.
chisq.test(x, p = p) # maybe doubtful, but is ok!
chisq.test(x, p = p, simulate.p.value = TRUE)

## Case B. Raw data
x <- trunc(5 * runif(100))
chisq.test(table(x)) # NOT 'chisq.test(x)'!
```
Chisquare

The (non-central) Chi-Squared Distribution

Description

Density, distribution function, quantile function and random generation for the chi-squared ($\chi^2$) distribution with df degrees of freedom and optional non-centrality parameter ncp.

Usage

dchisq(x, df, ncp = 0, log = FALSE)
pchisq(q, df, ncp = 0, lower.tail = TRUE, log.p = FALSE)
qchisq(p, df, ncp = 0, lower.tail = TRUE, log.p = FALSE)
rchisq(n, df, ncp = 0)

Arguments

x, q vector of quantiles.
p vector of probabilities.
n number of observations. If length(n) > 1, the length is taken to be the number required.
df degrees of freedom (non-negative, but can be non-integer).
ncp non-centrality parameter (non-negative).
log, log.p logical; if TRUE, probabilities p are given as log(p).
lower.tail logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The chi-squared distribution with df = $n \geq 0$ degrees of freedom has density

$$f_n(x) = \frac{1}{2^{n/2} \Gamma(n/2)} x^{n/2-1} e^{-x/2}$$

for $x > 0$, where $f_0(x) := \lim_{n \to 0} f_n(x) = \delta_0(x)$, a point mass at zero, is not a density function proper, but a "$\delta$ distribution".

The mean and variance are $n$ and $2n$.

The non-central chi-squared distribution with df = $n$ degrees of freedom and non-centrality parameter ncp = $\lambda$ has density

$$f(x) = f_{n,\lambda}(x) = e^{-\lambda/2} \sum_{r=0}^{\infty} \frac{(\lambda/2)^r}{r!} f_{n+2r}(x)$$

for $x \geq 0$. For integer $n$, this is the distribution of the sum of squares of $n$ normals each with variance one, $\lambda$ being the sum of squares of the normal means; further, $E(X) = n + \lambda$, $Var(X) = 2(n + 2 \ast \lambda)$, and $E((X - E(X))^3) = 8(n + 3 \ast \lambda)$.

Note that the degrees of freedom df = $n$, can be non-integer, and also $n = 0$ which is relevant for non-centrality $\lambda > 0$, see Johnson et al (1995, chapter 29). In that (noncentral, zero df) case, the distribution is a mixture of a point mass at $x = 0$ (of size pchisq(0, df=0, ncp=ncp)) and a continuous part, and dchisq() is not a density with respect to that mixture measure but rather the limit of the density for df $\to 0$.

Note that ncp values larger than about 1e5 (and even smaller) may give inaccurate results with many warnings for pchisq and qchisq.
Value

dchisq gives the density, pchisq gives the distribution function, qchisq gives the quantile function, and rchisq generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

The length of the result is determined by n for rchisq, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

Supplying ncp = 0 uses the algorithm for the non-central distribution, which is not the same algorithm used if ncp is omitted. This is to give consistent behaviour in extreme cases with values of ncp very near zero.

The code for non-zero ncp is principally intended to be used for moderate values of ncp: it will not be highly accurate, especially in the tails, for large values.

Source

The central cases are computed via the gamma distribution.

The non-central dchisq and rchisq are computed as a Poisson mixture of central chi-squares (Johnson et al, 1995, p.436).

The non-central pchisq is for ncp < 80 computed from the Poisson mixture of central chi-squares and for larger ncp via a C translation of


which computes the lower tail only (so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant).

The non-central qchisq is based on inversion of pchisq.

References


See Also

Distributions for other standard distributions.

A central chi-squared distribution with n degrees of freedom is the same as a Gamma distribution with shape $\alpha = n/2$ and scale $\sigma = 2$. Hence, see dgamma for the Gamma distribution.

The central chi-squared distribution with 2 d.f. is identical to the exponential distribution with rate 1/2: $\chi_2^2 = Exp(1/2)$, see dexp.
Examples

```r
require(graphics)

dchisq(1, df = 1:3)
pchisq(1, df = 3)
pchisq(1, df = 3, ncp = 0:4) # includes the above

x <- 1:10
## Chi-squared(df = 2) is a special exponential distribution
all.equal(dchisq(x, df = 2), dexp(x, 1/2))
all.equal(pchisq(x, df = 2), pexp(x, 1/2))

x <- 1:10
## Chi-squared(df = 2) is a special exponential distribution
all.equal(dchisq(x, df = 2), dexp(x, 1/2))
all.equal(pchisq(x, df = 2), pexp(x, 1/2))

## non-central RNG -- df = 0 with ncp > 0: Z0 has point mass at 0!
Z0 <- rchisq(100, df = 0, ncp = 2.)

## visual testing
L <- 1.2; n <- 1000; pp <- ppoints(n)

for(df in 2^(4*rnorm(9))) {
  plot(pp, sort(pchisq(rr <- rchisq(n, df = df, ncp = L), df = df, ncp = L)),
       ylab = "pchisq(rchisq(.),.)", pch = ".")
  mtext(paste("df = ", formatC(df, digits = 4)), line = -2, adj = 0.05)
  abline(0, 1, col = 2)
}

mtext(expression("P-P plots : Noncentral "* 
                  \chi^2 \ "(n=1000, df=X, ncp= 1.2)"),
       cex = 1.5, font = 2, outer = TRUE)

par(op)
```

```
## "analytical" test
lam <- seq(0, 100, by = .25)
p00 <- pchisq(0, df = df, ncp = lam)
p.0 <- pchisq(1e-300, df = 0, ncp = lam)
stopifnot(all.equal(p00, exp(-lam/2)),
          all.equal(p.0, exp(-lam/2)))
```

---

CMDSCAL

Classical (Metric) Multidimensional Scaling

Description

Classical multidimensional scaling (MDS) of a data matrix. Also known as principal coordinates analysis (Gower, 1966).

Usage

```r
cmdsce(d, k = 2, eig = FALSE, add = FALSE, x.ret = FALSE, 

list. = eig || add || x.ret)
```
Arguments

d
A distance structure such as that returned by dist or a full symmetric matrix containing the dissimilarities.

k
The maximum dimension of the space which the data are to be represented in; must be in \(\{1, 2, \ldots, n - 1\}\).

eig
Indicates whether eigenvalues should be returned.

add
Logical indicating if an additive constant \(c^*\) should be computed, and added to the non-diagonal dissimilarities such that the modified dissimilarities are Euclidean.

x.ret
Indicates whether the doubly centred symmetric distance matrix should be returned.

list
Logical indicating if a list should be returned or just the \(n \times k\) matrix, see 'Value'.

Details

Multidimensional scaling takes a set of dissimilarities and returns a set of points such that the distances between the points are approximately equal to the dissimilarities. (It is a major part of what ecologists call 'ordination'.)

A set of Euclidean distances on \(n\) points can be represented exactly in at most \(n - 1\) dimensions. cmdscale follows the analysis of Mardia (1978), and returns the best-fitting \(k\)-dimensional representation, where \(k\) may be less than the argument \(k\).

The representation is only determined up to location (cmdscale takes the column means of the configuration to be at the origin), rotations and reflections. The configuration returned is given in principal-component axes, so the reflection chosen may differ between \(R\) platforms (see prcomp).

When add = TRUE, a minimal additive constant \(c^*\) is computed such that the dissimilarities \(d_{ij} + c^*\) are Euclidean and hence can be represented in \(n - 1\) dimensions. Whereas S (Becker et al, 1988) computes this constant using an approximation suggested by Torgerson, \(R\) uses the analytical solution of Cailliez (1983), see also Cox and Cox (2001). Note that because of numerical errors the computed eigenvalues need not all be non-negative, and even theoretically the representation could be in fewer than \(n - 1\) dimensions.

Value

If .list is false (as per default), a matrix with \(k\) columns whose rows give the coordinates of the points chosen to represent the dissimilarities.

Otherwise, a list containing the following components.

- **points**
  A matrix with up to \(k\) columns whose rows give the coordinates of the points chosen to represent the dissimilarities.

- **eig**
  The \(n\) eigenvalues computed during the scaling process if eig is true. NB: versions of \(R\) before 2.12.1 returned only \(k\) but were documented to return \(n - 1\).

- **x**
  The doubly centered distance matrix if x.ret is true.

- **ac**
  The additive constant \(c^*, 0\) if add = FALSE.

- **GOF**
  A numeric vector of length 2, equal to say \((g_1, g_2)\), where \(g_i = (\sum_{j=1}^{k} \lambda_j) / (\sum_{j=1}^{n} T_i(\lambda_j))\), where \(\lambda_j\) are the eigenvalues (sorted in decreasing order), \(T_1(v) = |v|\), and \(T_2(v) = \max(v, 0)\).
References


See Also

dist.

`isoMDS` and `sammon` in package MASS provide alternative methods of multidimensional scaling.

Examples

```r
require(graphics)

loc <- cmdscale(euirdist)
x <- loc[, 1]
y <- -loc[, 2] # reflect so North is at the top
## note asp = 1, to ensure Euclidean distances are represented correctly
plot(x, y, type = "n", xlab = "", ylab = "", asp = 1, axes = FALSE,
     main = "cmdscale(euirdist)")
text(x, y, rownames(loc), cex = 0.6)
```

---

### coef

#### Extract Model Coefficients

**Description**

`coef` is a generic function which extracts model coefficients from objects returned by modeling functions. `coefficients` is an alias for it.

**Usage**

```r
coeff(object, ...)
coefficients(object, ...)
## Default S3 method:
coeff(object, complete = TRUE, ...)
## S3 method for class 'aov'
coeff(object, complete = FALSE, ...)
```
Arguments

- **object**: an object for which the extraction of model coefficients is meaningful.
- **complete**: for the default (used for `lm`, etc) and `aov` methods: logical indicating if the full coefficient vector should be returned also in case of an over-determined system where some coefficients will be set to `NA`, see also `alias`. Note that the default differs for `lm()` and `aov()` results.

... other arguments.

Details

All object classes which are returned by model fitting functions should provide a `coef` method or use the default one. (Note that the method is for `coef` and not `coefficients`.)

The "aov" method does not report aliased coefficients (see `alias`) by default where `complete = FALSE`.

The `complete` argument also exists for compatibility with `vcov` methods, and `coef` and `aov` methods for other classes should typically also keep the `complete = *` behavior in sync. By that, with `p <- length(coef(obj, complete = TF))`, `dim(vcov(obj, complete = TF)) == c(p, p)` will be fulfilled for both `complete` settings and the default.

Value

Coefficients extracted from the model object `object`.

For standard model fitting classes this will be a named numeric vector. For "maov" objects (produced by `aov`) it will be a matrix.

References


See Also

- `fitted.values` and `residuals` for related methods; `glm`, `lm` for model fitting.

Examples

```r
x <- 1:5; coef(lm(c(1:3, 7, 6) ~ x))
```

---

**complete.cases**

*Find Complete Cases*

Description

Return a logical vector indicating which cases are complete, i.e., have no missing values.

Usage

```r
complete.cases(...)```

Arguments

- ... a sequence of vectors, matrices and data frames.
Value

A logical vector specifying which observations/rows have no missing values across the entire sequence.

Note

A current limitation of this function is that it uses low level functions to determine lengths and missingness, ignoring the class. This will lead to spurious errors when some columns have classes with \texttt{length} or \texttt{is.na} methods, for example “\texttt{POSIXlt}”, as described in PR\#16648.

See Also

\texttt{is.na, na.omit, na.fail}.

Examples

\begin{verbatim}
x <- airquality[, -1] # x is a regression design matrix
y <- airquality[, 1] # y is the corresponding response

stopifnot(complete.cases(y) != is.na(y))
ok <- complete.cases(x, y)
sum(!ok) # how many are not "ok" ?
x <- x[ok,]
y <- y[ok]
\end{verbatim}

\texttt{confint} \hspace{1cm} \textit{Confidence Intervals for Model Parameters}

\begin{verbatim}
Description

Computes confidence intervals for one or more parameters in a fitted model. There is a default and a method for objects inheriting from class \texttt{"lm"}.

Usage

\texttt{confint(object, parm, level = 0.95, \ldots)}

## Default S3 method:
\texttt{confint(object, parm, level = 0.95, \ldots)}

## S3 method for class \texttt{"lm"}
\texttt{confint(object, parm, level = 0.95, \ldots)}

Arguments

\begin{verbatim}
oobject \hspace{1cm} \texttt{a fitted model object.}

parm \hspace{1cm} \texttt{a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.}

level \hspace{1cm} \texttt{the confidence level required.}

\ldots \hspace{1cm} \texttt{additional argument(s) for methods.}
\end{verbatim}
Details

`confint` is a generic function. The default method assumes normality, and needs suitable `coef` and `vcov` methods to be available. The default method can be called directly for comparison with other methods.

For objects of class "lm" the direct formulae based on $t$ values are used.

There are stub methods in package `stats` for classes "glm" and "nls" which call those in package `MASS` (if installed): if the `MASS` namespace has been loaded, its methods will be used directly. (Those methods are based on profile likelihood.)

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1-level)/2 and 1 - (1-level)/2 in % (by default 2.5% and 97.5%).

See Also

`confint.glm` and `confint.nls` in package `MASS`.

Examples

```r
fit <- lm(100/mpg ~ disp + hp + wt + am, data = mtcars)
confint(fit)
confint(fit, "wt")

## from example(glm)
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3, 1, 9); treatment <- gl(3, 3)
glm.D93 <- glm(counts ~ outcome + treatment, family = poisson())
confint(glm.D93) # needs MASS to be installed
cconfint.default(glm.D93) # based on asymptotic normality
```

---

**constrOptim**  
*Linearly Constrained Optimization*

Description

Minimise a function subject to linear inequality constraints using an adaptive barrier algorithm.

Usage

```r
constrOptim(theta, f, grad, ui, ci, mu = 1e-04, control = list(),
method = if(is.null(grad)) "Nelder-Mead" else "BFGS",
outer.iterations = 100, outer.eps = 1e-05, ..., 
hessian = FALSE)
```

Arguments

- `theta` numeric (vector) starting value (of length $p$): must be in the feasible region.
- `f` function to minimise (see below).
- `grad` gradient of $f$ (a `function` as well), or `NULL` (see below).
The feasible region is defined by \( u_i \times \theta - c_i \geq 0 \). The starting value must be in the interior of the feasible region, but the minimum may be on the boundary.

A logarithmic barrier is added to enforce the constraints and then `optim` is called. The barrier function is chosen so that the objective function should decrease at each outer iteration. Minima in the interior of the feasible region are typically found quite quickly, but a substantial number of outer iterations may be needed for a minimum on the boundary.

The tuning parameter \( \mu \) multiplies the barrier term. Its precise value is often relatively unimportant. As \( \mu \) increases the augmented objective function becomes closer to the original objective function but also less smooth near the boundary of the feasible region.

Any `optim` method that permits infinite values for the objective function may be used (currently all but "L-BFGS-B").

The objective function \( f \) takes as first argument the vector of parameters over which minimisation is to take place. It should return a scalar result. Optional arguments ... will be passed to `optim` and then (if not used by `optim`) to \( f \). As with `optim`, the default is to minimise, but maximisation can be performed by setting `control$fnscale` to a negative value.

The gradient function \( \text{grad} \) must be supplied except with `method = "Nelder-Mead"`. It should take arguments matching those of \( f \) and return a vector containing the gradient.

### Value

As for `optim`, but with two extra components: `barrier.value` giving the value of the barrier function at the optimum and `outer.iterations` gives the number of outer iterations (calls to `optim`). The `counts` component contains the sum of all `optim()`$counts.

### References

K. Lange *Numerical Analysis for Statisticians*. Springer 2001, p185ff

### See Also

`optim`, especially method = "L-BFGS-B" which does box-constrained optimisation.
Examples

```r
## from optim
fr <- function(x) { ## Rosenbrock Banana function
  x1 <- x[1]
  x2 <- x[2]
  100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
  x1 <- x[1]
  x2 <- x[2]
  c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
      200 * (x2 - x1 * x1))
}
optim(c(-1.2,1), fr, grr)
#Box-constraint, optimum on the boundary
constrOptim(c(-1.2,0.9), fr, grr, ui = rbind(c(-1,0), c(0,-1)), ci = c(-1,-1))
# x <= 0.9, y - x > 0.1
constrOptim(c(-1.5,0), fr, grr, ui = rbind(c(-1,0), c(1,-1)), ci = c(-0.9,0.1))

## Solves linear and quadratic programming problems
## but needs a feasible starting value
##
## from example(solve.QP) in 'quadprog'
## no derivative
fQP <- function(b) {-sum(c(0,5,0)*b)+0.5*sum(b*b)}
Amat <- matrix(c(-4,-3,0,2,1,0,0,-2,1), 3, 3)
bvec <- c(-8, 2, 0)
constrOptim(c(2,-1,-1), fQP, NULL, ui = t(Amat), ci = bvec)
# derivative
gQP <- function(b) {-c(0, 5, 0) + b}
constrOptim(c(2,-1,-1), fQP, gQP, ui = t(Amat), ci = bvec)

## Now with maximisation instead of minimisation
hQP <- function(b) {sum(c(0,5,0)*b)-0.5*sum(b*b)}
constrOptim(c(2,-1,-1), hQP, NULL, ui = t(Amat), ci = bvec, control = list(fnscale = -1))
```

**Description**

Return a matrix of contrasts.

**Usage**

```r
contr.helmert(n, contrasts = TRUE, sparse = FALSE)
contr.poly(n, scores = 1:n, contrasts = TRUE, sparse = FALSE)
contr.sum(n, contrasts = TRUE, sparse = FALSE)
contr.treatment(n, base = 1, contrasts = TRUE, sparse = FALSE)
contr.SAS(n, contrasts = TRUE, sparse = FALSE)
```
**Arguments**

- `n`: a vector of levels for a factor, or the number of levels.
- `contrasts`: a logical indicating whether contrasts should be computed.
- `sparse`: logical indicating if the result should be sparse (of class `dgCMatrix`), using package `Matrix`.
- `scores`: the set of values over which orthogonal polynomials are to be computed.
- `base`: an integer specifying which group is considered the baseline group. Ignored if `contrasts` is `FALSE`.

**Details**

These functions are used for creating contrast matrices for use in fitting analysis of variance and regression models. The columns of the resulting matrices contain contrasts which can be used for coding a factor with `n` levels. The returned value contains the computed contrasts. If the argument `contrasts` is `FALSE` a square indicator matrix (the dummy coding) is returned except for `contr.poly` (which includes the 0-degree, i.e. constant, polynomial when `contrasts = FALSE`).

- `contr.helmert` returns Helmert contrasts, which contrast the second level with the first, the third with the average of the first two, and so on. `contr.poly` returns contrasts based on orthogonal polynomials. `contr.sum` uses ‘sum to zero contrasts’.
- `contr.treatment` contrasts each level with the baseline level (specified by `base`): the baseline level is omitted. Note that this does not produce ‘contrasts’ as defined in the standard theory for linear models as they are not orthogonal to the intercept.
- `contr.SAS` is a wrapper for `contr.treatment` that sets the base level to be the last level of the factor. The coefficients produced when using these contrasts should be equivalent to those produced by many (but not all) SAS procedures.

For consistency, `sparse` is an argument to all these contrast functions, however `sparse = TRUE` for `contr.poly` is typically pointless and is rarely useful for `contr.helmert`.

**Value**

A matrix with `n` rows and `k` columns, with `k=n-1` if `contrasts` is `TRUE` and `k=n` if `contrasts` is `FALSE`.

**References**


**See Also**

- `contrasts`, `C`, and `aov`, `glm`, `lm`.

**Examples**

```r
(cH <- contr.helmert(4))
apply(cH, 2, sum) # column sums are 0
crossprod(ch) # diagonal -- columns are orthogonal
contr.helmert(4, contrasts = FALSE) # just the 4 x 4 identity matrix

(cT <- contr.treatment(5))
all(crossprod(cT) == diag(4)) # TRUE: even orthonormal
```
contrasts

Get and Set Contrast Matrices

Description
Set and view the contrasts associated with a factor.

Usage
contrasts(x, contrasts = TRUE, sparse = FALSE)
contrasts(x, how.many = NULL) <- value

Arguments
x a factor or a logical variable.
contrasts logical. See ‘Details’.
sparse logical indicating if the result should be sparse (of class dgCMatrix), using package Matrix.
how.many integer number indicating how many contrasts should be made. Defaults to one less than the number of levels of x. This need not be the same as the number of columns of value.
value either a numeric matrix (or a sparse or dense matrix of a class extending dMatrix from package Matrix) whose columns give coefficients for contrasts in the levels of x, or (the quoted name of) a function which computes such matrices.

Details
If contrasts are not set for a factor the default functions from options("contrasts") are used.
A logical vector x is converted into a two-level factor with levels c(FALSE, TRUE) (regardless of which levels occur in the variable).
The argument contrasts is ignored if x has a matrix contrasts attribute set. Otherwise if contrasts = TRUE it is passed to a contrasts function such as contr.treatment and if contrasts = FALSE an identity matrix is returned. Suitable functions have a first argument which is the character vector of levels, a named argument contrasts (always called with contrasts = TRUE) and optionally a logical argument sparse.

If value supplies more than how.many contrasts, the first how.many are used. If too few are supplied, a suitable contrast matrix is created by extending value after ensuring its columns are contrasts (orthogonal to the constant term) and not collinear.

References
See Also
R, contr.helmert, contr.poly, contr.sum, contr.treatment; glm, aov, lm.

Examples

```r
utils::example(factor)
fff <- ff[, drop = TRUE] # reduce to 5 levels.
contrasts(fff) # treatment contrasts by default
contrasts(C(fff, sum))
contrasts(fff, contrasts = FALSE) # the 5x5 identity matrix

contrasts(fff) <- contr.sum(5); contrasts(fff) # set sum contrasts
contrasts(fff, 2) <- contr.sum(5); contrasts(fff) # set 2 contrasts
# supply 2 contrasts, compute 2 more to make full set of 4.
contrasts(fff) <- contr.sum(5)[, 1:2]; contrasts(fff)

## using sparse contrasts: % useful, once model.matrix() works with these :
ffs <- fff
contrasts(ffs) <- contr.sum(5, sparse = TRUE)[, 1:2]; contrasts(ffs)
stopifnot(all.equal(ffs, fff))
contrasts(ffs) <- contr.sum(5, sparse = TRUE); contrasts(ffs)
```

convolve

Convolution of Sequences via FFT

Description

Use the Fast Fourier Transform to compute the several kinds of convolutions of two sequences.

Usage

```r
convolve(x, y, conj = TRUE, type = c("circular", "open", "filter"))
```

Arguments

- `x, y`: numeric sequences of the same length to be convolved.
- `conj`: logical; if TRUE, take the complex conjugate before back-transforming (default, and used for usual convolution).
- `type`: character; partially matched to "circular", "open", "filter". For "circular", the two sequences are treated as circular, i.e., periodic. For "open" and "filter", the sequences are padded with 0s (from left and right) first; "filter" returns the middle sub-vector of "open", namely, the result of running a weighted mean of x with weights y.

Details

The Fast Fourier Transform, `fft`, is used for efficiency.

The input sequences `x` and `y` must have the same length if circular is true.

Note that the usual definition of convolution of two sequences `x` and `y` is given by `convolve(x, rev(y), type = "o")`. 

Examples

```r
utils::example(factor)
fff <- ff[, drop = TRUE] # reduce to 5 levels.
contrasts(fff) # treatment contrasts by default
contrasts(C(fff, sum))
contrasts(fff, contrasts = FALSE) # the 5x5 identity matrix

contrasts(fff) <- contr.sum(5); contrasts(fff) # set sum contrasts
contrasts(fff, 2) <- contr.sum(5); contrasts(fff) # set 2 contrasts
# supply 2 contrasts, compute 2 more to make full set of 4.
contrasts(fff) <- contr.sum(5)[, 1:2]; contrasts(fff)

## using sparse contrasts: % useful, once model.matrix() works with these :
ffs <- fff
contrasts(ffs) <- contr.sum(5, sparse = TRUE)[, 1:2]; contrasts(ffs)
stopifnot(all.equal(ffs, fff))
contrasts(ffs) <- contr.sum(5, sparse = TRUE); contrasts(ffs)
```
Value

If \( r <- \texttt{convolve}(x, y, \text{type} = \text{"open"}) \) and \( n <- \text{length}(x), m <- \text{length}(y) \), then

\[
r_k = \sum_i x_{k-m+i} y_i
\]

where the sum is over all valid indices \( i \), for \( k = 1, \ldots, n + m - 1 \).

If \( \text{type} = \text{"circular"} \), \( n = m \) is required, and the above is true for \( i, k = 1, \ldots, n \) when \( x_j := x_{n+j} \) for \( j < 1 \).

References


See Also

\texttt{fft}, \texttt{nextn}, and particularly \texttt{filter} (from the \texttt{stats} package) which may be more appropriate.

Examples

```r
require(graphics)
x <- c(0,0,0,100,0,0,0)
y <- c(0,0,1,2,1,0,0)/4
zapsmall(convolve(x, y)) # *NOT* what you first thought.
zapsmall(convolve(x, y[3:5], type = "f")) # rather
x <- rnorm(50)
y <- rnorm(50)
# Circular convolution *has* this symmetry:
all.equal(convolve(x, y, conj = FALSE), rev(convolve(rev(y),x)))

n <- length(x <- -20:24)
y <- (x-10)^2/1000 + rnorm(x)/8
Han <- function(y) # Hanning
  convolve(y, c(1,2,1)/4, type = "filter")
plot(x, y, main = "Using convolve(.) for Hanning filters")
lines(x[-c(1 , n )], Han(y), col = "red")
lines(x[-c(1:2, (n-1):n)], Han(Han(y)), lwd = 2, col = "dark blue")
```

**cophenetic**

*Cophenetic Distances for a Hierarchical Clustering*

Description

Computes the cophenetic distances for a hierarchical clustering.
Usage

cophenetic(x)

## Default S3 method:
cophenetic(x)

## S3 method for class 'dendrogram'
cophenetic(x)

Arguments

x  
an R object representing a hierarchical clustering. For the default method, an object of class "hclust" or with a method for \texttt{as.hclust()} such as "agnes" in package \texttt{cluster}.

Details

The cophenetic distance between two observations that have been clustered is defined to be the intergroup dissimilarity at which the two observations are first combined into a single cluster. Note that this distance has many ties and restrictions.

It can be argued that a dendrogram is an appropriate summary of some data if the correlation between the original distances and the cophenetic distances is high. Otherwise, it should simply be viewed as the description of the output of the clustering algorithm.

cophenetic is a generic function. Support for classes which represent hierarchical clusterings (total indexed hierarchies) can be added by providing an \texttt{as.hclust()} or, more directly, a \texttt{cophenetic()} method for such a class.

The method for objects of class "dendrogram" requires that all leaves of the dendrogram object have non-null labels.

Value

An object of class "dist".

Author(s)

Robert Gentleman

References


See Also

dist, hclust

Examples

require(graphics)

d1 <- dist(USArrests)
hc <- hclust(d1, "ave")
d2 <- cophenetic(hc)
cor(d1, d2) # 0.7659
## Example from Sneath & Sokal, Fig. 5-29, p.279

d0 <- c(1,3.8,4.4,5.1, 4,4.2,5, 2.6,5.3, 5.4)
attributes(d0) <- list(Size = 5, diag = TRUE)
class(d0) <- "dist"
names(d0) <- letters[1:5]
d0
utils::str(upgma <- hclust(d0, method = "average"))
plot(upgma, hang = -1)
#
(d.coph <- cophenetic(upgma))
cor(d0, d.coph) # 0.9911

---

### Correlation, Variance and Covariance (Matrices)

#### Description

`var`, `cov` and `cor` compute the variance of `x` and the covariance or correlation of `x` and `y` if these are vectors. If `x` and `y` are matrices then the covariances (or correlations) between the columns of `x` and the columns of `y` are computed.

`cov2cor` scales a covariance matrix into the corresponding correlation matrix efficiently.

#### Usage

```r
var(x, y = NULL, na.rm = FALSE, use)
cov(x, y = NULL, use = "everything", method = c("pearson", "kendall", "spearman"))
cor(x, y = NULL, use = "everything", method = c("pearson", "kendall", "spearman"))
cov2cor(V)
```

#### Arguments

- **x**: a numeric vector, matrix or data frame.
- **y**: `NULL` (default) or a vector, matrix or data frame with compatible dimensions to `x`. The default is equivalent to `y = x` (but more efficient).
- **na.rm**: logical. Should missing values be removed?
- **use**: an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs".
- **method**: a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman": can be abbreviated.
- **V**: symmetric numeric matrix, usually positive definite such as a covariance matrix.
Details

For `cov` and `cor` one must *either* give a matrix or data frame for `x` or give both `x` and `y`.
The inputs must be numeric (as determined by `is.numeric`; logical values are also allowed for
historical compatibility): the "kendall" and "spearman" methods make sense for ordered inputs
but `xtfrm` can be used to find a suitable prior transformation to numbers.

`var` is just another interface to `cov`, where `na.rm` is used to determine the default for use when
that is unspecified. If `na.rm` is TRUE then the complete observations (rows) are used (`use = "na.or.complete"`) to compute the variance. Otherwise, by default use = "everything".
If `use` is "everything", `NA`s will propagate conceptually, i.e., a resulting value will be `NA` whenever
one of its contributing observations is `NA`.
If `use` is "all.obs", then the presence of missing observations will produce an error. If `use` is
"complete.obs" then missing values are handled by casewise deletion (and if there are no complete
cases, that gives an error).
"na.or.complete" is the same unless there are no complete cases, that gives `NA`. Finally, if `use`
has the value "pairwise.complete.obs" then the correlation or covariance between each pair of
variables is computed using all complete pairs of observations on those variables. This can result in
covariance or correlation matrices which are not positive semi-definite, as well as `NA` entries if there
are no complete pairs for that pair of variables. For `cov` and `var`, "pairwise.complete.obs" only
works with the "pearson" method. Note that (the equivalent of) `var(double(0), use = *)` gives
`NA` for `use` = "everything" and "na.or.complete", and gives an error in the other cases.
The denominator `n - 1` is used which gives an unbiased estimator of the (co)variance for i.i.d.
observations. These functions return `NA` when there is only one observation (whereas S-PLUS has
been returning NaN).
For `cor()`, if method is "kendall" or "spearman", Kendall’s τ or Spearman’s ρ statistic is used to
estimate a rank-based measure of association. These are more robust and have been recommended
if the data do not necessarily come from a bivariate normal distribution.
For `cov()`, a non-Pearson method is unusual but available for the sake of completeness. Note
that "spearman" basically computes `cor(R(x), R(y))` (or `cov(., .)`) where `R(u) := rank(u,
na.last = "keep")`. In the case of missing values, the ranks are calculated depending on the value
of `use`, either based on complete observations, or based on pairwise completeness with reranking
for each pair.
When there are ties, Kendall’s τₖ is computed, as proposed by Kendall (1945).
Scaling a covariance matrix into a correlation one can be achieved in many ways, mathematically
most appealing by multiplication with a diagonal matrix from left and right, or more efficiently by
using `sweep(., FUN = "/")` twice. The `cov2cor` function is even a bit more efficient, and provided
mostly for didactical reasons.

Value

For `r <- cor(*, use = "all.obs")`, it is now guaranteed that `all(abs(r) <= 1)`.

Note

Some people have noted that the code for Kendall’s tau is slow for very large datasets (many more
than 1000 cases). It rarely makes sense to do such a computation, but see function `cor.fk` in
package `pcaPP`.

References

Brooks/Cole.


**See Also**

- `cor.test` for confidence intervals (and tests).
- `cov.wt` for weighted covariance computation.
- `sd` for standard deviation (vectors).

**Examples**

```r
var(1:10) # 9.166667
var(1:5, 1:5) # 2.5

## Two simple vectors
cor(1:10, 2:11) # == 1

## Correlation Matrix of Multivariate sample:
(Cl <- cor(longley))
## Graphical Correlation Matrix:
symnum(Cl) # highly correlated

## Spearman's rho and Kendall's tau
symnum(c1S <- cor(longley, method = "spearman"))
symnum(c1K <- cor(longley, method = "kendall"))

## How much do they differ?
i <- lower.tri(Cl)
cor(cbind(P = Cl[i], S = c1S[i], K = c1K[i]))

## cov2cor() scales a covariance matrix by its diagonal
## to become the correlation matrix.
cov2cor # see the function definition (and learn ..)
stopifnot(all.equal(Cl, cov2cor(cov(longley)));
  all.equal(cor(longley, method = "kendall"),
            cov2cor(cov(longley, method = "kendall"))))

##--- Missing value treatment:
(C. <- cov(swiss))
range(eigen(C1)$values) # 6.19 1921

## swM := "swiss" with 3 "missing"s :
swM <- swiss
colnames(swM) <- abbreviate(colnames(swiss), minlength=6)
swM[1,2] <- swM[7,3] <- swM[25,5] <- NA # create 3 "missing"

## Consider all 5 "use" cases :
(C2 <- cov(swM)) # use="everything" quite a few NA's in cov.matrix
try(cov(swM, use = "all")) # Error: missing obs...

## how much do they differ?
(i <- lower.tri(C1))
cor(cbind(P = C1[i], S = c1S[i], K = c1K[i]))
```

```r
## cov2cor() scales a covariance matrix by its diagonal
## to become the correlation matrix.
cov2cor # see the function definition (and learn ..)
stopifnot(all.equal(Cl, cov2cor(cov(longley)));
  all.equal(cor(longley, method = "kendall"),
            cov2cor(cov(longley, method = "kendall"))))

##--- Missing value treatment:
(C. <- cov(swiss))
range(eigen(C1)$values) # 6.19 1921

## swM := "swiss" with 3 "missing"s :
swM <- swiss
colnames(swM) <- abbreviate(colnames(swiss), minlength=6)
swM[1,2] <- swM[7,3] <- swM[25,5] <- NA # create 3 "missing"

## Consider all 5 "use" cases :
(C2 <- cov(swM)) # use="everything" quite a few NA's in cov.matrix
try(cov(swM, use = "all")) # Error: missing obs...

## how much do they differ?
(i <- lower.tri(C1))
cor(cbind(P = C1[i], S = c1S[i], K = c1K[i]))
```
C3 <- cov(swM, use = "pairwise")
range(eigen(C3, only.values = TRUE)$values) # 6.19 1938
## Kendall's tau doesn't change much:
symnum(Rc <- cor(swM, method = "kendall", use = "complete"))
symnum(Rp <- cor(swM, method = "kendall", use = "pairwise"))
symnum(R. <- cor(swiss, method = "kendall"))
## "pairwise" is closer componentwise,
symsum(abs(c(1 - Rp/R.)))
symsum(abs(c(1 - Rc/R.)))
## but "complete" is closer in Eigen space:
EV <- function(m) eigen(m, only.values=TRUE)$values
summary(abs(1 - EV(Rp)/EV(R.))/abs(1 - EV(Rc)/EV(R.)))

Description
Test for association between paired samples, using one of Pearson's product moment correlation coefficient, Kendall's $\tau$ or Spearman's $\rho$.

Usage

cor.test(x, ...)
## Default S3 method:
cor.test(x, y, 
alternative = c("two.sided", "less", "greater"),
method = c("pearson", "kendall", "spearman"),
exact = NULL, conf.level = 0.95, continuity = FALSE, ...)

## S3 method for class 'formula'
cor.test(formula, data, subset, na.action, ...)

Arguments

x, y numeric vectors of data values. x and y must have the same length.
alternative indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association.
method a character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated.
exact a logical indicating whether an exact p-value should be computed. Used for Kendall's $\tau$ and Spearman's $\rho$. See 'Details' for the meaning of NULL (the default).
conf.level confidence level for the returned confidence interval. Currently only used for the Pearson product moment correlation coefficient if there are at least 4 complete pairs of observations.
cor.test

continuity logical: if true, a continuity correction is used for Kendall’s \( \tau \) and Spearman’s \( \rho \) when not computed exactly.

formula a formula of the form \( ~ u + v \), where each of \( u \) and \( v \) are numeric variables giving the data values for one sample. The samples must be of the same length.

data an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).

subset an optional vector specifying a subset of observations to be used.

na.action a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").

... further arguments to be passed to or from methods.

Details

The three methods each estimate the association between paired samples and compute a test of the value being zero. They use different measures of association, all in the range \([-1, 1]\) with 0 indicating no association. These are sometimes referred to as tests of no correlation, but that term is often confined to the default method.

If method is "pearson", the test statistic is based on Pearson’s product moment correlation coefficient \( \text{cor}(x, y) \) and follows a \( t \) distribution with \( \text{length}(x) - 2 \) degrees of freedom if the samples follow independent normal distributions. If there are at least 4 complete pairs of observation, an asymptotic confidence interval is given based on Fisher’s Z transform.

If method is "kendall" or "spearman", Kendall’s \( \tau \) or Spearman’s \( \rho \) statistic is used to estimate a rank-based measure of association. These tests may be used if the data do not necessarily come from a bivariate normal distribution.

For Kendall’s test, by default (if exact is NULL), an exact p-value is computed if there are less than 50 paired samples containing finite values and there are no ties. Otherwise, the test statistic is the estimate scaled to zero mean and unit variance, and is approximately normally distributed.

For Spearman’s test, p-values are computed using algorithm AS 89 for \( n < 1290 \) and exact = TRUE, otherwise via the asymptotic \( t \) approximation. Note that these are ‘exact’ for \( n < 10 \), and use an Edgeworth series approximation for larger sample sizes (the cutoff has been changed from the original paper).

Value

A list with class "htest" containing the following components:

- statistic the value of the test statistic.
- parameter the degrees of freedom of the test statistic in the case that it follows a \( t \) distribution.
- p.value the p-value of the test.
- estimate the estimated measure of association, with name "cor", "tau", or "rho" corresponding to the method employed.
- null.value the value of the association measure under the null hypothesis, always 0.
- alternative a character string describing the alternative hypothesis.
- method a character string indicating how the association was measured.
- data.name a character string giving the names of the data.
- conf.int a confidence interval for the measure of association. Currently only given for Pearson’s product moment correlation coefficient in case of at least 4 complete pairs of observations.
References


See Also

Kendall in package Kendall.
pKendall and pSpearman in package SuppDists, spearman.test in package pspearman, which supply different (and often more accurate) approximations.

Examples

## Assessment of tuna quality. We compare the Hunter L measure of
## lightness to the averages of consumer panel scores (recoded as
## integer values from 1 to 6 and averaged over 80 such values) in
## 9 lots of canned tuna.

x <- c(44.4, 45.9, 41.9, 53.3, 44.7, 44.1, 50.7, 45.2, 60.1)
y <- c(2.6, 3.1, 2.5, 5.0, 3.6, 4.0, 5.2, 2.8, 3.8)

## The alternative hypothesis of interest is that the
## Hunter L value is positively associated with the panel score.

cor.test(x, y, method = "kendall", alternative = "greater")
## => p=0.05972

cor.test(x, y, method = "kendall", alternative = "greater",
exact = FALSE) # using large sample approximation
## => p=0.04765

## Compare this to
cor.test(x, y, method = "spearm", alternative = "g")
cor.test(x, y, alternative = "g")

## Formula interface.
require(graphics)
pairs(USJudgeRatings)
cor.test(~ CONT + INTG, data = USJudgeRatings)

---

cov.wt

Weighted Covariance Matrices

Description

Returns a list containing estimates of the weighted covariance matrix and the mean of the data, and optionally of the (weighted) correlation matrix.

Usage

cov.wt(x, wt = rep(1/nrow(x), nrow(x)), cor = FALSE, center = TRUE,
method = c("unbiased", "ML"))
Arguments

x
a matrix or data frame. As usual, rows are observations and columns are variables.

wt
a non-negative and non-zero vector of weights for each observation. Its length must equal the number of rows of x.

cor
a logical indicating whether the estimated correlation weighted matrix will be returned as well.

center
either a logical or a numeric vector specifying the centers to be used when computing covariances. If TRUE, the (weighted) mean of each variable is used, if FALSE, zero is used. If center is numeric, its length must equal the number of columns of x.

method
string specifying how the result is scaled, see ‘Details’ below. Can be abbreviated.

Details

By default, method = "unbiased". The covariance matrix is divided by one minus the sum of squares of the weights, so if the weights are the default (1/n) the conventional unbiased estimate of the covariance matrix with divisor (n − 1) is obtained. This differs from the behaviour in S-PLUS which corresponds to method = "ML" and does not divide.

Value

A list containing the following named components:

cov
the estimated (weighted) covariance matrix

center
an estimate for the center (mean) of the data.

n.obs
the number of observations (rows) in x.

wt
the weights used in the estimation. Only returned if given as an argument.

cor
the estimated correlation matrix. Only returned if cor is TRUE.

See Also

cov and var.

Examples

(xy <- cbind(x = 1:10, y = c(1:3, 8:5, 8:10)))
w1 <- c(0,0,0,1,1,1,1,1,0,0)
cov.wt(xy, wt = w1) # i.e. method = "unbiased"
cov.wt(xy, wt = w1, method = "ML", cor = TRUE)
**cpgram**

*Plot Cumulative Periodogram*

**Description**

Plots a cumulative periodogram.

**Usage**

```r
cpgram(ts, taper = 0.1,
       main = paste("Series: ", deparse1(substitute(ts))),
       ci.col = "blue")
```

**Arguments**

- `ts`: a univariate time series
- `taper`: proportion tapered in forming the periodogram
- `main`: main title
- `ci.col`: colour for confidence band.

**Value**

None.

**Side Effects**

Plots the cumulative periodogram in a square plot.

**Note**

From package **MASS**.

**Author(s)**

B.D. Ripley

**Examples**

```r
require(graphics)
par(pty = "s", mfrow = c(1,2))
cpgram(lh)
lh.ar <- ar(lh, order.max = 9)
cpgram(lh.ar$resid, main = "AR(3) fit to lh")
cpgram(ldeaths)
```
cutree

Cut a Tree into Groups of Data

Description
Cuts a tree, e.g., as resulting from hclust, into several groups either by specifying the desired number(s) of groups or the cut height(s).

Usage
cutree(tree, k = NULL, h = NULL)

Arguments
tree a tree as produced by hclust. cutree() only expects a list with components merge, height, and labels, of appropriate content each.
k an integer scalar or vector with the desired number of groups
h numeric scalar or vector with heights where the tree should be cut.

At least one of k or h must be specified, k overrides h if both are given.

Details
Cutting trees at a given height is only possible for ultrametric trees (with monotone clustering heights).

Value
cutree returns a vector with group memberships if k or h are scalar, otherwise a matrix with group memberships is returned where each column corresponds to the elements of k or h, respectively (which are also used as column names).

References

See Also
hclust, dendrogram for cutting trees themselves.

Examples
hc <- hclust(dist(USArrests))
cutree(hc, k = 1:5) #k = 1 is trivial
cutree(hc, h = 250)

## Compare the 2 and 4 grouping:
g24 <- cutree(hc, c(2,4))
table(grp2 = g24[,"2"], grp4 = g24[,"4"])

---

**Description**

Cuts a tree, e.g., as resulting from `hclust`, into several groups either by specifying the desired number(s) of groups or the cut height(s).

**Usage**

```r
cutree(tree, k = NULL, h = NULL)
```

**Arguments**

- `tree` a tree as produced by `hclust`. `cutree()` only expects a list with components `merge`, `height`, and `labels`, of appropriate content each.
- `k` an integer scalar or vector with the desired number of groups
- `h` numeric scalar or vector with heights where the tree should be cut.

At least one of `k` or `h` must be specified, `k` overrides `h` if both are given.

**Details**

Cutting trees at a given height is only possible for ultrametric trees (with monotone clustering heights).

**Value**

`cutree` returns a vector with group memberships if `k` or `h` are scalar, otherwise a matrix with group memberships is returned where each column corresponds to the elements of `k` or `h`, respectively (which are also used as column names).

**References**


**See Also**

`hclust`, `dendrogram` for cutting trees themselves.

**Examples**

```r
hc <- hclust(dist(USArrests))
cutree(hc, k = 1:5) #k = 1 is trivial
cutree(hc, h = 250)

## Compare the 2 and 4 grouping:
g24 <- cutree(hc, c(2,4))
table(grp2 = g24[,"2"], grp4 = g24[,"4"])
```
decompose

Classical Seasonal Decomposition by Moving Averages

Description
Decompose a time series into seasonal, trend and irregular components using moving averages. Deals with additive or multiplicative seasonal component.

Usage

decompose(x, type = c("additive", "multiplicative"), filter = NULL)

Arguments

x
A time series.
type
The type of seasonal component. Can be abbreviated.
filter
A vector of filter coefficients in reverse time order (as for AR or MA coefficients), used for filtering out the seasonal component. If NULL, a moving average with symmetric window is performed.

Details

The additive model used is:

\[ Y_t = T_t + S_t + e_t \]

The multiplicative model used is:

\[ Y_t = T_t S_t e_t \]

The function first determines the trend component using a moving average (if filter is NULL, a symmetric window with equal weights is used), and removes it from the time series. Then, the seasonal figure is computed by averaging, for each time unit, over all periods. The seasonal figure is then centered. Finally, the error component is determined by removing trend and seasonal figure (recycled as needed) from the original time series.

This only works well if x covers an integer number of complete periods.

Value

An object of class "decomposed.ts" with following components:

x
The original series.
seasonal
The seasonal component (i.e., the repeated seasonal figure).
figure
The estimated seasonal figure only.
trend
The trend component.
random
The remainder part.
type
The value of type.

Note

The function stl provides a much more sophisticated decomposition.
delete.response

Author(s)
David Meyer <David.Meyer@wu.ac.at>

References

See Also
stl

Examples

```r
require(graphics)

m <- decompose(co2)
m$figure
plot(m)

## example taken from Kendall/Stuart
x <- c(-58, 175, 149, 214, 247, 237, 225, 329, 729, 809,
      530, 489, 540, 457, 195, 176, 337, 239, 128, 102, 232, 429, 3,
      98, 43, -141, -77, -13, 125, 361, -45, 184)
x <- ts(x, start = c(1951, 1), end = c(1958, 4), frequency = 4)
m <- decompose(x)
## seasonal figure: 6.25, 8.62, -8.84, -6.03
round(decompose(x)$figure / 10, 2)
```

delete.response  Modify Terms Objects

Description

delete.response returns a terms object for the same model but with no response variable.
drop.terms removes variables from the right-hand side of the model. There is also a "[.terms" method to perform the same function (with keep.response = TRUE).
reformulate creates a formula from a character vector. If length(termlabels) > 1, its elements are concatenated with +. Non-syntactic names (e.g. containing spaces or special characters; see make.names) must be protected with backticks (see examples). A non-parseable response still works for now, back compatibly, with a deprecation warning.

Usage

delete.response(termobj)

reformulate(termlabels, response = NULL, intercept = TRUE, env = parent.frame())
drop.terms(termobj, dropx = NULL, keep.response = FALSE)
delete.response

Arguments

- **termobj**: A terms object
- **termlabels**: character vector giving the right-hand side of a model formula. Cannot be zero-length.
- **response**: character string, symbol or call giving the left-hand side of a model formula, or NULL.
- **intercept**: logical: should the formula have an intercept?
- **env**: the environment of the formula returned.
- **dropx**: vector of positions of variables to drop from the right-hand side of the model.
- **keep.response**: Keep the response in the resulting object?

Value

delete.response and drop.terms return a terms object.
reformulate returns a formula.

See Also

terms

Examples

```r
ff <- y ~ z + x + w
tt <- terms(ff)
tt
delete.response(tt)
drop.terms(tt, 2:3, keep.response = TRUE)
tt[-1]
tt[2:3]
reformulate(attr(tt, "term.labels"))

## keep LHS:
reformulate("x+w", ff[[2]])
fS <- surv(ft, case) ~ a + b
reformulate(c("a", "b*f"), fS[[2]])

## using non-syntactic names:
reformulate(c("`P/E`", "`% Growth`"), response = as.name("+-"))

x <- c("a name", "another name")
tryCatch( reformulate(x), error = function(e) "Syntax error." )
## rather backquote the strings in x:
reformulate(sprintf("`%s`", x))

stopifnot(identical( ~ var, reformulate("var")),
            identical(~ a + b + c, reformulate(letters[1:3])),
            identical( ~ y - a + b, reformulate(letters[1:2], "y")))
```
dendrapply

Apply a Function to All Nodes of a Dendrogram

Description

Apply function FUN to each node of a dendrogram recursively. When \( y \leftarrow \text{dendrapply}(x, \text{fn}) \), then \( y \) is a dendrogram of the same graph structure as \( x \) and for each node, \( y.\text{node}[j] \leftarrow \text{FUN}(x.\text{node}[j], \ldots) \) (where \( y.\text{node}[j] \) is an (invalid!) notation for the \( j \)-th node of \( y \)).

Usage

dendrapply(X, FUN, ...)

Arguments

- **X**: an object of class "dendrogram".
- **FUN**: an R function to be applied to each dendrogram node, typically working on its attributes alone, returning an altered version of the same node.
- **...**: potential further arguments passed to FUN.

Value

Usually a dendrogram of the same (graph) structure as \( X \). For that, the function must be conceptually of the form \( \text{FUN} \leftarrow \text{function}(X) \{ \text{attributes}(X) \leftarrow \ldots ; X \} \), i.e., returning the node with some attributes added or changed.

Note

The implementation is somewhat experimental and suggestions for enhancements (or nice examples of usage) are very welcome. The current implementation is recursive and inefficient for dendrograms with many non-leaves. See the ‘Warning’ in dendrogram.

Author(s)

Martin Maechler

See Also

as.dendrogram, lapply for applying a function to each component of a list, rapply for doing so to each non-list component of a nested list.

Examples

```r
require(graphics)

## a smallish simple dendrogram
dhc <- as.dendrogram(hc <- hclust(dist(USArrests), "ave"))
(dhc21 <- dhc[[2]][[1]])

## too simple:
dendrapply(dhc21, function(n) utils::str(attributes(n)))
```
## toy example to set colored leaf labels:

```r
local(
  collab <- function(n) {
    if(is.leaf(n)) {
      a <- attributes(n)
      i <<- i+1
      attr(n, "nodePar") <-
      c(a$nodePar, list(lab.col = mycols[i], lab.font = i%%3))
    }
    n
  }
  mycols <- grDevices::rainbow(attr(dhc21, "members"))
  i <<- 0
}

dl <- dendrapply(dhc21, collab)
op <- par(mfrow = 2:1)
plot(dhc21)
plot(dl) ## --> colored labels!
par(op)
```

dendrogram

### General Tree Structures

**Description**

Class "dendrogram" provides general functions for handling tree-like structures. It is intended as a replacement for similar functions in hierarchical clustering and classification/regression trees, such that all of these can use the same engine for plotting or cutting trees.

**Usage**

```r
as.dendrogram(object, ...)  
## S3 method for class 'hclust'
as.dendrogram(object, hang = -1, check = TRUE, ...)

## S3 method for class 'dendrogram'
as.hclust(x, ...)

## S3 method for class 'dendrogram'
plot(x, type = c("rectangle", "triangle"),
     center = FALSE,
     edge.root = is.leaf(x) || !is.null(attr(x,"edgetext")),
     nodePar = NULL, edgePar = list(),
     leaflab = c("perpendicular", "textlike", "none"),
     dLeaf = NULL, xlab = ",", ylab = ",", xaxt = "n", yaxt = "s",
     horiz = FALSE, frame.plot = FALSE, xlim, ylim, ...)

## S3 method for class 'dendrogram'
cut(x, h, ...)

## S3 method for class 'dendrogram'
merge(x, y, ..., height,
     upper = "average", lower = "average", diss = TRUE, method = "complete")
```

adjunct = c("auto", "add.max", "none")

## S3 method for class 'dendrogram'
nobs(object, ...)

## S3 method for class 'dendrogram'
print(x, digits, ...)

## S3 method for class 'dendrogram'
rev(x)

## S3 method for class 'dendrogram'
str(object, max.level = NA, digits.d = 3,
give.attr = FALSE, wid = getOption("width"),
nest.lev = 0, indent.str = "",
last.str = getOption("str.dendrogram.last"), stem = "--",
...)

is.leaf(object)

Arguments

object any R object that can be made into one of class "dendrogram".
x, y object(s) of class "dendrogram".

hang numeric scalar indicating how the height of leaves should be computed from the heights of their parents; see plot.hclust.

check logical indicating if object should be checked for validity. This check is not necessary when x is known to be valid such as when it is the direct result of hclust(). The default is check=TRUE, e.g. for protecting against memory explosion with invalid inputs.

type type of plot.

center logical; if TRUE, nodes are plotted centered with respect to the leaves in the branch. Otherwise (default), plot them in the middle of all direct child nodes.

dLeaf a number specifying the distance in user coordinates between the tip of a leaf and its label. If NULL as per default, 3/4 of a letter width or height is used.

Arguments

object any R object that can be made into one of class "dendrogram".
x, y object(s) of class "dendrogram".

hang numeric scalar indicating how the height of leaves should be computed from the heights of their parents; see plot.hclust.

check logical indicating if object should be checked for validity. This check is not necessary when x is known to be valid such as when it is the direct result of hclust(). The default is check=TRUE, e.g. for protecting against memory explosion with invalid inputs.

type type of plot.

center logical; if TRUE, nodes are plotted centered with respect to the leaves in the branch. Otherwise (default), plot them in the middle of all direct child nodes.

edge.root logical; if true, draw an edge to the root node.

nodePar a list of plotting parameters to use for the nodes (see points) or NULL by default which does not draw symbols at the nodes. The list may contain components named pch, cex, col, xpd, and/or bg each of which can have length two for specifying separate attributes for inner nodes and leaves. Note that the default of pch is 1:2, so you may want to use pch = NA if you specify nodePar.

eedgePar a list of plotting parameters to use for the edge segments and labels (if there’s an edgetext). The list may contain components named col, lty and lwd (for the segments), p.col, p.lwd, and p.lty (for the polygon around the text) and t.col for the text color. As with nodePar, each can have length two for differentiating leaves and inner nodes.

leaflab a string specifying how leaves are labeled. The default "perpendicular" write text vertically (by default). "textlike" writes text horizontally (in a rectangle), and "none" suppresses leaf labels.

is.leaf(object)

Arguments

object any R object that can be made into one of class "dendrogram".
x, y object(s) of class "dendrogram".

hang numeric scalar indicating how the height of leaves should be computed from the heights of their parents; see plot.hclust.

check logical indicating if object should be checked for validity. This check is not necessary when x is known to be valid such as when it is the direct result of hclust(). The default is check=TRUE, e.g. for protecting against memory explosion with invalid inputs.

type type of plot.

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leaflab a string specifying how leaves are labeled. The default "perpendicular" write text vertically (by default). "textlike" writes text horizontally (in a rectangle), and "none" suppresses leaf labels.

dLeaf a number specifying the distance in user coordinates between the tip of a leaf and its label. If NULL as per default, 3/4 of a letter width or height is used.
The dendrogram is directly represented as a nested list where each component corresponds to a branch of the tree. Hence, the first branch of tree \( z \) is \( z[[1]] \), the second branch of the corresponding subtree is \( z[[1]][[2]] \), or shorter \( z[[c(1,2)]] \), etc.. Each node of the tree carries some information needed for efficient plotting or cutting as attributes, of which only members, height and leaf for leaves are compulsory:

- **members** total number of leaves in the branch
- **height** numeric non-negative height at which the node is plotted.
- **midpoint** numeric horizontal distance of the node from the left border (the leftmost leaf) of the branch (unit 1 between all leaves). This is used for \( \text{plot(*, center = FALSE)} \).
- **label** character; the label of the node
- **x.member** for \( \text{cut()} \$\text{upper} \), the number of former members; more generally a substitute for the members component used for ‘horizontal’ (when \( \text{horiz} = \text{FALSE} \), else ‘vertical’) alignment.
- **edgetext** character; the label for the edge leading to the node
- **nodePar** a named list (of length-1 components) specifying node-specific attributes for points plotting, see the nodePar argument above.
- **edgePar** a named list (of length-1 components) specifying attributes for segments plotting of the edge leading to the node, and drawing of the edgetext if available, see the edgePar argument above.
- **leaf** logical, if \( \text{TRUE} \), the node is a leaf of the tree.

Details

The dendrogram is directly represented as a nested list where each component corresponds to a branch of the tree. Hence, the first branch of tree \( z \) is \( z[[1]] \), the second branch of the corresponding subtree is \( z[[1]][[2]] \), or shorter \( z[[c(1,2)]] \), etc.. Each node of the tree carries some information needed for efficient plotting or cutting as attributes, of which only members, height and leaf for leaves are compulsory:

- **members** total number of leaves in the branch
- **height** numeric non-negative height at which the node is plotted.
- **midpoint** numeric horizontal distance of the node from the left border (the leftmost leaf) of the branch (unit 1 between all leaves). This is used for \( \text{plot(*, center = FALSE)} \).
- **label** character; the label of the node
- **x.member** for \( \text{cut()} \$\text{upper} \), the number of former members; more generally a substitute for the members component used for ‘horizontal’ (when \( \text{horiz} = \text{FALSE} \), else ‘vertical’) alignment.
- **edgetext** character; the label for the edge leading to the node
- **nodePar** a named list (of length-1 components) specifying node-specific attributes for points plotting, see the nodePar argument above.
- **edgePar** a named list (of length-1 components) specifying attributes for segments plotting of the edge leading to the node, and drawing of the edgetext if available, see the edgePar argument above.
- **leaf** logical, if \( \text{TRUE} \), the node is a leaf of the tree.
cut.dendrogram() returns a list with components $upper and $lower, the first is a truncated version of the original tree, also of class dendrogram, the latter a list with the branches obtained from cutting the tree, each a dendrogram.

There are [, print, and str methods for "dendrogram" objects where the first one (extraction) ensures that selecting sub-branches keeps the class, i.e., returns a dendrogram even if only a leaf. On the other hand, (single bracket) extraction returns the underlying list structure.

Objects of class "hclust" can be converted to class "dendrogram" using method as.dendrogram(), and since R 2.13.0, there is also a as.hclust() method as an inverse.

rev.dendrogram simply returns the dendrogram x with reversed nodes, see also reorder.dendrogram.

The merge(x, y, ...) method merges two or more dendrograms into a new one which has x and y (and optional further arguments) as branches. Note that before R 3.1.2, adjust = "none" was used implicitly, which is invalid when, e.g., the dendrograms are from as.dendrogram(hclust(..)).

nobs(object) returns the total number of leaves (the members attribute, see above).

is.leaf(object) returns logical indicating if object is a leaf (the most simple dendrogram).

plotNode() and plotNodeLimit() are helper functions.

Warning
Some operations on dendrograms such as merge() make use of recursion. For deep trees it may be necessary to increase options("expressions"): if you do, you are likely to need to set the C stack size (Cstack_info()["size"]) larger than the default where possible.

Note
plot(): When using type = "triangle", center = TRUE often looks better.

str(d): If you really want to see the internal structure, use str(unclass(d)) instead.

See Also
dendrapply for applying a function to each node. order.dendrogram and reorder.dendrogram; further, the labels method.

Examples

```r
require(graphics); requireutils)

hc <- hclust(dist(USArrests), "ave")
(dend1 <- as.dendrogram(hc)) # "print()" method
str(dend1) # "str()" method
str(dend1, max.level = 2, last.str = "") # only the first two sub-levels
oo <- options(str.dendrogram.last = ")") # yet another possibility
str(dend1, max.level = 2) # only the first two sub-levels
options(oo) # .. resetting them

op <- par(mfrow = c(2,2), mar = c(5,2,1,4))
plot(dend1)
## "triangle" type and show inner nodes:
plot(dend1, nodePar = list(pch = c(1,NA), cex = 0.8, lab.cex = 0.8),
     type = "t", center = TRUE)
plot(dend1, edgePar = list(col = 1:2, lty = 2:3),
     dLeaf = 1, edge.root = TRUE)
```
plot(dend1, nodePar = list(pch = 2:1, cex = .4*2:1, col = 2:3),
    horiz = TRUE)

## simple test for as.hclust() as the inverse of as.dendrogram():
stopifnot(identical(as.hclust(dend1)[1:4], hc[1:4]))

dend2 <- cut(dend1, h = 70)
## leaves are wrong horizontally in R 4.0 and earlier:
plot(dend2$upper)
## dend2$lower is *NOT* a dendrogram, but a list of .. :
plot(dend2$lower[[3]], nodePar = list(col = 4), horiz = TRUE, type = "tr")
## "inner" and "leaf" edges in different type & color :
plot(dend2$lower[[2]], nodePar = list(col = 1),
     edgePar = list(lty = 1:2, col = 2:1),
     horiz = TRUE)

## merge() to join dendrograms:
(d13 <- merge(dend2$lower[[1]], dend2$lower[[3]]))
## merge() all parts back (using default 'height' instead of original one):
den.1 <- Reduce(merge, dend2$lower)
## or merge() all four parts at same height --> 4 branches (!)
d. <- merge(dend2$lower[[1]], dend2$lower[[2]], dend2$lower[[3]], dend2$lower[[4]])
## (with a warning) or the same using do.call :
stopifnot(identical(d., do.call(merge, dend2$lower)))

## "Zoom" in to the first dendrogram :
plot(dend1, xlim = c(1,20), ylim = c(1,50))
nP <- list(col = 3:2, cex = c(2.0, 0.75), pch = 21:22,
       bg = c("light blue", "pink"),
       lab.cex = 0.75, lab.col = "tomato")

plot(d3, nodePar= nP, edgePar = list(col = "gray", lwd = 2), horiz = TRUE)

addE <- function(n) {
  if(!is.leaf(n)) {
    attr(n, "edgePar") <- list(p.col = "plum")
    attr(n, "edgetext") <- paste(attr(n, "members"), "members")
  }
  n
}
d3e <- dendrapply(d3, addE)

plot(d3e, nodePar = nP)

plot(d3e, nodePar = nP, leaflab = "textlike")
density

Kernel Density Estimation

Description

The (S3) generic function density computes kernel density estimates. Its default method does so with the given kernel and bandwidth for univariate observations.

Usage

density(x, ...)

## Default S3 method:
density(x, bw = "nrd0", adjust = 1,
kernel = c("gaussian", "epanechnikov", "rectangular",
"triangular", "biweight",
"cosine", "optcosine"),
weights = NULL, window = kernel, width,
give.Rkern = FALSE, subdensity = FALSE,
warnWbw = var(weights) > 0,
n = 512, from, to, cut = 3, na.rm = FALSE, ...)

Arguments

x
the data from which the estimate is to be computed. For the default method a numeric vector: long vectors are not supported.

bw
the smoothing bandwidth to be used. The kernels are scaled such that this is the standard deviation of the smoothing kernel. (Note this differs from the reference books cited below, and from S-PLUS.) bw can also be a character string giving a rule to choose the bandwidth. See bw.nrd. The default, "nrd0", has remained the default for historical and compatibility reasons, rather than as a general recommendation, where e.g., "SJ" would rather fit, see also Venables and Ripley (2002).

The specified (or computed) value of bw is multiplied by adjust.

adjust
the bandwidth used is actually adjust*bw. This makes it easy to specify values like ‘half the default’ bandwidth.

kernel, window
a character string giving the smoothing kernel to be used. This must partially match one of "gaussian", "rectangular", "triangular", "epanechnikov", "biweight", "cosine" or "optcosine", with default "gaussian", and may be abbreviated to a unique prefix (single letter). "cosine" is smoother than "optcosine", which is the usual ‘cosine’ kernel in the literature and almost MSE-efficient. However, "cosine" is the version used by S.

weights
numeric vector of non-negative observation weights, hence of same length as x. The default NULL is equivalent to weights = rep(1/nx, nx) where nx is the length of (the finite entries of) x[]. If na.rm = TRUE and there are NA’s in x, they and the corresponding weights are removed before computations. In that case, when the original weights have summed to one, they are re-scaled to keep doing so.
Note that weights are not taken into account for automatic bandwidth rules, i.e., when bw is a string. When the weights are proportional to true counts cn, \( \text{density}(x = \text{rep}(x, cn)) \) may be used instead of weights.

**width**

This exists for compatibility with S; if given, and bw is not, will set bw to width if this is a character string, or to a kernel-dependent multiple of width if this is numeric.

**give.Rkern**

Logical; if true, no density is estimated, and the "canonical bandwidth" of the chosen kernel is returned instead.

**subdensity**

Used only when weights are specified which do not sum to one. When true, it indicates that a "sub-density" is desired and no warning should be signalled. By default, when false, a warning is signalled when the weights do not sum to one.

**warnWbw**

Logical, used only when weights are specified and bw is character, i.e., automatic bandwidth selection is chosen (as by default). When true (as by default), a warning is signalled to alert the user that automatic bandwidth selection will not take the weights into account and hence may be suboptimal.

**n**

The number of equally spaced points at which the density is to be estimated. When \( n > 512 \), it is rounded up to a power of 2 during the calculations (as \( \text{fft} \) is used) and the final result is interpolated by \( \text{approx} \). So it almost always makes sense to specify \( n \) as a power of two.

**from**, **to**

The left and right-most points of the grid at which the density is to be estimated; the defaults are \( \text{cut} \times \text{bw} \) outside of range(\( x \)).

**cut**

By default, the values of from and to are cut bandwidths beyond the extremes of the data. This allows the estimated density to drop to approximately zero at the extremes.

**na.rm**

Logical; if TRUE, missing values are removed from \( x \). If FALSE any missing values cause an error.

... further arguments for (non-default) methods.

**Details**

The algorithm used in \texttt{density.default} disperses the mass of the empirical distribution function over a regular grid of at least 512 points and then uses the fast Fourier transform to convolve this approximation with a discretized version of the kernel and then uses linear approximation to evaluate the density at the specified points.

The statistical properties of a kernel are determined by \( \sigma_K^2 = \int t^2 K(t) dt \) which is always \( = 1 \) for our kernels (and hence the bandwidth bw is the standard deviation of the kernel) and \( R(K) = \int K^2(t) dt \).

MSE-equivalent bandwidths (for different kernels) are proportional to \( \sigma_K R(K) \) which is scale invariant and for our kernels equal to \( R(K) \). This value is returned when \texttt{give.Rkern = TRUE}. See the examples for using exact equivalent bandwidths.

Infinite values in \( x \) are assumed to correspond to a point mass at +/-\( \text{Inf} \) and the density estimate is of the sub-density on \( (-\text{Inf}, +\text{Inf}) \).

**Value**

If \texttt{give.Rkern} is true, the number \( R(K) \), otherwise an object with class "density" whose underlying structure is a list containing the following components.

\[ \text{x} \]

the \( n \) coordinates of the points where the density is estimated.

\[ \text{y} \]

the estimated density values. These will be non-negative, but can be zero.
bw  the bandwidth used.
n  the sample size after elimination of missing values.
call  the call which produced the result.
data.name  the deparsed name of the x argument.
has.na  logical, for compatibility (always FALSE).

The print method reports summary values on the x and y components.

References


See Also

*bw.nrd, plot.density, hist.*

Examples

```r
require(graphics)

plot(density(c(-20, rep(0,98), 20)), xlim = c(-4, 4)) # IQR = 0

# The Old Faithful geyser data
d <- density(faithful$eruptions, bw = "sj")
d
plot(d)

plot(d, type = "n")
polygon(d, col = "wheat")

## Missing values:
x <- xx <- faithful$eruptions
x[i.out <- sample(length(x), 10)] <- NA
doR <- density(x, bw = 0.15, na.rm = TRUE)
lines(doR, col = "blue")
points(xx[i.out], rep(0.01, 10))

## Weighted observations:
fe <- sort(faithful$eruptions) # has quite a few non-unique values
## use 'counts / n' as weights:
dw <- density(unique(fe), weights = table(fe)/length(fe), bw = d$bw)
utils::str(dw) ## smaller n: only 126, but identical estimate:
stopifnot(all.equal(d[1:3], dw[1:3]))

## simulation from a density() fit:
```

# a kernel density fit is an equally-weighted mixture.
fit <- density(xx)
N <- 1e6
x.new <- rnorm(N, sample(xx, size = N, replace = TRUE), fit$bw)
plot(fit)
lines(density(x.new), col = "blue")

(kernels <- eval(formals(density.default)$kernel))

## show the kernels in the R parametrization
plot(density(0, bw = 1), xlab = "", main = "R's density() kernels with bw = 1")
for(i in 2:length(kernels))
  lines(density(0, bw = 1, kernel = kernels[i]), col = i)
legend(1.5,.4, legend = kernels, col = seq(kernels), lty = 1, cex = .8, y.intersp = 1)

## show the kernels in the S parametrization
plot(density(0, from = -1.2, to = 1.2, width = 2, kernel = "gaussian"),
     type = "l", ylim = c(0, 1), xlab = "", main = "R's density() kernels with width = 1")
for(i in 2:length(kernels))
  lines(density(0, width = 2, kernel = kernels[i]), col = i)
legend(0.6, 1.0, legend = kernels, col = seq(kernels), lty = 1)

##-------- Semi-advanced theoretic from here on ------------
(RKs <- cbind(sapply(kernels,
      function(k) density(kernel = k, give.Rkern = TRUE))))
100*round(RKs["epanechnikov",]/RKs, 4) ## Efficiencies

bw <- bw.SJ(precip) ## sensible automatic choice
plot(density(precip, bw = bw),
     main = "same sd bandwidths, 7 different kernels")
for(i in 2:length(kernels))
  lines(density(precip, bw = bw, kernel = kernels[i]), col = i)

## Bandwidth Adjustment for "Exactly Equivalent Kernels"
(h.f <- sapply(kernels, function(k)density(kernel = k, give.Rkern = TRUE)))
(h.f <- (h.f["gaussian"] / h.f)^ .2)
## -> 1, 1.01, .995, 1.007,... close to 1 => adjustment barely visible..

plot(density(precip, bw = bw),
     main = "equivalent bandwidths, 7 different kernels")
for(i in 2:length(kernels))
  lines(density(precip, bw = bw, adjust = h.f[i], kernel = kernels[i]), col = i)
legend(55, 0.035, legend = kernels, col = seq(kernels), lty = 1)
Description

Compute derivatives of simple expressions, symbolically and algorithmically.

Usage

\[
\begin{align*}
D \text{ (expr, name)} \\
\text{deriv(expr, ...)} \\
\text{deriv3(expr, ...)} \\
\text{## Default S3 method:} \\
\text{deriv(expr, namevec, function.arg = NULL, tag = ".expr",} \\
\text{hessian = FALSE, ...)} \\
\text{## S3 method for class 'formula'} \\
\text{deriv(expr, namevec, function.arg = NULL, tag = ".expr",} \\
\text{hessian = FALSE, ...)} \\
\text{## Default S3 method:} \\
\text{deriv3(expr, namevec, function.arg = NULL, tag = ".expr",} \\
\text{hessian = TRUE, ...)} \\
\text{## S3 method for class 'formula'} \\
\text{deriv3(expr, namevec, function.arg = NULL, tag = ".expr",} \\
\text{hessian = TRUE, ...)}
\end{align*}
\]

Arguments

- **expr**: a **expression** or **call** (except D) a formula with no lhs.
- **name, namevec**: character vector, giving the variable names (only one for D()) with respect to which derivatives will be computed.
- **function.arg**: if specified and non-NULL, a character vector of arguments for a function return, or a function (with empty body) or TRUE, the latter indicating that a function with argument names namevec should be used.
- **tag**: character; the prefix to be used for the locally created variables in result. Must be no longer than 60 bytes when translated to the native encoding.
- **hessian**: a logical value indicating whether the second derivatives should be calculated and incorporated in the return value.
- **...**: arguments to be passed to or from methods.

Details

D is modelled after its S namesake for taking simple symbolic derivatives.

deriv is a **generic** function with a default and a **formula** method. It returns a **call** for computing the expr and its (partial) derivatives, simultaneously. It uses so-called **algorithmic derivatives**. If function.arg is a function, its arguments can have default values, see the fx example below.

Currently, deriv.formula just calls deriv.default after extracting the expression to the right of `~`.

deriv3 and its methods are equivalent to deriv and its methods except that hessian defaults to TRUE for deriv3.

The internal code knows about the arithmetic operators +, -, *, / and ^, and the single-variable functions exp, log, sin, cos, tan, sinh, cosh, sqrt, pnorm, dnorm, asin, acos, atan, gamma, lgamma, digamma and trigamma, as well as psigamma for one or two arguments (but derivative only
with respect to the first. (Note that only the standard normal distribution is considered.)
Since $R$ 3.4.0, the single-variable functions \texttt{log1p}, \texttt{expm1}, \texttt{log2}, \texttt{log10}, \texttt{cospi}, \texttt{sinpi}, \texttt{tanpi}, \texttt{factorial}, and \texttt{lfactorial} are supported as well.

**Value**

\texttt{D} returns a call and therefore can easily be iterated for higher derivatives.
\texttt{deriv} and \texttt{deriv3} normally return an \texttt{expression} object whose evaluation returns the function values with a "gradient" attribute containing the gradient matrix. If \texttt{hessian} is TRUE the evaluation also returns a "hessian" attribute containing the Hessian array.
If \texttt{function.arg} is not \texttt{NULL}, \texttt{deriv} and \texttt{deriv3} return a function with those arguments rather than an expression.

**References**


**See Also**

\texttt{nlm} and \texttt{optim} for numeric minimization which could make use of derivatives,

**Examples**

```r
## formula argument :
dx2x <- deriv(~ x^2, "x") ; dx2x
## Not run: expression({
    .value <- x^2
    .grad <- array(0, c(length(.value), 1), list(NULL, c("x")))
    .grad[, "x"] <- 2 * x
    attr(.value, "gradient") <- .grad
    .value
})
## End(Not run)
mode(dx2x)
x <- -1:2
eval(dx2x)

## Something 'tougher':
trig.exp <- expression(sin(cos(x + y^2)))
(D.sc <- D(trig.exp, "x") )
all.equal(D(trig.exp[[1]], "x"), D.sc)
(dxy <- deriv(trig.exp, c("x", "y")) )
y <- 1
eval(dxy)
eval(D.sc)

## function returned:
deriv(y ~ sin(cos(x) * y)), c("x","y"), function.arg = TRUE)

## function with defaulted arguments:
(fx <- deriv(y ~ b0 + b1 * 2^(-x/th), c("b0", "b1", "th"),
```
deviance

Model Deviance

Description

Returns the deviance of a fitted model object.
df.residual

Usage

deviance(object, ...)

Arguments

object an object for which the deviance is desired.
... additional optional argument.

Details

This is a generic function which can be used to extract deviances for fitted models. Consult the individual modeling functions for details on how to use this function.

Value

The value of the deviance extracted from the object object.

References


See Also

df.residual, extractAIC, glm, lm.

---------

df.residual  Residual Degrees-of-Freedom

Description

Returns the residual degrees-of-freedom extracted from a fitted model object.

Usage

df.residual(object, ...)

Arguments

object an object for which the degrees-of-freedom are desired.
... additional optional arguments.

Details

This is a generic function which can be used to extract residual degrees-of-freedom for fitted models. Consult the individual modeling functions for details on how to use this function.

The default method just extracts the df.residual component.

Value

The value of the residual degrees-of-freedom extracted from the object x.
Discrete Integration: Inverse of Differencing

Description
Computes the inverse function of the lagged differences function `diff`.

Usage
`diffinv(x, ...)`

## Default S3 method:
`diffinv(x, lag = 1, differences = 1, xi, ...)`

## S3 method for class 'ts'
`diffinv(x, lag = 1, differences = 1, xi, ...)`

Arguments
- `x`: a numeric vector, matrix, or time series.
- `lag`: a scalar lag parameter.
- `differences`: an integer representing the order of the difference.
- `xi`: a numeric vector, matrix, or time series containing the initial values for the integrals. If missing, zeros are used.
- `...`: arguments passed to or from other methods.

Details
`diffinv` is a generic function with methods for class "ts" and default for vectors and matrices. Missing values are not handled.

Value
A numeric vector, matrix, or time series (the latter for the "ts" method) representing the discrete integral of `x`.

Author(s)
A. Trapletti

See Also
diff

Examples
```r
s <- 1:10
d <- diff(s)
diffinv(d, xi = 1)
```
distance matrix computation

Description

This function computes and returns the distance matrix computed by using the specified distance measure to compute the distances between the rows of a data matrix.

Usage

```
dist(x, method = "euclidean", diag = FALSE, upper = FALSE, p = 2)

as.dist(m, diag = FALSE, upper = FALSE)
```

Arguments

- `x` a numeric matrix, data frame or "dist" object.
- `method` the distance measure to be used. This must be one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski". Any unambiguous substring can be given.
- `diag` logical value indicating whether the diagonal of the distance matrix should be printed by `print.dist`.
- `upper` logical value indicating whether the upper triangle of the distance matrix should be printed by `print.dist`.
- `p` The power of the Minkowski distance.
- `m` An object with distance information to be converted to a "dist" object. For the default method, a "dist" object, or a matrix (of distances) or an object which can be coerced to such a matrix using `as.matrix()`. (Only the lower triangle of the matrix is used, the rest is ignored).
- `digits, justify` passed to `format` inside of `print()`. 
- `right,...` further arguments, passed to other methods.

Details

Available distance measures are (written for two vectors `x` and `y`):

- **euclidean**: Usual distance between the two vectors (2 norm aka $L_2$), $\sqrt{\sum_i (x_i - y_i)^2}$. 
- **maximum**: Maximum distance between two components of `x` and `y` (supremum norm)
manhattan: Absolute distance between the two vectors (1 norm aka \( L_1 \)).

canberra: \( \sum_i |x_i - y_i|/(|x_i| + |y_i|) \). Terms with zero numerator and denominator are omitted from the sum and treated as if the values were missing.

This is intended for non-negative values (e.g., counts), in which case the denominator can be written in various equivalent ways; Originally, \( R \) used \( x_i + y_i \), then from 1998 to 2017, \( |x_i + y_i| \), and then the correct \( |x_i| + |y_i| \).

binary: (aka asymmetric binary): The vectors are regarded as binary bits, so non-zero elements are ‘on’ and zero elements are ‘off’. The distance is the proportion of bits in which only one is on amongst those in which at least one is on. This also called “Jaccard” distance in some contexts. Here, two all-zero observations have distance 0, whereas in traditional Jaccard definitions, the distance would be undefined for that case and give \( \text{NaN} \) numerically.

minkowski: The \( p \) norm, the \( p \)th root of the sum of the \( p \)th powers of the differences of the components.

Missing values are allowed, and are excluded from all computations involving the rows within which they occur. Further, when \( \text{Inf} \) values are involved, all pairs of values are excluded when their contribution to the distance gave \( \text{NaN} \) or \( \text{NA} \). If some columns are excluded in calculating a Euclidean, Manhattan, Canberra or Minkowski distance, the sum is scaled up proportionally to the number of columns used. If all pairs are excluded when calculating a particular distance, the value is \( \text{NA} \).

The "dist" method of \( \text{as.matrix()} \) and \( \text{as.dist()} \) can be used for conversion between objects of class "dist" and conventional distance matrices.

\( \text{as.dist()} \) is a generic function. Its default method handles objects inheriting from class "dist", or coercible to matrices using \( \text{as.matrix()} \). Support for classes representing distances (also known as dissimilarities) can be added by providing an \( \text{as.matrix()} \) or, more directly, an \( \text{as.dist} \) method for such a class.

Value

dist returns an object of class "dist".

The lower triangle of the distance matrix stored by columns in a vector, say \( \text{do} \). If \( n \) is the number of observations, i.e., \( n \leftarrow \text{attr(} \text{do, "Size"\)} \), then for \( i < j \leq n \), the dissimilarity between (row) \( i \) and \( j \) is \( \text{do[}n*(i-1) - i*(i-1)/2 + j-i\text{]} \). The length of the vector is \( n*(n-1)/2 \), i.e., of order \( n^2 \).

The object has the following attributes (besides "class" equal to "dist"):

- **Size**: integer, the number of observations in the dataset.
- **Labels**: optionally, contains the labels, if any, of the observations of the dataset.
- **Diag, Upper**: logicals corresponding to the arguments \( \text{diag} \) and \( \text{upper} \) above, specifying how the object should be printed.
- **call**: optionally, the \( \text{call} \) used to create the object.
- **method**: optionally, the distance method used; resulting from \( \text{dist()} \), the \( \text{(match.arg())ed} \) method argument.

References


See Also
daisy in the cluster package with more possibilities in the case of mixed (continuous / categorical) variables. hclust.

Examples

```
require(graphics)

x <- matrix(rnorm(100), nrow = 5)
dist(x)
dist(x, diag = TRUE)
dist(x, upper = TRUE)
m <- as.matrix(dist(x))
d <- as.dist(m)
stopifnot(d == dist(x))

## Use correlations between variables "as distance"

dd <- as.dist((1 - cor(USJudgeRatings))/2)
round(1000 * dd) # (prints more nicely)
plot(hclust(dd)) # to see a dendrogram of clustered variables

## example of binary and canberra distances.
x <- c(0, 0, 1, 1, 1, 1)
y <- c(1, 0, 1, 1, 0, 1)
dist(rbind(x, y), method = "binary")
## answer 0.4 = 2/5

dist(rbind(x, y), method = "canberra")
## answer 2 * (6/5)

## To find the names
labels(eurodist)
```

## Examples involving "Inf":
```
## 1)
x[6] <- Inf
(m2 <- rbind(x, y))
dist(m2, method = "binary")
# warning, answer 0.5 = 2/4

## These all give "Inf":
stopifnot(Inf == dist(m2, method = "euclidean"),
          Inf == dist(m2, method = "maximum"),
          Inf == dist(m2, method = "manhattan"))

## "Inf" is same as very large number:
x1 <- x; x1[6] <- 1e100
stopifnot(dist(cbind(x1, y), method = "canberra") ==
          print(dist(cbind(x1, y), method = "canberra"))))

## 2)
y[6] <- Inf #-> 6-th pair is excluded
dist(rbind(x, y), method = "binary")
# warning; 0.5

dist(rbind(x, y), method = "canberra")
# 3
dist(rbind(x, y), method = "maximum")
# 1
dist(rbind(x, y), method = "manhattan")
# 2.4
```
Distributions

**Description**

Density, cumulative distribution function, quantile function and random variate generation for many standard probability distributions are available in the `stats` package.

**Details**

The functions for the density/mass function, cumulative distribution function, quantile function and random variate generation are named in the form `dxxx`, `pxxx`, `qxxx` and `rxxx` respectively.

For the beta distribution see `dbeta`.
For the binomial (including Bernoulli) distribution see `dbinom`.
For the Cauchy distribution see `dcauchy`.
For the chi-squared distribution see `dchisq`.
For the exponential distribution see `dexp`.
For the F distribution see `df`.
For the gamma distribution see `dgamma`.
For the geometric distribution see `dgeom`. (This is also a special case of the negative binomial.)
For the hypergeometric distribution see `dhyper`.
For the log-normal distribution see `dlnorm`.
For the multinomial distribution see `dmultinom`.
For the negative binomial distribution see `dnbinom`.
For the normal distribution see `dnorm`.
For the Poisson distribution see `dpois`.
For the Student's t distribution see `dt`.
For the uniform distribution see `dunif`.
For the Weibull distribution see `dweibull`.
For less common distributions of test statistics see `pbirthday`, `dsignrank`, `ptukey` and `dwilcox` (and see the 'See Also' section of `cor.test`).

**See Also**

`RNG` about random number generation in R.

The CRAN task view on distributions, [https://CRAN.R-project.org/view=Distributions](https://CRAN.R-project.org/view=Distributions), mentioning several CRAN packages for additional distributions.
**dummy.coef**  

*Extract Coefficients in Original Coding*

**Description**

This extracts coefficients in terms of the original levels of the coefficients rather than the coded variables.

**Usage**

```r
dummy.coef(object, ...)
```

## S3 method for class 'lm'

dummy.coef(object, use.na = FALSE, ...)

## S3 method for class 'aovlist'

dummy.coef(object, use.na = FALSE, ...)

**Arguments**

- **object** a linear model fit.
- **use.na** logical flag for coefficients in a singular model. If use.na is true, undetermined coefficients will be missing; if false they will get one possible value.
- **...** arguments passed to or from other methods.

**Details**

A fitted linear model has coefficients for the contrasts of the factor terms, usually one less in number than the number of levels. This function re-expresses the coefficients in the original coding; as the coefficients will have been fitted in the reduced basis, any implied constraints (e.g., zero sum for `contr.helmert` or `contr.sum`) will be respected. There will be little point in using `dummy.coef` for `contr.treatment` contrasts, as the missing coefficients are by definition zero.

The method used has some limitations, and will give incomplete results for terms such as `poly(x, 2)`. However, it is adequate for its main purpose, `aov` models.

**Value**

A list giving for each term the values of the coefficients. For a multistratum `aov` model, such a list for each stratum.

**Warning**

This function is intended for human inspection of the output: it should not be used for calculations. Use coded variables for all calculations.

The results differ from S for singular values, where S can be incorrect.

**See Also**

- `aov`, `model.tables`
Examples

```r
options(contrasts = c("contr.helmert", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
dummy.coef(npk.aov)

npk.aovE <- aov(yield ~ N*P*K + Error(block), npk)
dummy.coef(npk.aovE)
```

---

**ecdf**

*Empirical Cumulative Distribution Function*

Description

Compute an empirical cumulative distribution function, with several methods for plotting, printing and computing with such an “ecdf” object.

Usage

```r
ecdf(x)
```

## S3 method for class 'ecdf'
plot(x, ..., ylab="Fn(x)", verticals = FALSE, 
col.01line = "gray70", pch = 19)

## S3 method for class 'ecdf'
print(x, digits= getOption("digits") - 2, ...)

## S3 method for class 'ecdf'
summary(object, ...)

## S3 method for class 'ecdf'
quantile(x, ...)
```

Arguments

- `x, object` numeric vector of the observations for `ecdf`; for the methods, an object inheriting from class "ecdf".
- `...` arguments to be passed to subsequent methods, e.g., `plot.stepfun` for the plot method.
- `ylab` label for the y-axis.
- `verticals` see `plot.stepfun`.
- `col.01line` numeric or character specifying the color of the horizontal lines at \( y = 0 \) and \( 1 \), see `colors`.
- `pch` plotting character.
- `digits` number of significant digits to use, see `print`.
The e.c.d.f. (empirical cumulative distribution function) \( F_n \) is a step function with jumps \( i/n \) at observation values, where \( i \) is the number of tied observations at that value. Missing values are ignored.

For observations \( x = (x_1, x_2, \ldots, x_n) \), \( F_n \) is the fraction of observations less or equal to \( t \), i.e.,

\[
F_n(t) = \frac{\#\{x_i \leq t\}}{n} = \frac{1}{n} \sum_{i=1}^{n} \mathbf{1}[x_i \leq t].
\]

The function `plot.ecdf` which implements the `plot` method for `ecdf` objects, is implemented via a call to `plot.stepfun`; see its documentation.

**Value**

For `ecdf`, a function of class "ecdf", inheriting from the "stepfun" class, and hence inheriting a `knots()` method.

For the `summary` method, a summary of the knots of object with a "header" attribute.

The `quantile(obj, ...)` method computes the same quantiles as `quantile(x, ...)` would where \( x \) is the original sample.

**Note**

The objects of class "ecdf" are not intended to be used for permanent storage and may change structure between versions of \( R \) (and did at \( R \) 3.0.0). They can usually be re-created by

\[
\text{eval(attr(old_obj, "call"), environment(old_obj))}
\]

since the data used is stored as part of the object’s environment.

**Author(s)**

Martin Maechler; fixes and new features by other R-core members.

**See Also**

`stepfun`, the more general class of step functions, `approxfun` and `splinefun`.

**Examples**

```r
# Simple didactical ecdf example :
x <- rnorm(12)
Fn <- ecdf(x)
Fn  # a *function*
Fn(x) # returns the percentiles for x
tt <- seq(-2, 2, by = 0.1)
12 * Fn(tt) # Fn is a 'simple' function (with values k/12)
summary(Fn)
###-- see below for graphics
knots(Fn) # the unique data values (12 of them if there were no ties)

y <- round(rnorm(12), 1); y[3] <- y[1]
Fn12 <- ecdf(y)
Fn12
```

##-- Simple didactical ecdf example :
x <- rnorm(12)
Fn <- ecdf(x)
Fn  # a *function*
Fn(x) # returns the percentiles for x
tt <- seq(-2, 2, by = 0.1)
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knots(Fn) # the unique data values (12 of them if there were no ties)

y <- round(rnorm(12), 1); y[3] <- y[1]
Fn12 <- ecdf(y)
Fn12
```
eff.aovlist

Compute Efficiencies of Multistratum Analysis of Variance

Description

Computes the efficiencies of fixed-effect terms in an analysis of variance model with multiple strata.

Usage

eff.aovlist(aovlist)

Arguments

aovlist The result of a call to aov with an Error term.
Fixed-effect terms in an analysis of variance model with multiple strata may be estimable in more than one stratum, in which case there is less than complete information in each. The efficiency for a term is the fraction of the maximum possible precision (inverse variance) obtainable by estimating in just that stratum. Under the assumption of balance, this is the same for all contrasts involving that term.

This function is used to pick strata in which to estimate terms in model.tables.aovlist and se.contrast.aovlist.

In many cases terms will only occur in one stratum, when all the efficiencies will be one: this is detected and no further calculations are done.

The calculation used requires orthogonal contrasts for each term, and will throw an error if non-orthogonal contrasts (e.g., treatment contrasts or an unbalanced design) are detected.

A matrix giving for each non-pure-error stratum (row) the efficiencies for each fixed-effect term in the model.


Examples

```r
## An example from Yates (1932),
## a 2^3 design in 2 blocks replicated 4 times
Block <- gl(8, 4)
A <- factor(c(0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1))
B <- factor(c(0,0,1,1,0,0,1,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1))
C <- factor(c(0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1))
aovdat <- data.frame(Block, A, B, C, Yield)
old <- getOption("contrasts")
options(contrasts = c("contr.helmert", "contr.poly"))
## IGNORE_RDIFF_BEGIN
(fit <- aov(Yield ~ A*B*C + Error(Block), data = aovdat))
## IGNORE_RDIFF_END
eff.aovlist(fit)
options(contrasts = old)
```
effects

Effects from Fitted Model

Description

Returns (orthogonal) effects from a fitted model, usually a linear model. This is a generic function, but currently only has a methods for objects inheriting from classes "lm" and "glm".

Usage

effects(object, ...)

## S3 method for class 'lm'
effects(object, set.sign = FALSE, ...)

Arguments

object
an R object; typically, the result of a model fitting function such as lm.

set.sign
logical. If TRUE, the sign of the effects corresponding to coefficients in the model will be set to agree with the signs of the corresponding coefficients, otherwise the sign is arbitrary.

... arguments passed to or from other methods.

Details

For a linear model fitted by lm or aov, the effects are the uncorrelated single-degree-of-freedom values obtained by projecting the data onto the successive orthogonal subspaces generated by the QR decomposition during the fitting process. The first \( r \) (the rank of the model) are associated with coefficients and the remainder span the space of residuals (but are not associated with particular residuals).

Empty models do not have effects.

Value

A (named) numeric vector of the same length as residuals, or a matrix if there were multiple responses in the fitted model, in either case of class "coef".

The first \( r \) rows are labelled by the corresponding coefficients, and the remaining rows are unlabelled. Note that in rank-deficient models the corresponding coefficients will be in a different order if pivoting occurred.

References


See Also

coeff
Examples

```r
y <- c(1:3, 7, 5)
x <- c(1:3, 6:7)
( ee <- effects(lm(y ~ x)) )
c( round(ee - effects(lm(y+10 ~ I(x-3.8))), 3) )
# just the first is different
```

---

**embed**  
*Embedding a Time Series*

Description

Embeds the time series `x` into a low-dimensional Euclidean space.

Usage

```r
embed (x, dimension = 1)
```

Arguments

- `x` a numeric vector, matrix, or time series.
- `dimension` a scalar representing the embedding dimension.

Details

Each row of the resulting matrix consists of sequences `x[t]`, `x[t-1]`, ..., `x[t-dimension+1]`, where `t` is the original index of `x`. If `x` is a matrix, i.e., `x` contains more than one variable, then `x[t]` consists of the `t`th observation on each variable.

Value

A matrix containing the embedded time series `x`.

Author(s)

A. Trapletti, B.D. Ripley

Examples

```r
x <- 1:10
embed (x, 3)
```
expand.model.frame  Add new variables to a model frame

Description

Evaluates new variables as if they had been part of the formula of the specified model. This ensures that the same na.action and subset arguments are applied and allows, for example, x to be recovered for a model using sin(x) as a predictor.

Usage

```r
expand.model.frame(model, extras,
                   envir = environment(formula(model)),
                   na.expand = FALSE)
```

Arguments

- **model**: a fitted model
- **extras**: one-sided formula or vector of character strings describing new variables to be added
- **envir**: an environment to evaluate things in
- **na.expand**: logical; see below

Details

If `na.expand = FALSE` then NA values in the extra variables will be passed to the na.action function used in model. This may result in a shorter data frame (with `na.omit`) or an error (with `na.fail`). If `na.expand = TRUE` the returned data frame will have precisely the same rows as `model.frame(model)`, but the columns corresponding to the extra variables may contain NA.

Value

A data frame.

See Also

`model.frame`, `predict`

Examples

```r
model <- lm(log(Volume) ~ log(Girth) + log(Height), data = trees)
expand.model.frame(model, ~ Girth)  # prints data.frame like

dd <- data.frame(x = 1:5, y = rnorm(5), z = c(1,2,NA,4,5))
model <- glm(y ~ x, data = dd, subset = 1:4, na.action = na.omit)
expand.model.frame(model, "z", na.expand = FALSE)  # = default
expand.model.frame(model, "z", na.expand = TRUE)
```
The Exponential Distribution

Description

Density, distribution function, quantile function and random generation for the exponential distribution with rate rate (i.e., mean 1/rate).

Usage

\[
\begin{align*}
dexp(x, rate = 1, log = FALSE) \\
pexp(q, rate = 1, lower.tail = TRUE, log.p = FALSE) \\
qexp(p, rate = 1, lower.tail = TRUE, log.p = FALSE) \\
rexp(n, rate = 1)
\end{align*}
\]

Arguments

- `x, q` vector of quantiles.
- `p` vector of probabilities.
- `n` number of observations. If `length(n) > 1`, the length is taken to be the number required.
- `rate` vector of rates.
- `log, log.p` logical; if TRUE, probabilities p are given as log(p).
- `lower.tail` logical; if TRUE (default), probabilities are \(P[X \leq x]\), otherwise, \(P[X > x]\).

Details

If `rate` is not specified, it assumes the default value of 1.

The exponential distribution with rate \(\lambda\) has density

\[
f(x) = \lambda e^{-\lambda x}
\]

for \(x \geq 0\).

Value

`dexp` gives the density, `pexp` gives the distribution function, `qexp` gives the quantile function, and `rexp` generates random deviates.

The length of the result is determined by `n` for `rexp`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The cumulative hazard \(H(t) = -\log(1 - F(t))\) is \(-\text{pexp}(t, r, \text{lower} = \text{FALSE}, \text{log} = \text{TRUE})\).
Source

dexp, pexp and qexp are all calculated from numerically stable versions of the definitions.
rexp uses

References


See Also

exp for the exponential function.

Distributions for other standard distributions, including dgamma for the gamma distribution and dweibull for the Weibull distribution, both of which generalize the exponential.

Examples

dexp(1) - exp(-1) #-> 0

```r
## a fast way to generate *sorted* U[0,1] random numbers:
rsunif <- function(n) { n1 <- n+1
cE <- cumsum(rexp(n1)); cE[seq_len(n)]/cE[n1] }
plot(rsunif(1000), ylim=0:1, pch=".")
abline(0,1/(1000+1), col=adjustcolor(1, 0.5))
```

---

**extractAIC**

*Extract AIC from a Fitted Model*

Description

Computes the (generalized) Akaike *An Information Criterion* for a fitted parametric model.

Usage

```r
extractAIC(fit, scale, k = 2, ...)
```

Arguments

- **fit**
  - fitted model, usually the result of a fitter like `lm`.
- **scale**
  - optional numeric specifying the scale parameter of the model, see `scale` in `step`. Currently only used in the "lm" method, where `scale` specifies the estimate of the error variance, and `scale = 0` indicates that it is to be estimated by maximum likelihood.
- **k**
  - numeric specifying the ‘weight’ of the equivalent degrees of freedom (≡ edf) part in the AIC formula.
- **...**
  - further arguments (currently unused in base R).
extractAIC

Details

This is a generic function, with methods in base \( \mathbb{R} \) for classes "aov", "glm" and "lm" as well as for "negbin" (package MASS) and "coxph" and "survreg" (package survival).

The criterion used is

\[
AIC = -2 \log L + k \times edf,
\]

where \( L \) is the likelihood and edf the equivalent degrees of freedom (i.e., the number of free parameters for usual parametric models) of \( \text{fit} \).

For linear models with unknown scale (i.e., for \( \text{lm} \) and \( \text{aov} \)), \(-2 \log L \) is computed from the deviance and uses a different additive constant to \( \logLk \) and hence \( \text{AIC} \). If \( \text{RSS} \) denotes the (weighted) residual sum of squares then \( \text{extractAIC} \) uses for \(-2 \log L \) the formulae \( \text{RSS}/s - n \) (corresponding to Mallows’ \( C_p \)) in the case of known scale \( s \) and \( n \log(\text{RSS}/n) \) for unknown scale. \( \text{AIC} \) only handles unknown scale and uses the formula \( n \log(\text{RSS}/n) + n + n \log 2\pi - \sum \log w \) where \( w \) are the weights. Further \( \text{AIC} \) counts the scale estimation as a parameter in the edf and \( \text{extractAIC} \) does not.

For \( \text{glm} \) fits the family’s \text{aic()} function is used to compute the AIC: see the note under \text{logLk} about the assumptions this makes.

\( k = 2 \) corresponds to the traditional AIC, using \( k = \log(n) \) provides the BIC (Bayesian IC) instead.

Note that the methods for this function may differ in their assumptions from those of methods for \( \text{AIC} \) (usually via a method for \text{logLk}). We have already mentioned the case of "lm" models with estimated scale, and there are similar issues in the "glm" and "negbin" methods where the dispersion parameter may or may not be taken as 'free'. This is immaterial as \( \text{extractAIC} \) is only used to compare models of the same class (where only differences in AIC values are considered).

Value

A numeric vector of length 2, with first and second elements giving

\begin{align*}
edf & \quad \text{the ‘equivalent degrees of freedom’ for the fitted model \text{fit}.} \\
\text{AIC} & \quad \text{the (generalized) Akaike Information Criterion for \text{fit}.}
\end{align*}

Note

This function is used in \text{add1}, \text{drop1} and \text{step} and the similar functions in package MASS from which it was adopted.

Author(s)

B. D. Ripley

References


See Also

\text{AIC, deviance, add1, step}

Examples

\begin{verbatim}
utils::example(glm)
extractAIC(glm.D93) #>> 5 15.129
\end{verbatim}
Factor Analysis

Description

Perform maximum-likelihood factor analysis on a covariance matrix or data matrix.

Usage

```r
factanal(x, factors, data = NULL, covmat = NULL, n.obs = NA,
        subset, na.action, start = NULL,
        scores = c("none", "regression", "Bartlett"),
        rotation = "varimax", control = NULL, ...)
```

Arguments

- `x`: A formula or a numeric matrix or an object that can be coerced to a numeric matrix.
- `factors`: The number of factors to be fitted.
- `data`: An optional data frame (or similar: see `model.frame`), used only if `x` is a formula. By default the variables are taken from `environment(formula)`.
- `covmat`: A covariance matrix, or a covariance list as returned by `cov.wt`. Of course, correlation matrices are covariance matrices.
- `n.obs`: The number of observations, used if `covmat` is a covariance matrix.
- `subset`: A specification of the cases to be used, if `x` is used as a matrix or formula.
- `na.action`: The `na.action` to be used if `x` is used as a matrix or formula.
- `start`: NULL or a matrix of starting values, each column giving an initial set of uniquenesses.
- `scores`: Type of scores to produce, if any. The default is none, "regression" gives Thompson’s scores, "Bartlett" given Bartlett’s weighted least-squares scores. Partial matching allows these names to be abbreviated.
- `rotation`: character. "none" or the name of a function to be used to rotate the factors: it will be called with first argument the loadings matrix, and should return a list with component `loadings` giving the rotated loadings, or just the rotated loadings.
- `control`: A list of control values.
- `nstart`: The number of starting values to be tried if `start = NULL`. Default 1.
- `trace`: logical. Output tracing information? Default FALSE.
- `lower`: The lower bound for uniquenesses during optimization. Should be > 0. Default 0.005.
- `opt`: A list of control values to be passed to `optim`’s control argument.
- `rotate`: a list of additional arguments for the rotation function.
- `...`: Components of `control` can also be supplied as named arguments to `factanal`.
The factor analysis model is
\[ x = \Lambda f + e \]
for a \( p \)-element vector \( x \), a \( p \times k \) matrix \( \Lambda \) of loadings, a \( k \)-element vector \( f \) of scores and a \( p \)-element vector \( e \) of errors. None of the components other than \( x \) is observed, but the major restriction is that the scores be uncorrelated and of unit variance, and that the errors be independent with variances \( \Psi \), the uniquenesses. It is also common to scale the observed variables to unit variance, and done in this function.

Thus factor analysis is in essence a model for the correlation matrix of \( x \),
\[ \Sigma = \Lambda \Lambda' + \Psi \]

There is still some indeterminacy in the model for it is unchanged if \( \Lambda \) is replaced by \( G \Lambda \) for any orthogonal matrix \( G \). Such matrices \( G \) are known as rotations (although the term is applied also to non-orthogonal invertible matrices).

If covmat is supplied it is used. Otherwise \( x \) is used if it is a matrix, or a formula \( x \) is used with data to construct a model matrix, and that is used to construct a covariance matrix. (It makes no sense for the formula to have a response, and all the variables must be numeric.) Once a covariance matrix is found or calculated from \( x \), it is converted to a correlation matrix for analysis. The correlation matrix is returned as component correlation of the result.

The fit is done by optimizing the log likelihood assuming multivariate normality over the uniquenesses. (The maximizing loadings for given uniquenesses can be found analytically: Lawley & Maxwell (1971, p. 27).) All the starting values supplied in start are tried in turn and the best fit obtained is used. If start = NULL then the first fit is started at the value suggested by Jöreskog (1963) and given by Lawley & Maxwell (1971, p. 31), and then \( \text{control}\$\text{start} - 1 \) other values are tried, randomly selected as equal values of the uniquenesses.

The uniquenesses are technically constrained to lie in \([0, 1]\), but near-zero values are problematical, and the optimization is done with a lower bound of \( \text{control}\$\text{lower} \), default 0.005 (Lawley & Maxwell, 1971, p. 32).

Scores can only be produced if a data matrix is supplied and used. The first method is the regression method of Thomson (1951), the second the weighted least squares method of Bartlett (1937, 8). Both are estimates of the unobserved scores \( f \). Thomson’s method regresses (in the population) the unknown \( f \) on \( x \) to yield
\[ \hat{f} = \Lambda \Sigma^{-1} x \]
and then substitutes the sample estimates of the quantities on the right-hand side. Bartlett’s method minimizes the sum of squares of standardized errors over the choice of \( f \), given (the fitted) \( \Lambda \).

If \( x \) is a formula then the standard NA-handling is applied to the scores (if requested): see napredict.

The print method (documented under loadings) follows the factor analysis convention of drawing attention to the patterns of the results, so the default precision is three decimal places, and small loadings are suppressed.

Value

An object of class "factanal" with components

loadings A matrix of loadings, one column for each factor. The factors are ordered in decreasing order of sums of squares of loadings, and given the sign that will make the sum of the loadings positive. This is of class "loadings": see loadings for its print method.

uniquenesses The uniquenesses computed.
correlation  The correlation matrix used.
criteria  The results of the optimization: the value of the criterion (a linear function of
          the negative log-likelihood) and information on the iterations used.
factors  The argument factors.
dof  The number of degrees of freedom of the factor analysis model.
method  The method: always "mle".
rotnam  The rotation matrix if relevant.
scores  If requested, a matrix of scores. napredict is applied to handle the treatment
          of values omitted by the na.action.
n.obs  The number of observations if available, or NA.
call  The matched call.
n.a.action  If relevant.
STATISTIC, PVAL  The significance-test statistic and P value, if it can be computed.

Note
There are so many variations on factor analysis that it is hard to compare output from different
programs. Further, the optimization in maximum likelihood factor analysis is hard, and many other
examples we compared had less good fits than produced by this function. In particular, solutions
which are ‘Heywood cases’ (with one or more uniquenesses essentially zero) are much more common
than most texts and some other programs would lead one to believe.

References
Bartlett, M. S. (1937). The statistical conception of mental factors. British Journal of Psychology,
141246a0.
Butterworths.

See Also
loadings (which explains some details of the print method), varimax, princomp, ability.cov,
Harman23.cor, Harman74.cor.

Other rotation methods are available in various contributed packages, including GPArotation
and psych.

Examples
# A little demonstration, v2 is just v1 with noise,
# and same for v4 vs. v3 and v6 vs. v5
# Last four cases are there to add noise
# and introduce a positive manifold (g factor)
v1 <- c(1,1,1,1,1,1,1,1,1,1,3,3,3,3,3,4,5,6)
v2 <- c(1,2,1,1,1,2,1,2,1,3,4,3,3,3,4,6,5)
v3 <- c(3,3,3,3,3,1,1,1,1,1,1,1,1,1,1,5,4,6)
v4 <- c(3,3,4,3,1,1,2,1,1,1,2,1,5,6,4)
v5 <- c(1,1,1,1,3,3,3,3,1,1,1,1,6,4,5)
v6 <- c(1,1,1,2,1,3,3,4,3,1,1,2,1,6,5,4)
m1 <- cbind(v1,v2,v3,v4,v5,v6)
cor(m1)
factanal(m1, factors = 3) # varimax is the default
factanal(m1, factors = 3, rotation = "promax")
# The following shows the g factor as PC1
prcomp(m1) # signs may depend on platform

## formula interface
factanal(~v1+v2+v3+v4+v5+v6, factors = 3, 
          scores = "Bartlett")$scores

## a realistic example from Bartholomew (1987, pp. 61-65)
utils::example(ability.cov)

---

## factor.scope

*Compute Allowed Changes in Adding to or Dropping from a Formula*

**Description**

Add. scope and drop. scope compute those terms that can be individually added to or dropped from a model while respecting the hierarchy of terms.

**Usage**

```r
add.scope(terms1, terms2)
drop.scope(terms1, terms2)
factor.scope(factor, scope)
```

**Arguments**

- `terms1`: the terms or formula for the base model.
- `terms2`: the terms or formula for the upper (add. scope) or lower (drop. scope) scope. If missing for drop. scope it is taken to be the null formula, so all terms (except any intercept) are candidates to be dropped.
- `factor`: the "factor" attribute of the terms of the base object.
- `scope`: a list with one or both components drop and add giving the "factor" attribute of the lower and upper scopes respectively.

**Details**

Factor. scope is not intended to be called directly by users.

**Value**

For add. scope and drop. scope a character vector of terms labels. For factor. scope, a list with components drop and add, character vectors of terms labels.
Family objects provide a convenient way to specify the details of the models used by functions such as `glm`. See the documentation for `glm` for the details on how such model fitting takes place.

**Usage**

```r
class(family) = c("link-glm", "link-family")
class(link) = "link-glm"
```

**Arguments**

- `link` a specification for the model link function. This can be a name/expression, a literal character string, a length-one character vector, or an object of class "link-glm" (such as generated by `make.link`) provided it is not specified via one of the standard names given next.

  The `binomial` family accepts the links (as names) `identity`, `log` and `inverse`; the `binomial` family the links `logit`, `probit`, `cauchit`, (corresponding to logistic, normal and Cauchy CDFs respectively) `log` and `cloglog` (complementary log-log); the `Gamma` family the links `inverse`, `identity` and `log`; the `poisson` family the links `log`, `identity`, and `sqrt`; and the inverse `gaussian` family the links `1/mu^2`, `inverse`, `identity` and `log`.

  The quasi family accepts the links `logit`, `probit`, `cloglog`, `identity`, `inverse`, `log`, `1/mu^2` and `sqrt`, and the function `power` can be used to create a power link function.

- `variance` for all families other than quasi, the variance function is determined by the family. The quasi family will accept the literal character string (or unquoted as a name/expression) specifications "constant", "mu(1-mu)"., "mu", "mu^2" and "mu^3", a length-one character vector taking one of those values, or a list containing components `varfun`, `validmu`, `dev.resids`, `initialize` and `name`. 
family

the function family accesses the family objects which are stored within objects created by modelling functions (e.g., glm).

... further arguments passed to methods.

Details

family is a generic function with methods for classes "glm" and "lm" (the latter returning gaussian()).

For the binomial and quasibinomial families the response can be specified in one of three ways:

1. As a factor: 'success' is interpreted as the factor not having the first level (and hence usually of having the second level).
2. As a numerical vector with values between 0 and 1, interpreted as the proportion of successful cases (with the total number of cases given by the weights).
3. As a two-column integer matrix: the first column gives the number of successes and the second the number of failures.

The quasibinomial and quasipoisson families differ from the binomial and poisson families only in that the dispersion parameter is not fixed at one, so they can model over-dispersion. For the binomial case see McCullagh and Nelder (1989, pp. 124–8). Although they show that there is (under some restrictions) a model with variance proportional to mean as in the quasi-binomial model, note that glm does not compute maximum-likelihood estimates in that model. The behaviour of S is closer to the quasi-variants.

Value

An object of class "family" (which has a concise print method). This is a list with elements

- family character: the family name.
- link character: the link name.
- linkfun function: the link.
- linkinv function: the inverse of the link function.
- variance function: the variance as a function of the mean.
- dev.resids function giving the deviance for each observation as a function of (y, mu, wt), used by the residuals method when computing deviance residuals.
- aic function giving the AIC value if appropriate (but NA for the quasi- families). More precisely, this function returns \(-2\ell + 2s\), where \(\ell\) is the log-likelihood and \(s\) is the number of estimated scale parameters. Note that the penalty term for the location parameters (typically the "regression coefficients") is added elsewhere, e.g., in glm.fit(), or AIC(), see the AIC example in glm. See logLik for the assumptions made about the dispersion parameter.
- mu.eta function: derivative of the inverse-link function with respect to the linear predictor. If the inverse-link function is \(\mu = g^{-1}(\eta)\) where \(\eta\) is the value of the linear predictor, then this function returns \(d(g^{-1})/d\eta = d\mu/d\eta\).
- initialize expression. This needs to set up whatever data objects are needed for the family as well as \(n\) (needed for AIC in the binomial family) and mustart (see glm).
- validmu logical function. Returns TRUE if a mean vector mu is within the domain of variance.
- valideta logical function. Returns TRUE if a linear predictor eta is within the domain of linkinv.
simulate (optional) function simulate(object, nsim) to be called by the "lm" method of simulate. It will normally return a matrix with nsim columns and one row for each fitted value, but it can also return a list of length nsim. Clearly this will be missing for 'quasi-' families.

dispersion (optional since R version 4.3.0) numeric: value of the dispersion parameter, if fixed, or NA_real_ if free.

Note

The link and variance arguments have rather awkward semantics for back-compatibility. The recommended way is to supply them as quoted character strings, but they can also be supplied unquoted (as names or expressions). Additionally, they can be supplied as a length-one character vector giving the name of one of the options, or as a list (for link, of class "link-glm"). The restrictions apply only to links given as names: when given as a character string all the links known to make.link are accepted.

This is potentially ambiguous: supplying link = logit could mean the unquoted name of a link or the value of object logit. It is interpreted if possible as the name of an allowed link, then as an object. (You can force the interpretation to always be the value of an object via logit[1].)

Author(s)

The design was inspired by S functions of the same names described in Hastie & Pregibon (1992) (except quasibinomial and quasipoisson).

References


See Also

glm, power, make.link.

For binomial coefficients, choose; the binomial and negative binomial distributions, Binomial, and NegBinomial.

Examples

require(utils) # for str
nf <- gaussian() # Normal family
nf
str(nf)

gf <- Gamma()
gf
str(gf)
gf$linkinv
gf$variance(-3:4) #== (. )^2
## Binomial with default 'logit' link: Check some properties visually:
bi <- binomial()
et <- seq(-10, 10, by=1/8)
plot(et, bi$mu.eta(et), type="l")
## show that mu.eta() is derivative of linkinv() :
lines((et[-1]+et[-length(et)])/2, col=adjustcolor("red", 1/4),
diff(bi$linkinv(et))/diff(et), type="l", lwd=4)
## which here is the logistic density:
lines(et, dlogis(et), lwd=3, col=adjustcolor("blue", 1/4))
stopifnot(exprs = {
  all.equal(bi$ mu.eta(et), dlogis(et))
  all.equal(bi$linkinv(et), plogis(et) -> m)
  all.equal(bi$linkfun(m ), qlogis(m)) # logit(.) == qlogis(.) !
})

## Data from example(glm) :
d.AD <- data.frame(treatment = gl(3,3),
                   outcome = gl(3,1,9),
                   counts = c(18,17,15, 20,10,20, 25,13,12))
glm.D93 <- glm(counts ~ outcome + treatment, d.AD, family = poisson())
## Quasipoisson: compare with above / example(glm) :
glm.qD93 <- glm(counts ~ outcome + treatment, d.AD, family = quasipoisson())
glm.qD93
anova (glm.qD93, test = "F")
summary(glm.qD93)
## for Poisson results (same as from 'glm.D93' !) use
anova (glm.qD93, dispersion = 1, test = "Chisq")
summary(glm.qD93, dispersion = 1)

## Example of user-specified link, a logit model for p^days
logexp <- function(days = 1)
{
  linkfun <- function(mu) qlogis(mu^(1/days))
  linkinv <- function(eta) plogis(eta)^days
  mu.eta <- function(eta) days * plogis(eta)^(days-1) *
            binomial()$mu.eta(eta)
  valideta <- function(eta) TRUE
  link <- paste0("logexp(", days, ")")
  structure(list(linkfun = linkfun, linkinv = linkinv,
                mu.eta = mu.eta, valideta = valideta, name = link),
            class = "link-glm")
}
(bil3 <- binomial(logexp(3)))

## in practice this would be used with a vector of 'days', in
## which case use an offset of 0 in the corresponding formula
## to get the null deviance right.

## Binomial with identity link: often not a good idea, as both
## computationally and conceptually difficult:
binomial(link = "identity") ## is exactly the same as
binomial(link = make.link("identity"))
## tests of quasi

```r
x <- rnorm(100)
y <- rpois(100, exp(1+x))
glm(y ~ x, family = quasi(variance = "mu", link = "log"))
# which is the same as
glm(y ~ x, family = poisson)
glm(y ~ x, family = quasi(variance = "mu^2", link = "log"))
## Not run: glm(y ~ x, family = quasi(variance = "mu^3", link = "log")) # fails
y <- rbinom(100, 1, plogis(x))
# need to set a starting value for the next fit
glm(y ~ x, family = quasi(variance = "mu(1-mu)", link = "logit"), start = c(0,1))
```

---

### FDist

**The F Distribution**

Density, distribution function, quantile function and random generation for the F distribution with `df1` and `df2` degrees of freedom (and optional non-centrality parameter `ncp`).

**Usage**

```r
df(x, df1, df2, ncp, log = FALSE)
pf(q, df1, df2, ncp, lower.tail = TRUE, log.p = FALSE)
qf(p, df1, df2, ncp, lower.tail = TRUE, log.p = FALSE)
rf(n, df1, df2, ncp)
```

**Arguments**

- `x, q` vector of quantiles.
- `p` vector of probabilities.
- `n` number of observations. If `length(n) > 1`, the length is taken to be the number required.
- `df1, df2` degrees of freedom. Inf is allowed.
- `ncp` non-centrality parameter. If omitted the central F is assumed.
- `log, log.p` logical; if TRUE, probabilities `p` are given as log(p).
- `lower.tail` logical; if TRUE (default), probabilities are \( P(X \leq x) \), otherwise, \( P(X > x) \).

**Details**

The F distribution with \( \nu_1 \) and \( \nu_2 \) degrees of freedom has density

\[
f(x) = \frac{\Gamma(\nu_1/2 + \nu_2/2)}{\Gamma(\nu_1/2)\Gamma(\nu_2/2)} \left( \frac{\nu_1}{\nu_2} \right)^{\nu_1/2} x^{\nu_1/2-1} \left( 1 + \frac{\nu_1 x}{\nu_2} \right)^{-(\nu_1+\nu_2)/2}
\]

for \( x > 0 \).

The F distribution’s cumulative distribution function (cdf), \( F_{\nu_1,\nu_2} \) fulfills (Abramowitz & Stegun 26.6.2, p.946) \( F_{\nu_1,\nu_2}(qF) = 1 - I_x(\nu_2/2, \nu_1/2) = I_{1-x}(\nu_1/2, \nu_2/2) \), where \( x := \frac{\nu_2}{\nu_2 + \nu_1 qF} \), and \( I_x(a,b) \) is the incomplete beta function; in R, \( \text{pbeta}(x, a, b) \).
It is the distribution of the ratio of the mean squares of \( \nu_1 \) and \( \nu_2 \) independent standard normals, and hence of the ratio of two independent chi-squared variates each divided by its degrees of freedom. Since the ratio of a normal and the root mean-square of \( m \) independent normals has a Student’s \( t_m \) distribution, the square of a \( t_m \) variate has a F distribution on 1 and \( m \) degrees of freedom.

The non-central F distribution is again the ratio of mean squares of independent normals of unit variance, but those in the numerator are allowed to have non-zero means and \( \text{ncp} \) is the sum of squares of the means. See Chisquare for further details on non-central distributions.

**Value**

df gives the density, pf gives the distribution function qf gives the quantile function, and rf generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

The length of the result is determined by n for rf, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

**Note**

Supplying \( \text{ncp} = 0 \) uses the algorithm for the non-central distribution, which is not the same algorithm used if \( \text{ncp} \) is omitted. This is to give consistent behaviour in extreme cases with values of \( \text{ncp} \) very near zero.

The code for non-zero \( \text{ncp} \) is principally intended to be used for moderate values of \( \text{ncp} \): it will not be highly accurate, especially in the tails, for large values.

**Source**

For the central case of df, computed via a binomial probability, code contributed by Catherine Loader (see dbinom); for the non-central case computed via dbeta, code contributed by Peter Ruckdeschel.

For pf, via pbeta (or for large \( df_2 \), via pchisq).

For qf, via qchisq for large \( df_2 \), else via qbeta.

**References**


**See Also**

Distributions for other standard distributions, including dchisq for chi-squared and dt for Student’s t distributions.
Examples

## Equivalence of pt(.,nu) with pf(.^2, 1,nu):

x <- seq(0.001, 5, length.out = 100)
nu <- 4
stopifnot(all.equal(2*pt(x,nu) - 1, pf(x^2, 1,nu)),
  ## upper tails:
  all.equal(2*pt(x, nu, lower.tail=FALSE),
            pf(x^2, 1,nu, lower.tail=FALSE)))

## the density of the square of a t_m is 2*dt(x, m)/(2*x)
all.equal(df(x^2, 1, 5), dt(x, 5)/x)

## Identity (F <-> t): qf(2*p - 1, 1, df) == qt(p, df)^2 for p >= 1/2
p <- seq(1/2, .99, length.out = 50); df <- 10
rel.err <- function(x, y) ifelse(x == y, 0, abs(x-y)/mean(abs(c(x,y))))
stopifnot(all.equal(qf(2*p - 1, 1, df),
                  qt(p, df)^2))

## Identity (F <-> Beta <-> incompl.beta):
n1 <- 7 ; n2 <- 12; qF <- c((0:4)/4, 1.5, 2:16)
x <- n2/(n2 + n1*qF)
stopifnot(all.equal(pf(qF, n1, n2, lower.tail=FALSE),
                   pbeta(x, n2/2, n1/2)))

fft

Fast Discrete Fourier Transform (FFT)

Description

Computes the Discrete Fourier Transform (DFT) of an array with a fast algorithm, the “Fast Fourier Transform” (FFT).

Usage

fft(z, inverse = FALSE)
mvfft(z, inverse = FALSE)

Arguments

z

a real or complex array containing the values to be transformed. Long vectors are not supported.

inverse

if TRUE, the unnormalized inverse transform is computed (the inverse has a + i in the exponent of e, but here, we do not divide by 1/length(x)).

Value

When z is a vector, the value computed and returned by fft is the unnormalized univariate discrete Fourier transform of the sequence of values in z. Specifically, y <- fft(z) returns

\[ y[h] = \sum_{k=1}^{n} z[k] \exp(-2\pi i (k - 1)(h - 1)/n) \]
for \( h = 1, \ldots, n \) where \( n = \text{length}(y) \). If \text{inverse} is \text{TRUE}, \exp(-2\pi \ldots) \) is replaced with \exp(2\pi \ldots).

When \( z \) contains an array, \texttt{fft} computes and returns the multivariate (spatial) transform. If \text{inverse} is \text{TRUE}, the (unnormalized) inverse Fourier transform is returned, i.e., if \( y \leftarrow \text{fft}(z) \), then \( z \) is \texttt{fft}(y, \text{inverse = TRUE}) / \text{length}(y) \).

By contrast, \texttt{mvfft} takes a real or complex matrix as argument, and returns a similar shaped matrix, but with each column replaced by its discrete Fourier transform. This is useful for analyzing vector-valued series.

The FFT is fastest when the length of the series being transformed is highly composite (i.e., has many factors). If this is not the case, the transform may take a long time to compute and will use a large amount of memory.

Source


References


See Also

\texttt{convolve, nextn}.

Examples

```r
x <- 1:4
fft(x)
fft(fft(x), inverse = TRUE)/length(x)
## Slow Discrete Fourier Transform (DFT) - e.g., for checking the formula
fft0 <- function(z, inverse=FALSE) {
  n <- length(z)
  if(n == 0) return(z)
  k <- 0:(n-1)
  ff <- (if(inverse) 1 else -1) * 2*pi * 1i * k/n
  vapply(1:n, function(h) sum(z * exp(ff*(h-1))), complex(1))
}
relD <- function(x,y) 2* abs(x - y) / abs(x + y)
n <- 2^8
z <- complex(n, rnorm(n), rnorm(n))
## relative differences in the order of 4*10^(-14) :
summary(relD(fft(z), fft0(z)))
summary(relD(fft(z, inverse=TRUE), fft0(z, inverse=TRUE)))
```
filter

Linear Filtering on a Time Series

Description

Applies linear filtering to a univariate time series or to each series separately of a multivariate time series.

Usage

filter(x, filter, method = c("convolution", "recursive"),
       sides = 2, circular = FALSE, init)

Arguments

x
a univariate or multivariate time series.

filter
a vector of filter coefficients in reverse time order (as for AR or MA coefficients).

method
Either "convolution" or "recursive" (and can be abbreviated). If "convolution" a moving average is used: if "recursive" an autoregression is used.

sides
for convolution filters only. If sides = 1 the filter coefficients are for past values only; if sides = 2 they are centred around lag 0. In this case the length of the filter should be odd, but if it is even, more of the filter is forward in time than backward.

circular
for convolution filters only. If TRUE, wrap the filter around the ends of the series, otherwise assume external values are missing (NA).

init
for recursive filters only. Specifies the initial values of the time series just prior to the start value, in reverse time order. The default is a set of zeros.

Details

Missing values are allowed in x but not in filter (where they would lead to missing values everywhere in the output).

Note that there is an implied coefficient 1 at lag 0 in the recursive filter, which gives

\[ y_t = x_t + f_1 y_{t-1} + \cdots + f_p y_{t-p} \]

No check is made to see if recursive filter is invertible: the output may diverge if it is not.

The convolution filter is

\[ y_t = f_1 x_{t+o} + \cdots + f_p x_{t+o-(p-1)} \]

where \( o \) is the offset: see sides for how it is determined.

Value

A time series object.
Note

`convolve`, type = "filter") uses the FFT for computations and so may be faster for long filters on univariate series, but it does not return a time series (and so the time alignment is unclear), nor does it handle missing values. `filter` is faster for a filter of length 100 on a series of length 1000, for example.

See Also

`convolve`, `arima.sim`

Examples

```r
x <- 1:100
filter(x, rep(1, 3))
filter(x, rep(1, 3), sides = 1)
filter(x, rep(1, 3), sides = 1, circular = TRUE)

filter(presidents, rep(1, 3))
```

---

`fisher.test`  
*Fisher’s Exact Test for Count Data*

Description

Performs Fisher’s exact test for testing the null of independence of rows and columns in a contingency table with fixed marginals.

Usage

```r
fisher.test(x, y = NULL, workspace = 200000, hybrid = FALSE,  
hybridPars = c(expect = 5, percent = 80, Emin = 1),  
control = list(), or = 1, alternative = "two.sided",  
conf.int = TRUE, conf.level = 0.95,  
simulate.p.value = FALSE, B = 2000)
```

Arguments

- `x`  
either a two-dimensional contingency table in matrix form, or a factor object.
- `y`  
a factor object; ignored if `x` is a matrix.
- `workspace`  
an integer specifying the size of the workspace used in the network algorithm. In units of 4 bytes. Only used for non-simulated p-values larger than $2 \times 2$ tables. Since R version 3.5.0, this also increases the internal stack size which allows larger problems to be solved, however sometimes needing hours. In such cases, `simulate.p.value=TRUE` may be more reasonable.
- `hybrid`  
a logical. Only used for larger than $2 \times 2$ tables, in which cases it indicates whether the exact probabilities (default) or a hybrid approximation thereof should be computed.
- `hybridPars`  
a numeric vector of length 3, by default describing “Cochran’s conditions” for the validity of the chi-square approximation, see ‘Details’.
control

a list with named components for low level algorithm control. At present the only one used is "mult", a positive integer \( \geq 2 \) with default 30 used only for larger than \( 2 \times 2 \) tables. This says how many times as much space should be allocated to paths as to keys: see file ‘fexact.c’ in the sources of this package.

or

the hypothesized odds ratio. Only used in the \( 2 \times 2 \) case.

alternative

indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. Only used in the \( 2 \times 2 \) case.

conf.int

logical indicating if a confidence interval for the odds ratio in a \( 2 \times 2 \) table should be computed (and returned).

conf.level

confidence level for the returned confidence interval. Only used in the \( 2 \times 2 \) case and if conf.int = TRUE.

simulate.p.value

a logical indicating whether to compute p-values by Monte Carlo simulation, in larger than \( 2 \times 2 \) tables.

B

an integer specifying the number of replicates used in the Monte Carlo test.

Details

If \( x \) is a matrix, it is taken as a two-dimensional contingency table, and hence its entries should be nonnegative integers. Otherwise, both \( x \) and \( y \) must be vectors or factors of the same length. Incomplete cases are removed, vectors are coerced into factor objects, and the contingency table is computed from these.

For \( 2 \times 2 \) cases, p-values are obtained directly using the (central or non-central) hypergeometric distribution. Otherwise, computations are based on a C version of the FORTRAN subroutine FEXACT which implements the network developed by Mehta and Patel (1983, 1986) and improved by Clarkson, Fan and Joe (1993). The FORTRAN code can be obtained from https://netlib.org/toms/643. Note this fails (with an error message) when the entries of the table are too large. (It transposes the table if necessary so it has no more rows than columns. One constraint is that the product of the row marginals be less than \( 2^{31} - 1 \).

For \( 2 \times 2 \) tables, the null of conditional independence is equivalent to the hypothesis that the odds ratio equals one. ‘Exact’ inference can be based on observing that in general, given all marginal totals fixed, the first element of the contingency table has a non-central hypergeometric distribution with non-centrality parameter given by the odds ratio (Fisher, 1935). The alternative for a one-sided test is based on the odds ratio, so alternative = "greater" is a test of the odds ratio being bigger than or.

Two-sided tests are based on the probabilities of the tables, and take as ‘more extreme’ all tables with probabilities less than or equal to that of the observed table, the p-value being the sum of such probabilities.

For larger than \( 2 \times 2 \) tables and hybrid = TRUE, asymptotic chi-squared probabilities are only used if the ‘Cochran conditions’ (or modified version thereof) specified by hybridPars = c(expect = 5, percent = 80, Emin = 1) are satisfied, that is if no cell has expected counts less than 1 (= Emin) and more than 80% (= percent) of the cells have expected counts at least 5 (= expect), otherwise the exact calculation is used. A corresponding if() decision is made for all sub-tables considered.

Accidentally, \( R \) has used 180 instead of 80 as percent, i.e., hybridPars[2] in \( R \) versions between 3.0.0 and 3.4.1 (inclusive), i.e., the 2nd of the hybridPars (all of which used to be hard-coded previous to \( R \) 3.5.0). Consequently, in these versions of \( R \), hybrid=TRUE never made a difference.

In the \( r \times c \) case with \( r > 2 \) or \( c > 2 \), internal tables can get too large for the exact test in which case an error is signalled. Apart from increasing workspace sufficiently, which then may lead to
very long running times, using simulate.p.value = TRUE may then often be sufficient and hence advisable.

Simulation is done conditional on the row and column marginals, and works only if the marginals are strictly positive. (A C translation of the algorithm of Patefield (1981) is used.) Note that the default number of replicates (B = 2000) implies a minimum p-value of about 0.0005 (1/(B + 1)).

Value

A list with class "htest" containing the following components:

- **p.value**  
  the p-value of the test.

- **conf.int**  
  a confidence interval for the odds ratio. Only present in the 2 × 2 case and if argument conf.int = TRUE.

- **estimate**  
  an estimate of the odds ratio. Note that the conditional Maximum Likelihood Estimate (MLE) rather than the unconditional MLE (the sample odds ratio) is used. Only present in the 2 × 2 case.

- **null.value**  
  the odds ratio under the null, or. Only present in the 2 × 2 case.

- **alternative**  
  a character string describing the alternative hypothesis.

- **method**  
  the character string "Fisher's Exact Test for Count Data".

- **data.name**  
  a character string giving the name(s) of the data.

References


See Also

- chisq.test
- fisher.exact in package exact2x2 for alternative interpretations of two-sided tests and confidence intervals for 2 × 2 tables.
Examples

## Agresti (1990, p. 61f; 2002, p. 91) Fisher’s Tea Drinker
## A British woman claimed to be able to distinguish whether milk or
## tea was added to the cup first. To test, she was given 8 cups of
## tea, in four of which milk was added first. The null hypothesis
## is that there is no association between the true order of pouring
## and the woman’s guess, the alternative that there is a positive
## association (that the odds ratio is greater than 1).
TeaTasting <-
matrix(c(3, 1, 1, 3),
      nrow = 2,
      dimnames = list(Guess = c("Milk", "Tea"),
                       Truth = c("Milk", "Tea")))
fisher.test(TeaTasting, alternative = "greater")
## => p = 0.2429, association could not be established

## Fisher (1962, 1970), Criminal convictions of like-sex twins
Convictions <- matrix(c(2, 10, 15, 3), nrow = 2,
                       dimnames =
                       list(c("Dizygotic", "Monozygotic"),
                            c("Convicted", "Not convicted")))
fisher.test(Convictions, alternative = "less")
fisher.test(Convictions, conf.int = FALSE)
fisher.test(Convictions, conf.level = 0.95)$conf.int
fisher.test(Convictions, conf.level = 0.99)$conf.int

## A r x c table Agresti (2002, p. 57) Job Satisfaction
Job <- matrix(c(1, 2, 1, 0, 3, 3, 6, 1, 10, 10, 14, 9, 6, 7, 12, 11), 4, 4,
               dimnames =
               list(income = c("< 15k", "15-25k", "25-40k", "+ 40k"),
                    satisfaction = c("VeryD", "LittleD", "ModerateS", "VeryS")))
fisher.test(Job) # 0.7827
fisher.test(Job, simulate.p.value = TRUE, B = 1e5) # also close to 0.78

## 6th example in Mehta & Patel’s JASA paper
MP6 <- rbind(
            c(1, 2, 2, 1, 0, 1),
            c(2, 0, 2, 3, 0, 0),
            c(0, 1, 1, 2, 7, 3),
            c(1, 2, 0, 0, 0, 1),
            c(0, 1, 1, 1, 0, 0))
fisher.test(MP6)
# Exactly the same p-value, as Cochran’s conditions are never met:
fisher.test(MP6, hybrid=TRUE)

---

fitted Extract Model Fitted Values

Description

fitted is a generic function which extracts fitted values from objects returned by modeling functions. fitted.values is an alias for it.

All object classes which are returned by model fitting functions should provide a fitted method. (Note that the generic is fitted and not fitted.values.)
Methods can make use of `napredict` methods to compensate for the omission of missing values. The default and `nls` methods do.

Usage

```r
fitted(object, ...) fitted.values(object, ...)
```

Arguments

- `object` an object for which the extraction of model fitted values is meaningful.
- `...` other arguments.

Value

Fitted values extracted from the object `object`.

References


See Also

`coefficients`, `glm`, `lm`, `residuals`.

---

### fivenum

**Tukey Five-Number Summaries**

Returns Tukey’s five number summary (minimum, lower-hinge, median, upper-hinge, maximum) for the input data.

Usage

```r
fivenum(x, na.rm = TRUE)
```

Arguments

- `x` numeric, maybe including NAs and ±Inf.s.
- `na.rm` logical; if TRUE, all NA and NaNs are dropped, before the statistics are computed.

Value

A numeric vector of length 5 containing the summary information. See `boxplot.stats` for more details.

See Also

`IQR`, `boxplot.stats`, `median`, `quantile`, `range`.

Examples

```r
fivenum(c(rnorm(100), -1:1/0))
```
Fligner-Killeen Test of Homogeneity of Variances

Description

Performs a Fligner-Killeen (median) test of the null that the variances in each of the groups (samples) are the same.

Usage

`fligner.test(x, ...)`

## Default S3 method:
`fligner.test(x, g, ...)`

## S3 method for class 'formula'
`fligner.test(formula, data, subset, na.action, ...)`

Arguments

- `x` a numeric vector of data values, or a list of numeric data vectors.
- `g` a vector or factor object giving the group for the corresponding elements of `x`. Ignored if `x` is a list.
- `formula` a formula of the form `lhs ~ rhs` where `lhs` gives the data values and `rhs` the corresponding groups.
- `data` an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
- `subset` an optional vector specifying a subset of observations to be used.
- `na.action` a function which indicates what should happen when the data contain NAs. Defaults to `getOption("na.action")`.
- `...` further arguments to be passed to or from methods.

Details

If `x` is a list, its elements are taken as the samples to be compared for homogeneity of variances, and hence have to be numeric data vectors. In this case, `g` is ignored, and one can simply use `fligner.test(x)` to perform the test. If the samples are not yet contained in a list, use `fligner.test(list(x, ...))`.

Otherwise, `x` must be a numeric data vector, and `g` must be a vector or factor object of the same length as `x` giving the group for the corresponding elements of `x`.

The Fligner-Killeen (median) test has been determined in a simulation study as one of the many tests for homogeneity of variances which is most robust against departures from normality, see Conover, Johnson & Johnson (1981). It is a $k$-sample simple linear rank which uses the ranks of the absolute values of the centered samples and weights $a(i) = \text{qnorm}((1+i/(n+1))/2)$. The version implemented here uses median centering in each of the samples (F-K:med $X^2$ in the reference).
Value

A list of class "htest" containing the following components:

- statistic: the Fligner-Killeen:med $X^2$ test statistic.
- parameter: the degrees of freedom of the approximate chi-squared distribution of the test statistic.
- p.value: the p-value of the test.
- method: the character string "Fligner-Killeen test of homogeneity of variances".
- data.name: a character string giving the names of the data.

References


See Also

- `ansari.test` and `mood.test` for rank-based two-sample test for a difference in scale parameters;
- `var.test` and `bartlett.test` for parametric tests for the homogeneity of variances.

Examples

```r
require(graphics)
plot(count ~ spray, data = InsectSprays)
fligner.test(InsectSprays$count, InsectSprays$spray)
fligner.test(count ~ spray, data = InsectSprays)
## Compare this to bartlett.test()
```

formula

**Model Formulae**

Description

The generic function `formula` and its specific methods provide a way of extracting formulae which have been included in other objects.

as.formula is almost identical, additionally preserving attributes when object already inherits from "formula".

Usage

- `formula(x, ...)`
- `DF2formula(x, env = parent.frame())`
- `as.formula(object, env = parent.frame())`

## S3 method for class 'formula'

- `print(x, showEnv = !identical(e, .GlobalEnv), ...)`
Arguments

- `x, object`: R object, for DF2formula() a data.frame.
- `...`: further arguments passed to or from other methods.
- `env`: the environment to associate with the result, if not already a formula.
- `showEnv`: logical indicating if the environment should be printed as well.

Details

The models fitted by, e.g., the `lm` and `glm` functions are specified in a compact symbolic form. The `~` operator is basic in the formation of such models. An expression of the form `y ~ model` is interpreted as a specification that the response `y` is modelled by a linear predictor specified symbolically by `model`. Such a model consists of a series of terms separated by `+` operators. The terms themselves consist of variable and factor names separated by `:` operators. Such a term is interpreted as the interaction of all the variables and factors appearing in the term.

In addition to `+` and `:`, a number of other operators are useful in model formulae.

- The `*` operator denotes factor crossing: `a*b` is interpreted as `a + b + a:b`.
- The `^` operator indicates crossing to the specified degree. For example `(a+b+c)^2` is identical to `(a+b+c)*(a+b+c)` which in turn expands to a formula containing the main effects for `a`, `b` and `c` together with their second-order interactions.
- The `%in%` operator indicates that the terms on its left are nested within those on the right. For example `a + b %in% a` expands to the formula `a + a:b`.
- The `/` operator provides a shorthand, so that `a / b` is equivalent to `a + b %in% a`.
- The `-` operator removes the specified terms, hence `(a+b+c)^2 - a:b` is identical to `a + b + c + b:c + a:c`. It can also be used to remove the intercept term: when fitting a linear model `y ~ x - 1` specifies a line through the origin. A model with no intercept can be also specified as `y ~ x + 0` or `y ~ 0 + x`.

While formulae usually involve just variable and factor names, they can also involve arithmetic expressions. The formula `log(y) ~ a + log(x)` is quite legal. When such arithmetic expressions involve operators which are also used symbolically in model formulae, there can be confusion between arithmetic and symbolic operator use.

To avoid this confusion, the function `I()` can be used to bracket those portions of a model formula where the operators are used in their arithmetic sense. For example, in the formula `y ~ a + I(b+c)`, the term `b+c` is to be interpreted as the sum of `b` and `c`.

Variable names can be quoted by backticks `like this` in formulae, although there is no guarantee that all code using formulae will accept such non-syntactic names.

Most model-fitting functions accept formulae with right-hand-side including the function `offset` to indicate terms with a fixed coefficient of one. Some functions accept other 'specials' such as `strata` or `cluster` (see the special argument of `terms.formula`).

There are two special interpretations of . in a formula. The usual one is in the context of a data argument of model fitting functions and means 'all columns not otherwise in the formula': see `terms.formula`. In the context of `update.formula, only`, it means 'what was previously in this part of the formula'.

When `formula` is called on a fitted model object, either a specific method is used (such as that for class "nls") or the default method. The default first looks for a "formula" component of the object (and evaluates it), then a "terms" component, then a `formula` parameter of the call (and evaluates its value) and finally a "formula" attribute.
There is a `formula` method for data frames. When there’s "terms" attribute with a formula, e.g., for a `model.frame()`, that formula is returned. If you’d like the previous (R ≤ 3.5.x) behavior, use the auxiliary `DF2formula()` which does not consider a "terms" attribute. Otherwise, if there is only one column this forms the RHS with an empty LHS. For more columns, the first column is the LHS of the formula and the remaining columns separated by `+` form the RHS.

**Value**

All the functions above produce an object of class "formula" which contains a symbolic model formula.

**Environments**

A formula object has an associated environment, and this environment (rather than the parent environment) is used by `model.frame` to evaluate variables that are not found in the supplied data argument.

Formulas created with the `~` operator use the environment in which they were created. Formulas created with `as.formula` will use the `env` argument for their environment.

**Note**

In R versions up to 3.6.0, character `x` of length more than one were parsed as separate lines of R code and the first complete expression was evaluated into a formula when possible. This silently truncates such vectors of characters inefficiently and to some extent inconsistently as this behaviour had been undocumented. For this reason, such use has been deprecated. If you must work via character `x`, do use a string, i.e., a character vector of length one.

E.g., `eval(call("~", quote(foo + bar)))` has been an order of magnitude more efficient than `formula(c("~", "foo + bar"))`.

Further, character “expressions” needing an `eval()` to return a formula are now deprecated.

**References**


**See Also**

`~`, `I`, `offset`.

For formula manipulation: `terms`, and `all.vars`. For typical use: `lm`, `glm`, and `coplot`. For formula construction: `reformulate`.

**Examples**

```r
class(fo <- y ~ x1*x2) # "formula"
fo
typeof(fo) # R internal : "language"
terms(fo)

environment(fo)
environment(as.formula("y ~ x"))
environment(as.formula("y ~ x", env = new.env()))
```
## Create a formula for a model with a large number of variables:
xnam <- paste0("x", 1:25)
(fmla <- as.formula(paste("y ~ ", paste(xnam, collapse = "+"))))
## Equivalent with reformulate():
flm2 <- reformulate(xnam, response = "y")
stopifnot(identical(fmla, flm2))

---

**formula.nls**

*Extract Model Formula from nls Object*

### Description

Returns the model used to fit object.

### Usage

```r
## S3 method for class 'nls'
formula(x, ...)
```

### Arguments

- `x`  
an object inheriting from class "nls", representing a nonlinear least squares fit.
- `...`  
further arguments passed to or from other methods.

### Value

A formula representing the model used to obtain object.

### Author(s)

José Pinheiro and Douglas Bates

### See Also

`nls, formula`

### Examples

```r
fm1 <- nls(circumference ~ A/(1+exp((B-age)/C)), Orange,
start = list(A = 160, B = 700, C = 350))
formula(fm1)
```
friedman.test

Friedman Rank Sum Test

Description

Performs a Friedman rank sum test with unreplicated blocked data.

Usage

friedman.test(y, ...)

## Default S3 method:
friedman.test(y, groups, blocks, ...)

## S3 method for class 'formula'
friedman.test(formula, data, subset, na.action, ...)

Arguments

y a vector giving the group for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.
groups a vector giving the block for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.
blocks a vector giving the block for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.
formula a formula of the form a ~ b | c, where a, b and c give the data values and corresponding groups and blocks, respectively.
data an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset an optional vector specifying a subset of observations to be used.
naction a function which indicates what should happen when the data contain NAs. Defaults togetOption("na.action").
... further arguments to be passed to or from methods.

Details

friedman.test can be used for analyzing unreplicated complete block designs (i.e., there is exactly one observation in y for each combination of levels of groups and blocks) where the normality assumption may be violated.

The null hypothesis is that apart from an effect of blocks, the location parameter of y is the same in each of the groups.

If y is a matrix, groups and blocks are obtained from the column and row indices, respectively. NA’s are not allowed in groups or blocks; if y contains NA’s, corresponding blocks are removed.
Value

A list with class "htest" containing the following components:

- **statistic** the value of Friedman's chi-squared statistic.
- **parameter** the degrees of freedom of the approximate chi-squared distribution of the test statistic.
- **p.value** the p-value of the test.
- **method** the character string "Friedman rank sum test".
- **data.name** a character string giving the names of the data.

References


See Also

- quade.test

Examples

```R
## Comparison of three methods ("round out", "narrow angle", and "wide angle") for rounding first base. For each of 18 players and the three method, the average time of two runs from a point on the first base line 35ft from home plate to a point 15ft short of second base is recorded.
RoundingTimes <-
matrix(c(5.40, 5.50, 5.55, 5.85, 5.70, 5.75, 5.20, 5.60, 5.50, 5.55, 5.50, 5.40, 5.90, 5.85, 5.70, 5.45, 5.55, 5.60, 5.40, 5.40, 5.35, 5.45, 5.50, 5.35, 5.25, 5.15, 5.00, 5.85, 5.80, 5.70, 5.25, 5.20, 5.10, 5.65, 5.55, 5.45, 5.60, 5.35, 5.45, 5.05, 5.00, 4.95, 5.50, 5.50, 5.40, 5.45, 5.55, 5.50, 5.55, 5.55, 5.55, 5.50, 5.45, 5.45, 5.45, 5.55, 5.55, 5.35, 5.45, 5.55, 5.50, 5.40, 5.70, 5.65, 5.55, 6.30, 6.30, 6.25),
nrow = 22,
byrow = TRUE,
dimnames = list(1:22,
c("Round Out", "Narrow Angle", "Wide Angle")))
friedman.test(RoundingTimes)
```
```r
## => strong evidence against the null that the methods are equivalent
## with respect to speed

wb <- aggregate(warpbreaks$breaks,
    by = list(w = warpbreaks$wool,
              t = warpbreaks$tension),
    FUN = mean)
wb
friedman.test(wb$x, wb$w, wb$t)
friedman.test(x ~ w | t, data = wb)
```

---

**ftable**

*Flat Contingency Tables*

**Description**

Create ‘flat’ contingency tables.

**Usage**

```r
ftable(x, ...)
```

**Arguments**

- `x, ...`  
  R objects which can be interpreted as factors (including character strings), or a list (or data frame) whose components can be so interpreted, or a contingency table object of class "table" or "ftable".

- `exclude`  
  values to use in the exclude argument of `factor` when interpreting non-factor objects.

- `row.vars`  
  a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables to be used for the rows of the flat contingency table.

- `col.vars`  
  a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables to be used for the columns of the flat contingency table.

**Details**

`ftable` creates ‘flat’ contingency tables. Similar to the usual contingency tables, these contain the counts of each combination of the levels of the variables (factors) involved. This information is then re-arranged as a matrix whose rows and columns correspond to unique combinations of the levels of the row and column variables (as specified by `row.vars` and `col.vars`, respectively). The combinations are created by looping over the variables in reverse order (so that the levels of the left-most variable vary the slowest). Displaying a contingency table in this flat matrix form (via `print.ftable`, the print method for objects of class "ftable") is often preferable to showing it as a higher-dimensional array.
ftable is a generic function. Its default method, ftable.default, first creates a contingency table in array form from all arguments except row.vars and col.vars. If the first argument is of class "table", it represents a contingency table and is used as is; if it is a flat table of class "ftable", the information it contains is converted to the usual array representation using as.table. Otherwise, the arguments should be R objects which can be interpreted as factors (including character strings), or a list (or data frame) whose components can be so interpreted, which are cross-tabulated using table. Then, the arguments row.vars and col.vars are used to collapse the contingency table into flat form. If neither of these two is given, the last variable is used for the columns. If both are given and their union is a proper subset of all variables involved, the other variables are summed out.

When the arguments are R expressions interpreted as factors, additional arguments will be passed to table to control how the variable names are displayed; see the last example below.

Function ftable.formula provides a formula method for creating flat contingency tables.

There are methods for as.table, as.matrix and as.data.frame.

Value

ftable returns an object of class "ftable", which is a matrix with counts of each combination of the levels of variables with information on the names and levels of the (row and columns) variables stored as attributes "row.vars" and "col.vars".

See Also

ftable.formula for the formula interface (which allows a data = . argument); read.ftable for information on reading, writing and coercing flat contingency tables; table for ordinary cross-tabulation; xtabs for formula-based cross-tabulation.

Examples

## Start with a contingency table.
ftable(Titanic, row.vars = 1:3)
ftable(Titanic, row.vars = 1:2, col.vars = "Survived")
ftable(Titanic, row.vars = 2:1, col.vars = "Survived")

## Start with a data frame.
x <- ftable(mtcars[c("cyl", "vs", "am", "gear")])
x
ftable(x, row.vars = c(2, 4))

## Start with expressions, use table()'s "dnn" to change labels
ftable(mtcars$ cyl, mtcars$ vs, mtcars$ am, mtcars$ gear, row.vars = c(2, 4),
       dnn = c("Cylinders", "V/S", "Transmission", "Gears"))
Usage

## S3 method for class 'formula'
ftable(formula, data = NULL, subset, na.action, ...)

Arguments

formula a formula object with both left and right hand sides specifying the column and row variables of the flat table.
data a data frame, list or environment (or similar: see model.frame) containing the variables to be cross-tabulated, or a contingency table (see below).
subset an optional vector specifying a subset of observations to be used. Ignored if data is a contingency table.
na.action a function which indicates what should happen when the data contain NAs. Ignored if data is a contingency table.
... further arguments to the default ftable method may also be passed as arguments, see ftable.default.

Details

This is a method of the generic function ftable.

The left and right hand side of formula specify the column and row variables, respectively, of the flat contingency table to be created. Only the + operator is allowed for combining the variables. A . may be used once in the formula to indicate inclusion of all the remaining variables.

If data is an object of class "table" or an array with more than 2 dimensions, it is taken as a contingency table, and hence all entries should be nonnegative. Otherwise, if it is not a flat contingency table (i.e., an object of class "ftable"), it should be a data frame or matrix, list or environment containing the variables to be cross-tabulated. In this case, na.action is applied to the data to handle missing values, and, after possibly selecting a subset of the data as specified by the subset argument, a contingency table is computed from the variables.

The contingency table is then collapsed to a flat table, according to the row and column variables specified by formula.

Value

A flat contingency table which contains the counts of each combination of the levels of the variables, collapsed into a matrix for suitably displaying the counts.

See Also

ftable, ftable.default; table.

Examples

Titanic
x <- ftable(Survived ~ ., data = Titanic)
x
ftable(Sex ~ Class + Age, data = x)
The Gamma Distribution

Description
Density, distribution function, quantile function and random generation for the Gamma distribution with parameters shape and scale.

Usage

dgamma(x, shape, rate = 1, scale = 1/rate, log = FALSE)
pgamma(q, shape, rate = 1, scale = 1/rate, lower.tail = TRUE, log.p = FALSE)
qgamma(p, shape, rate = 1, scale = 1/rate, lower.tail = TRUE, log.p = FALSE)
rgamma(n, shape, rate = 1, scale = 1/rate)

Arguments

x, q
vector of quantiles.
p
vector of probabilities.
n
number of observations. If length(n) > 1, the length is taken to be the number required.
rate
an alternative way to specify the scale.
shape, scale
shape and scale parameters. Must be positive, scale strictly.
log, log.p
logical; if TRUE, probabilities/densities p are returned as log(p).
lower.tail
logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details
If scale is omitted, it assumes the default value of 1.
The Gamma distribution with parameters shape = \( \alpha \) and scale = \( \sigma \) has density

$$f(x) = \frac{1}{\sigma^\alpha \Gamma(\alpha)} x^{\alpha-1} e^{-x/\sigma}$$

for \( x \geq 0, \alpha > 0 \) and \( \sigma > 0 \). (Here \( \Gamma(\alpha) \) is the function implemented by R’s \texttt{gamma()} and defined in its help. Note that \( \alpha = 0 \) corresponds to the trivial distribution with all mass at point 0.)
The mean and variance are $E(X) = \alpha \sigma$ and $Var(X) = \alpha \sigma^2$.
The cumulative hazard $H(t) = -\log(1 - F(t))$ is

-\texttt{pgamma(t, ..., lower = FALSE, log = TRUE)}

Note that for smallish values of shape (and moderate scale) a large parts of the mass of the Gamma distribution is on values of \( x \) so near zero that they will be represented as zero in computer arithmetic. So \texttt{rgamma} may well return values which will be represented as zero. (This will also happen for very large values of scale since the actual generation is done for scale = 1.)
Value
dgamma gives the density, pgamma gives the distribution function, qgamma gives the quantile function, and rgamma generates random deviates.
Invalid arguments will result in return value NaN, with a warning.
The length of the result is determined by n for rgamma, and is the maximum of the lengths of the numerical arguments for the other functions.
The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note
The S (Becker et al, 1988) parametrization was via shape and rate: S had no scale parameter. It is an error to supply both scale and rate.

pgamma is closely related to the incomplete gamma function. As defined by Abramowitz and Stegun 6.5.1 (and by ‘Numerical Recipes’) this is

\[ P(a, x) = \frac{1}{\Gamma(a)} \int_0^x t^{a-1}e^{-t}dt \]

where \( P(a, x) \) is pgamma(x, a). Other authors (for example Karl Pearson in his 1922 tables) omit the normalizing factor, defining the incomplete gamma function \( \gamma(a, x) \) as \( \gamma(a, x) = \int_0^x t^{a-1}e^{-t}dt \), i.e., pgamma(x, a) * gamma(a). Yet other use the ‘upper’ incomplete gamma function,

\[ \Gamma(a, x) = \int_x^\infty t^{a-1}e^{-t}dt, \]

which can be computed by pgamma(x, a, lower = FALSE) * gamma(a).
Note however that pgamma(x, a, ...) currently requires \( a > 0 \), whereas the incomplete gamma function is also defined for negative \( a \). In that case, you can use gamma_inc(a, x) (for \( \Gamma(a, x) \)) from package gsl.
See also https://en.wikipedia.org/wiki/Incomplete_gamma_function, or https://dlmf.nist.gov/8.2#i.

Source
dgamma is computed via the Poisson density, using code contributed by Catherine Loader (see dbinom).

pgamma uses an unpublished (and not otherwise documented) algorithm ‘mainly by Morten Welinder’.

qgamma is based on a C translation of
plus a final Newton step to improve the approximation.
rgamma for shape >= 1 uses
and for 0 < shape < 1 uses
Geometric

The Geometric Distribution

Description

Density, distribution function, quantile function and random generation for the geometric distribution with parameter prob.

Usage

dgeom(x, prob, log = FALSE)
pgeom(q, prob, lower.tail = TRUE, log.p = FALSE)
qgeom(p, prob, lower.tail = TRUE, log.p = FALSE)
rgeom(n, prob)

Arguments

x, q
vector of quantiles representing the number of failures in a sequence of Bernoulli trials before success occurs.

p
vector of probabilities.
Geometric

`n` number of observations. If `length(n) > 1`, the length is taken to be the number required.

`prob` probability of success in each trial. $0 < \text{prob} \leq 1$.

`log, log.p` logical; if TRUE, probabilities p are given as log(p).

`lower.tail` logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The geometric distribution with `prob = p` has density

$$p(x) = p(1 - p)^x$$

for $x = 0, 1, 2, \ldots$, $0 < p \leq 1$.

If an element of `x` is not integer, the result of `dgeom` is zero, with a warning.

The quantile is defined as the smallest value $x$ such that $F(x) \geq p$, where $F$ is the distribution function.

Value

dgeom gives the density, pgeom gives the distribution function, qgeom gives the quantile function, and rgeom generates random deviates.

Invalid `prob` will result in return value `NaN`, with a warning.

The length of the result is determined by `n` for rgeom, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

rgeom returns a vector of type integer unless generated values exceed the maximum representable integer when `double` values are returned.

Source

dgeom computes via dbinom, using code contributed by Catherine Loader (see dbinom).
pgeom and qgeom are based on the closed-form formulae.
rgeom uses the derivation as an exponential mixture of Poissons, see


See Also

Distributions for other standard distributions, including dnbimom for the negative binomial which generalizes the geometric distribution.

Examples

qgeom((1:9)/10, prob = .2)
Ni <- rgeom(20, prob = 1/4); table(factor(Ni, 0:max(Ni)))
getInitial  Get Initial Parameter Estimates

Description

This function evaluates initial parameter estimates for a nonlinear regression model. If data is a
data parameterized data frame or pframe object, its parameters attribute is returned. Otherwise the
object is examined to see if it contains a call to a selfStart object whose initial attribute can be
evaluated.

Usage

getInitial(object, data, ...)

Arguments

object a formula or a selfStart model that defines a nonlinear regression model
data a data frame in which the expressions in the formula or arguments to the
selfStart model can be evaluated
... optional additional arguments

Value

A named numeric vector or list of starting estimates for the parameters. The construction of many
selfStart models is such that these "starting" estimates are, in fact, the converged parameter
estimates.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart, selfStart.default, selfStart.formula. Further, nlsList from nlme.

Examples

PurTrt <- Puromycin[ Puromycin$state == "treated", ]
print(getInitial( rate ~ SSmicmen( conc, Vm, K ), PurTrt ), digits = 3)
glm is used to fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution.

Usage

```r
glm(formula, family = gaussian, data, weights, subset, na.action, start = NULL, etastart, mustart, offset, control = list(...), model = TRUE, method = "glm.fit", x = FALSE, y = TRUE, singular.ok = TRUE, contrasts = NULL, ...)
```

```r
glm.fit(x, y, weights = rep.int(1, nobs), start = NULL, etastart = NULL, mustart = NULL, offset = rep.int(0, nobs), family = gaussian(), control = list(), intercept = TRUE, singular.ok = TRUE)
```

## S3 method for class 'glm'
weights(object, type = c("prior", "working"), ...)

Arguments

- **formula**: an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
- **family**: a description of the error distribution and link function to be used in the model. For glm this can be a character string naming a family function, a family function or the result of a call to a family function. For glm.fit only the third option is supported. (See family for details of family functions.)
- **data**: an optional data frame, list or environment (or object coercible by `as.data.frame`) to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which glm is called.
- **weights**: an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
- **subset**: an optional vector specifying a subset of observations to be used in the fitting process.
- **na.action**: a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit. Another possible value is NULL, no action. Value na.exclude can be useful.
- **start**: starting values for the parameters in the linear predictor.
- **etastart**: starting values for the linear predictor.
- **mustart**: starting values for the vector of means.
offset this can be used to specify an *a priori* known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset.

control a list of parameters for controlling the fitting process. For glm.fit this is passed to glm.control.

model a logical value indicating whether model.frame should be included as a component of the returned value.

method the method to be used in fitting the model. The default method "glm.fit" uses iteratively reweighted least squares (IWLS): the alternative "model.frame" returns the model frame and does no fitting.

User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as glm.fit. If specified as a character string it is looked up from within the stats namespace.

x, y For glm: logical values indicating whether the response vector and model matrix used in the fitting process should be returned as components of the returned value.

For glm.fit: x is a design matrix of dimension n * p, and y is a vector of observations of length n.

singular.ok logical; if FALSE a singular fit is an error.

contrasts an optional list. See the contrasts.arg of model.matrix.default.

intercept logical. Should an intercept be included in the null model?

object an object inheriting from class "glm".

type character, partial matching allowed. Type of weights to extract from the fitted model object. Can be abbreviated.

... For glm: arguments to be used to form the default control argument if it is not supplied directly.

For weights: further arguments passed to or from other methods.

Details

A typical predictor has the form response ~ terms where response is the (numeric) response vector and terms is a series of terms which specifies a linear predictor for response. For binomial and quasibinomial families the response can also be specified as a factor (when the first level denotes failure and all others success) or as a two-column matrix with the columns giving the numbers of successes and failures. A terms specification of the form first + second indicates all the terms in first together with all the terms in second with any duplicates removed.

A specification of the form first:second indicates the set of terms obtained by taking the interactions of all terms in first with all terms in second. The specification first+second indicates the cross of first and second. This is the same as first + second + first:second.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.

Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in weights being inversely proportional to the dispersions); or equivalently, when the elements of weights are positive integers wi, that each response yi is the mean of wi unit-weight observations. For a binomial GLM prior weights are used to give the number of trials when the response is the proportion of successes: they would rarely be used for a Poisson GLM.
glm.fit is the workhorse function: it is not normally called directly but can be more efficient where the response vector, design matrix and family have already been calculated.

If more than one of etastart, start and mustart is specified, the first in the list will be used. It is often advisable to supply starting values for a quasi family, and also for families with unusual links such as gaussian("log").

All of weights, subset, offset, etastart and mustart are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula.

For the background to warning messages about ‘fitted probabilities numerically 0 or 1 occurred’ for binomial GLMs, see Venables & Ripley (2002, pp. 197–8).

Value

glm returns an object of class inheriting from "glm" which inherits from the class "lm". See later in this section. If a non-standard method is used, the object will also inherit from the class (if any) returned by that function.

The function summary (i.e., summary.glm) can be used to obtain or print a summary of the results and the function anova (i.e., anova.glm) to produce an analysis of variance table.

The generic accessor functions coefficients, effects, fitted.values and residuals can be used to extract various useful features of the value returned by glm.

weights extracts a vector of weights, one for each case in the fit (after subsetting and na.action). An object of class "glm" is a list containing at least the following components:

- coefficients a named vector of coefficients
- residuals the working residuals, that is the residuals in the final iteration of the IWLS fit. Since cases with zero weights are omitted, their working residuals are NA.
- fitted.values the fitted mean values, obtained by transforming the linear predictors by the inverse of the link function.
- rank the numeric rank of the fitted linear model.
- family the family object used.
- linear.predictors the linear fit on link scale.
- deviance up to a constant, minus twice the maximized log-likelihood. Where sensible, the constant is chosen so that a saturated model has deviance zero.
- aic A version of Akaike’s An Information Criterion, minus twice the maximized log-likelihood plus twice the number of parameters, computed via the aic component of the family. For binomial and Poison families the dispersion is fixed at one and the number of parameters is the number of coefficients. For gaussian, Gamma and inverse gaussian families the dispersion is estimated from the residual deviance, and the number of parameters is the number of coefficients plus one. For a gaussian family the MLE of the dispersion is used so this is a valid value of AIC, but for Gamma and inverse gaussian families it is not. For families fitted by quasi-likelihood the value is NA.
- null.deviance The deviance for the null model, comparable with deviance. The null model will include the offset, and an intercept if there is one in the model. Note that this will be incorrect if the link function depends on the data other than through the fitted mean: specify a zero offset to force a correct calculation.
- iter the number of iterations of IWLS used.
- weights the working weights, that is the weights in the final iteration of the IWLS fit.
prior.weights  the weights initially supplied, a vector of 1s if none were.
df.residual  the residual degrees of freedom.
df.null  the residual degrees of freedom for the null model.
y  if requested (the default) the y vector used. (It is a vector even for a binomial model.)
x  if requested, the model matrix.
model  if requested (the default), the model frame.
converged  logical. Was the IWLS algorithm judged to have converged?
boundary  logical. Is the fitted value on the boundary of the attainable values?
call  the matched call.
formula  the formula supplied.
terms  the terms object used.
data  the data argument.
offset  the offset vector used.
control  the value of the control argument used.
method  the name of the fitter function used (when provided as a character string to glm() or the fitter function (when provided as that).
contrasts  (where relevant) the contrasts used.
xlevels  (where relevant) a record of the levels of the factors used in fitting.
na.action  (where relevant) information returned by model.frame on the special handling of NAs.

In addition, non-empty fits will have components qr, R and effects relating to the final weighted linear fit.

Objects of class "glm" are normally of class c("glm", "lm"), that is inherit from class "lm", and well-designed methods for class "lm" will be applied to the weighted linear model at the final iteration of IWLS. However, care is needed, as extractor functions for class "glm" such as residuals and weights do not just pick out the component of the fit with the same name.

If a binomial glm model was specified by giving a two-column response, the weights returned by prior.weights are the total numbers of cases (factored by the supplied case weights) and the component y of the result is the proportion of successes.

Fitting functions

The argument method serves two purposes. One is to allow the model frame to be recreated with no fitting. The other is to allow the default fitting function glm.fit to be replaced by a function which takes the same arguments and uses a different fitting algorithm. If glm.fit is supplied as a character string it is used to search for a function of that name, starting in the stats namespace.

The class of the object return by the fitter (if any) will be prepended to the class returned by glm.

Author(s)

The original R implementation of glm was written by Simon Davies working for Ross Ihaka at the University of Auckland, but has since been extensively re-written by members of the R Core team.

The design was inspired by the S function of the same name described in Hastie & Pregibon (1992).
References


See Also

`anova.glm`, `summary.glm`, etc. for `glm` methods, and the generic functions `anova`, `summary`, `effects`, `fitted.values`, and `residuals`.

`lm` for non-generalized linear models (which SAS calls GLMs, for ‘general’ linear models).

`loglin` and `loglm` (package `MASS`) for fitting log-linear models (which binomial and Poisson GLMs are) to contingency tables.

`bigglm` in package `biglm` for an alternative way to fit GLMs to large datasets (especially those with many cases).

`esoph`, `infert` and `predict.glm` have examples of fitting binomial glms.

Examples

```r
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
data.frame(treatment, outcome, counts) # showing data
glm.D93 <- glm(counts ~ outcome + treatment, family = poisson())
anova(glm.D93)
summary(glm.D93)

## Computing AIC [in many ways]:
(A0 <- AIC(glm.D93))
(ll <- logLik(glm.D93))
A1 <- -2*logLik(glm.D93) + 2*attr(ll, "df")
A2 <- glm.D93$family$aic(counts, mu=fitted(glm.D93), wt=1) +
    2 * length(coef(glm.D93))
stopifnot(exprs = {
an.all.equal(A0, A1)
an.all.equal(A1, A2)
an.all.equal(A1, glm.D93$aic)
})

## an example with offsets from Venables & Ripley (2002, p.189)
utils::data(anorexia, package = "MASS")
anorex.1 <- glm(Postwt ~ Prewt + Treat + offset(Prewt),
                family = gaussian, data = anorexia)
summary(anorex.1)

# A Gamma example, from McCullagh & Nelder (1989, pp. 300-2)
clotting <- data.frame(u = c(5,10,15,20,30,40,60,80,100),
        lot1 = c(118,58,42,35,27,25,21,19,18),
        lot2 = c(58,39,30,27,25,20,19,18,17),
        lot3 = c(20,18,16,13,12,10,9,7,6))
clotting$lot <- gl(3, 3, labels = c("lot1", "lot2", "lot3"))
clotting$u <- as.numeric(clotting$u)
clotting$lot1 <- as.numeric(clotting$lot1)
clotting$lot2 <- as.numeric(clotting$lot2)
clotting$lot3 <- as.numeric(clotting$lot3)
clotting$u <- log(clotting$u)
clotting$lot1 <- log(clotting$lot1)
clotting$lot2 <- log(clotting$lot2)
clotting$lot3 <- log(clotting$lot3)

glm.G100 <- glm(u ~ lot + lot1 + lot2 + lot3, data = clotting,
                family = Gamma)
summary(glm.G100)
```
lot2 = c(69,35,26,21,18,16,13,12,12))
summary(glm(lot1 ~ log(u), data = clotting, family = Gamma))
summary(glm(lot2 ~ log(u), data = clotting, family = Gamma))
## Aliased ("S"ingular) -> 1 NA coefficient
(fS <- glm(lot2 ~ log(u) + log(u^2), data = clotting, family = Gamma))
tools::assertError(update(fS, singular.ok=FALSE), verbose=interactive())
## -> .. "singular fit encountered"
## Not run:
## for an example of the use of a terms object as a formula
demo(glm.vr)
## End(Not run)

glm.control

---

### Description

Auxiliary function for `glm` fitting. Typically only used internally by `glm.fit`, but may be used to construct a control argument to either function.

### Usage

```r
glm.control(epsilon = 1e-8, maxit = 25, trace = FALSE)
```

### Arguments

- `epsilon` positive convergence tolerance \( \epsilon \); the iterations converge when
  \[ \frac{|\text{dev} - \text{dev}_{old}|}{(|\text{dev}| + 0.1)} < \epsilon. \]
- `maxit` integer giving the maximal number of IWLS iterations.
- `trace` logical indicating if output should be produced for each iteration.

### Details

The control argument of `glm` is by default passed to the control argument of `glm.fit`, which uses its elements as arguments to `glm.control`: the latter provides defaults and sanity checking.

If `epsilon` is small (less than \(10^{-10}\)) it is also used as the tolerance for the detection of collinearity in the least squares solution.

When `trace` is true, calls to `cat` produce the output for each IWLS iteration. Hence, `options(digits = *)` can be used to increase the precision, see the example.

### Value

A list with components named as the arguments.

### References

See Also

`glm.fit`, the fitting procedure used by `glm`.

Examples

```r
### A variation on example(glm):
## Annette Dobson's example ...
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
oo <- options(digits = 12) # to see more when tracing :
glm.D93X <- glm(counts ~ outcome + treatment, family = poisson(),
                 trace = TRUE, epsilon = 1e-14)
options(o0)
coef(glm.D93X) # the last two are closer to 0 than in ?glm's glm.D93
```

---

`glm.summaries`  
*Accessing Generalized Linear Model Fits*

**Description**

These functions are all methods for class `glm` or `summary.glm` objects.

**Usage**

```r
## S3 method for class 'glm'
family(object, ...)

## S3 method for class 'glm'
residuals(object, type = c("deviance", "pearson", "working",
                          "response", "partial"), ...)
```

**Arguments**

- `object` an object of class `glm`, typically the result of a call to `glm`.
- `type` the type of residuals which should be returned. The alternatives are: "deviance" (default), "pearson", "working", "response", and "partial". Can be abbreviated.
- ... further arguments passed to or from other methods.

**Details**

The references define the types of residuals: Davison & Snell is a good reference for the usages of each.

The partial residuals are a matrix of working residuals, with each column formed by omitting a term from the model.

How `residuals` treats cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclue` they will appear, with residual value NA. See also `naresid`.

For fits done with `y = FALSE` the response values are computed from other components.
hclust

Hierarchical Clustering

Description

Hierarchical cluster analysis on a set of dissimilarities and methods for analyzing it.

Usage

hclust(d, method = "complete", members = NULL)

## S3 method for class 'hclust'
plot(x, labels = NULL, hang = 0.1, check = TRUE,
axes = TRUE, frame.plot = FALSE, ann = TRUE,
main = "Cluster Dendrogram",
sub = NULL, xlab = NULL, ylab = "Height", ...)

Arguments

d a dissimilarity structure as produced by dist.
method the agglomeration method to be used. This should be (an unambiguous abbreviation of) one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
members NULL or a vector with length size of d. See the ‘Details’ section.
x an object of the type produced by hclust.
hang The fraction of the plot height by which labels should hang below the rest of the plot. A negative value will cause the labels to hang down from 0.
check logical indicating if the x object should be checked for validity. This check is not necessary when x is known to be valid such as when it is the direct result of hclust(). The default is check=TRUE, as invalid inputs may crash R due to memory violation in the internal C plotting code.

See Also

glm for computing glm.obj, anova.glm; the corresponding generic functions, summary.glm, coef, deviance, df.residual, effects, fitted, residuals.
influence.measures for deletion diagnostics, including standardized (rstandard) and studentized (rstudent) residuals.

References


This function performs a hierarchical cluster analysis using a set of dissimilarities for the \( n \) objects being clustered. Initially, each object is assigned to its own cluster and then the algorithm proceeds iteratively, at each stage joining the two most similar clusters, continuing until there is just a single cluster. At each stage distances between clusters are recomputed by the Lance–Williams dissimilarity update formula according to the particular clustering method being used.

A number of different clustering methods are provided. **Ward's** minimum variance method aims at finding compact, spherical clusters. The **complete** linkage method finds similar clusters. The **single** linkage method (which is closely related to the minimal spanning tree) adopts a 'friends of friends' clustering strategy. The other methods can be regarded as aiming for clusters with characteristics somewhere between the single and complete link methods. Note however, that methods "median" and "centroid" are not leading to a **monotone distance** measure, or equivalently the resulting dendrograms can have so called **inversions** or **reversals** which are hard to interpret, but note the trichotomies in Legendre and Legendre (2012).

Two different algorithms are found in the literature for Ward clustering. The one used by option "ward.D" (equivalent to the only Ward option "ward" in R versions \( \leq 3.0.3 \)) does not implement Ward's (1963) clustering criterion, whereas option "ward.D2" implements that criterion (Murtagh and Legendre 2014). With the latter, the dissimilarities are squared before cluster updating. Note that \texttt{agnes(*, method="ward")} corresponds to \texttt{hclust(*, "ward.D2")}.

If \texttt{members} \neq \texttt{NULL}, then \( d \) is taken to be a dissimilarity matrix between clusters instead of dissimilarities between singletons and \texttt{members} gives the number of observations per cluster. This way the hierarchical cluster algorithm can be 'started in the middle of the dendrogram', e.g., in order to reconstruct the part of the tree above a cut (see examples). Dissimilarities between clusters can be efficiently computed (i.e., without \texttt{hclust} itself) only for a limited number of distance/linkage combinations, the simplest one being **squared** Euclidean distance and centroid linkage. In this case the dissimilarities between the clusters are the squared Euclidean distances between cluster means.

In hierarchical cluster displays, a decision is needed at each merge to specify which subtree should go on the left and which on the right. Since, for \( n \) observations there are \( n - 1 \) merges, there are \( 2^{(n-1)} \) possible orderings for the leaves in a cluster tree, or dendrogram. The algorithm used in \texttt{hclust} is to order the subtree so that the tighter cluster is on the left (the last, i.e., most recent, merge of the left subtree is at a lower value than the last merge of the right subtree). Single observations are the tightest clusters possible, and merges involving two observations place them in order by their observation sequence number.

**Value**

An object of class \texttt{hclust} which describes the tree produced by the clustering process. The object is a list with components:

- **labels**: A character vector of labels for the leaves of the tree. By default the row names or row numbers of the original data are used. If \texttt{labels = FALSE} no labels at all are plotted.
- **axes**, **frame.plot**, **ann**: logical flags as in \texttt{plot.default}.
- **main**, **sub**, **xlab**, **ylab**: character strings for \texttt{title}. **sub** and **xlab** have a non-NULL default when there's a \texttt{tree$call}.
- **...**: Further graphical arguments. E.g., \texttt{cex} controls the size of the labels (if plotted) in the same way as \texttt{text}.
merge  an \( n - 1 \) by 2 matrix. Row \( i \) of \( \text{merge} \) describes the merging of clusters at step \( i \) of the clustering. If an element \( j \) in the row is negative, then observation \( -j \) was merged at this stage. If \( j \) is positive then the merge was with the cluster formed at the (earlier) stage \( j \) of the algorithm. Thus negative entries in \( \text{merge} \) indicate agglomerations of singletons, and positive entries indicate agglomerations of non-singletons.

height  a set of \( n - 1 \) real values (non-decreasing for ultrametric trees). The clustering \( \text{height} \): that is, the value of the criterion associated with the clustering method for the particular agglomeration.

order  a vector giving the permutation of the original observations suitable for plotting, in the sense that a cluster plot using this ordering and matrix \( \text{merge} \) will not have crossings of the branches.

labels  labels for each of the objects being clustered.

call  the call which produced the result.

method  the cluster method that has been used.

dist.method  the distance that has been used to create \( d \) (only returned if the distance object has a "method" attribute).

There are \texttt{print}, \texttt{plot} and \texttt{identify} (see \texttt{identify.hclust}) methods and the \texttt{rect.hclust()} function for \texttt{hclust} objects.

Note

Method "centroid" is typically meant to be used with squared Euclidean distances.

Author(s)

The \texttt{hclust} function is based on Fortran code contributed to STATLIB by F. Murtagh.

References


Heatmap

See Also

identify.hclust, rect.hclust, cutree, dendrogram, kmeans.

For the Lance–Williams formula and methods that apply it generally, see agnes from package cluster.

Examples

require(graphics)

### Example 1: Violent crime rates by US state

hc <- hclust(dist(USArrests), "ave")
plot(hc)
plot(hc, hang = -1)

## Do the same with centroid clustering and squared Euclidean distance, cut the tree into ten clusters and reconstruct the upper part of the tree from the cluster centers.

hc <- hclust(dist(USArrests)^2, "cen")
memb <- cutree(hc, k = 10)
cent <- NULL
for(k in 1:10){
  cent <- rbind(cent, colMeans(USArrests[memb == k, , drop = FALSE]))
}

hc1 <- hclust(dist(cent)^2, method = "cen", members = table(memb))

opar <- par(mfrow = c(1, 2))
plot(hc, labels = FALSE, hang = -1, main = "Original Tree")
plot(hc1, labels = FALSE, hang = -1, main = "Re-start from 10 clusters")
par(opar)

### Example 2: Straight-line distances among 10 US cities

## Compare the results of algorithms "ward.D" and "ward.D2"

mds2 <- -cmdscale(UScitiesD)
plot(mds2, type="n", axes=FALSE, ann=FALSE)
text(mds2, labels=rownames(mds2), xpd = NA)

hc1.D <- hclust(UScitiesD, "ward.D") # "wrong"
hc1.D2 <- hclust(UScitiesD, "ward.D2")

opar <- par(mfrow = c(1, 2))
plot(hc1.D, hang=-1)
plot(hc1.D2, hang=-1)
par(opar)

Heatmap

Draw a Heat Map

Description

A heat map is a false color image (basically image(t(x))) with a dendrogram added to the left side and to the top. Typically, reordering of the rows and columns according to some set of values (row or column means) within the restrictions imposed by the dendrogram is carried out.
heatmap

Usage

heatmap(x, Rowv = NULL, Colv = if(symm)"Rowv" else NULL,
        distfun = dist, hclustfun = hclust,
        reorderfun = function(d, w) reorder(d, w),
        add.expr, symm = FALSE, revC = identical(Colv, "Rowv"),
        scale = c("row", "column", "none"), na.rm = TRUE,
        margins = c(5, 5), ColSideColors, RowSideColors,
        cexRow = 0.2 + 1/log10(nr), cexCol = 0.2 + 1/log10(nc),
        labRow = NULL, labCol = NULL, main = NULL,
        xlab = NULL, ylab = NULL,
        keep.dendro = FALSE, verbose = getOption("verbose"), ...)

Arguments

x numeric matrix of the values to be plotted.
Rowv determines if and how the row dendrogram should be computed and reordered. Either a dendrogram or a vector of values used to reorder the row dendrogram or NA to suppress any row dendrogram (and reordering) or by default, NULL, see 'Details' below.
Colv determines if and how the column dendrogram should be reordered. Has the same options as the Rowv argument above and additionally when x is a square matrix, Colv = "Rowv" means that columns should be treated identically to the rows (and so if there is to be no row dendrogram there will not be a column one either).
distfun function used to compute the distance (dissimilarity) between both rows and columns. Defaults to dist.
hclustfun function used to compute the hierarchical clustering when Rowv or Colv are not dendrograms. Defaults to hclust. Should take as argument a result of distfun and return an object to which as.dendrogram can be applied.
reorderfun function(d, w) of dendrogram and weights for reordering the row and column dendrograms. The default uses reorder.dendrogram.
add.expr expression that will be evaluated after the call to image. Can be used to add components to the plot.
symm logical indicating if x should be treated symmetrically; can only be true when x is a square matrix.
revC logical indicating if the column order should be reversed for plotting, such that e.g., for the symmetric case, the symmetry axis is as usual.
scale character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. The default is "row" if symm false, and "none" otherwise.
na.rm logical indicating whether NA's should be removed.
margins numeric vector of length 2 containing the margins (see par(mar = *)) for column and row names, respectively.
ColSideColors (optional) character vector of length ncol(x) containing the color names for a horizontal side bar that may be used to annotate the columns of x.
RowSideColors (optional) character vector of length nrow(x) containing the color names for a vertical side bar that may be used to annotate the rows of x.
heatmap

cexRow, cexCol positive numbers, used as cex.axis in for the row or column axis labeling. The
defaults currently only use number of rows or columns, respectively.
labRow, labCol character vectors with row and column labels to use; these default to
rownames(x) or colnames(x), respectively.
main, xlab, ylab main, x- and y-axis titles; defaults to none.
keep.dendro logical indicating if the dendrogram(s) should be kept as part of the result (when
Rowv and/or Colv are not NA).
verbose logical indicating if information should be printed.
... additional arguments passed on to image, e.g., col specifying the colors.

Details
If either Rowv or Colv are dendrograms they are honored (and not reordered). Otherwise, dendro-
grams are computed as dd <- as.dendrogram(hclustfun(distfun(X))) where X is either x or
t(x).
If either is a vector (of 'weights') then the appropriate dendrogram is reordered according to the
supplied values subject to the constraints imposed by the dendrogram, by reorder(dd, Rowv), in
the row case. If either is missing, as by default, then the ordering of the corresponding dendrogram
is by the mean value of the rows/columns, i.e., in the case of rows, Rowv <- rowMeans(x, na.rm =
na.rm). If either is NA, no reordering will be done for the corresponding side.
By default (scale = "row") the rows are scaled to have mean zero and standard deviation one.
There is some empirical evidence from genomic plotting that this is useful.

Value
Invisibly, a list with components

rowInd row index permutation vector as returned by order.dendrogram.
colInd column index permutation vector.
Rowv the row dendrogram; only if input Rowv was not NA and keep.dendro is true.
Colv the column dendrogram; only if input Colv was not NA and keep.dendro is true.

Note
Unless Rowv = NA (or Colv = NA), the original rows and columns are reordered in any case to
match the dendrogram, e.g., the rows by order.dendrogram(Rowv) where Rowv is the (possibly
reorder()ed) row dendrogram.
heatmap() uses layout and draws the image in the lower right corner of a 2x2 layout. Consequen-
tially, it can not be used in a multi column/row layout, i.e., when par(mfrow = *) or (mfcol = *)
has been called.

Author(s)
Andy Liaw, original; R. Gentleman, M. Maechler, W. Huber, revisions.

See Also
image, hclust
Examples

```r
require(graphics); require(grDevices)
x <- as.matrix(mtcars)
rc <- rainbow(nrow(x), start = 0, end = .3)
cc <- rainbow(ncol(x), start = 0, end = .3)
hv <- heatmap(x, col = cm.colors(256), scale = "column",
             RowSideColors = rc, ColSideColors = cc,
             margins = c(5,10),
             xlab = "specification variables", ylab = "Car Models",
             main = "heatmap(<Mtcars data>, ..., scale = \"column\")")
utils::str(hv) # the two re-ordering index vectors
```

HoltWinters

**Holt-Winters Filtering**

**Description**

Computes Holt-Winters Filtering of a given time series. Unknown parameters are determined by minimizing the squared prediction error.

**Usage**

`HoltWinters(x, alpha = NULL, beta = NULL, gamma = NULL,`
seasonal = c("additive", "multiplicative"),
start.periods = 2, l.start = NULL, b.start = NULL,
s.start = NULL,
optim.start = c(alpha = 0.3, beta = 0.1, gamma = 0.1),
optim.control = list())

Arguments

- **x**
  An object of class `ts`

- **alpha**
  `alpha` parameter of Holt-Winters Filter.

- **beta**
  `beta` parameter of Holt-Winters Filter. If set to `FALSE`, the function will do exponential smoothing.

- **gamma**
  `gamma` parameter used for the seasonal component. If set to `FALSE`, an non-seasonal model is fitted.

- **seasonal**
  Character string to select an “additive” (the default) or “multiplicative” seasonal model. The first few characters are sufficient. (Only takes effect if `gamma` is non-zero).

- **start.periods**
  Start periods used in the autodetection of start values. Must be at least 2.

- **l.start**
  Start value for level (a[0]).

- **b.start**
  Start value for trend (b[0]).

- **s.start**
  Vector of start values for the seasonal component (s[1][0]...s[p][0])

- **optim.start**
  Vector with named components `alpha`, `beta`, and `gamma` containing the starting values for the optimizer. Only the values needed must be specified. Ignored in the one-parameter case.

- **optim.control**
  Optional list with additional control parameters passed to `optim` if this is used. Ignored in the one-parameter case.

Details

The additive Holt-Winters prediction function (for time series with period length p) is

\[ \hat{Y}[t + h] = a[t] + hb[t] + s[t - p + 1 + (h - 1) \mod p], \]

where \( a[t] \), \( b[t] \) and \( s[t] \) are given by

\[
\begin{align*}
    a[t] &= \alpha (Y[t] - s[t - p]) + (1 - \alpha)(a[t - 1] + b[t - 1]) \\
    b[t] &= \beta(a[t] - a[t - 1]) + (1 - \beta)b[t - 1] \\
    s[t] &= \gamma(Y[t] - a[t]) + (1 - \gamma)s[t - p]
\end{align*}
\]

The multiplicative Holt-Winters prediction function (for time series with period length p) is

\[ \hat{Y}[t + h] = (a[t] + hb[t]) \times s[t - p + 1 + (h - 1) \mod p], \]

where \( a[t] \), \( b[t] \) and \( s[t] \) are given by

\[
\begin{align*}
    a[t] &= \alpha (Y[t]/s[t - p]) + (1 - \alpha)(a[t - 1] + b[t - 1]) \\
    b[t] &= \beta(a[t] - a[t - 1]) + (1 - \beta)b[t - 1] \\
    s[t] &= \gamma(Y[t]/a[t]) + (1 - \gamma)s[t - p]
\end{align*}
\]
The data in \( x \) are required to be non-zero for a multiplicative model, but it makes most sense if they are all positive.

The function tries to find the optimal values of \( \alpha \) and/or \( \beta \) and/or \( \gamma \) by minimizing the squared one-step prediction error if they are NULL (the default). `optimize` will be used for the single-parameter case, and `optim` otherwise.

For seasonal models, start values for \( a \), \( b \) and \( s \) are inferred by performing a simple decomposition in trend and seasonal component using moving averages (see function `decompose`) on the first periods (a simple linear regression on the trend component is used for starting level and trend). For level/trend-models (no seasonal component), start values for \( a \) and \( b \) are \( x[2] \) and \( x[2] - x[1] \), respectively. For level-only models (ordinary exponential smoothing), the start value for \( a \) is \( x[1] \).

**Value**

An object of class "HoltWinters", a list with components:

- `fitted`: A multiple time series with one column for the filtered series as well as for the level, trend and seasonal components, estimated contemporaneously (that is at time \( t \) and not at the end of the series).
- `x`: The original series
- `alpha`: alpha used for filtering
- `beta`: beta used for filtering
- `gamma`: gamma used for filtering
- `coefficients`: A vector with named components \( a, b, s1, \ldots, sp \) containing the estimated values for the level, trend and seasonal components
- `seasonal`: The specified seasonal parameter
- `SSE`: The final sum of squared errors achieved in optimizing
- `call`: The call used

**Author(s)**

David Meyer &lt;David.Meyer@wu.ac.at&gt;

**References**


**See Also**

`predict.HoltWinters`, `optim`. 

---

**HoltWinters**

The data in \( x \) are required to be non-zero for a multiplicative model, but it makes most sense if they are all positive.

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- `seasonal`: The specified seasonal parameter
- `SSE`: The final sum of squared errors achieved in optimizing
- `call`: The call used

**Author(s)**

David Meyer &lt;David.Meyer@wu.ac.at&gt;

**References**


**See Also**

`predict.HoltWinters`, `optim`. 

---
Examples

```r
require(graphics)

## Seasonal Holt-Winters
(m <- HoltWinters(co2))
plot(m)
plot(fitted(m))

(m <- HoltWinters(AirPassengers, seasonal = "mult"))
plot(m)

## Non-Seasonal Holt-Winters
x <- uspop + rnorm(uspop, sd = 5)
m <- HoltWinters(x, gamma = FALSE)
plot(m)

## Exponential Smoothing
m2 <- HoltWinters(x, gamma = FALSE, beta = FALSE)
lines(fitted(m2)[,1], col = 3)
```

Hypergeometric

The Hypergeometric Distribution

Description

Density, distribution function, quantile function and random generation for the hypergeometric distribution.

Usage

```r
dhyper(x, m, n, k, log = FALSE)
phyper(q, m, n, k, lower.tail = TRUE, log.p = FALSE)
qhyper(p, m, n, k, lower.tail = TRUE, log.p = FALSE)
rhyper(nn, m, n, k)
```

Arguments

- `x, q`: vector of quantiles representing the number of white balls drawn without replacement from an urn which contains both black and white balls.
- `m`: the number of white balls in the urn.
- `n`: the number of black balls in the urn.
- `k`: the number of balls drawn from the urn, hence must be in \(0, 1, \ldots, m + n\).
- `p`: probability, it must be between 0 and 1.
- `nn`: number of observations. If \(\text{length}(nn) > 1\), the length is taken to be the number required.
- `log, log.p`: logical; if TRUE, probabilities \(p\) are given as \(\log(p)\).
- `lower.tail`: logical; if TRUE (default), probabilities are \(P[X \leq x]\), otherwise, \(P[X > x]\).
Hypergeometric

Details

The hypergeometric distribution is used for sampling without replacement. The density of this distribution with parameters \( m, n \) and \( k \) (named \( Np, N-Np, \) and \( n \), respectively in the reference below, where \( N := m + n \) is also used in other references) is given by

\[
p(x) = \frac{\binom{m}{x} \binom{n}{k-x}}{\binom{m+n}{k}}
\]

for \( x = 0, \ldots, k \).

Note that \( p(x) \) is non-zero only for \( \max(0, k-n) \leq x \leq \min(k,m) \).

With \( p := m/(m+n) \) (hence \( Np = N \times p \) in the reference’s notation), the first two moments are mean

\[
E[X] = \mu = kp
\]

and variance

\[
Var(X) = kp(1-p)\frac{m+n-k}{m+n-1},
\]

which shows the closeness to the Binomial\((k,p)\) (where the hypergeometric has smaller variance unless \( k = 1 \)).

The quantile is defined as the smallest value \( x \) such that \( F(x) \geq p \), where \( F \) is the distribution function.

In \texttt{rhyper()}, if one of \( m, n, k \) exceeds \texttt{Machine$integer.max}, currently the equivalent of \texttt{qhyper(runif(nn), m,n,k)} \) is used which is comparably slow while instead a binomial approximation may be considerably more efficient.

Value

dhyper gives the density, phyper gives the distribution function, qhyper gives the quantile function, and rhyper generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

The length of the result is determined by \( n \) for \texttt{rhyper}, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than \( n \) are recycled to the length of the result. Only the first elements of the logical arguments are used.

Source

dhyper computes via binomial probabilities, using code contributed by Catherine Loader (see \texttt{dbinom}).

phyper is based on calculating \texttt{dhyper} and \texttt{phyper(...)}/\texttt{dhyper(...)} (as a summation), based on ideas of Ian Smith and Morten Welinder.

qhyper is based on inversion (of an earlier \texttt{phyper()} algorithm).

rhyper is based on a corrected version of


References

identify.hclust

See Also

Distributions for other standard distributions.

Examples

```r
m <- 10; n <- 7; k <- 8
x <- 0:(k+1)
rbind(phyper(x, m, n, k), dhyper(x, m, n, k))
all(phyper(x, m, n, k) == cumsum(dhyper(x, m, n, k)))  # FALSE
## but error is very small:
signif(phyper(x, m, n, k) - cumsum(dhyper(x, m, n, k)), digits = 3)
```

 identification.hclust

Identify Clusters in a Dendrogram

Description

identify.hclust reads the position of the graphics pointer when the (first) mouse button is pressed. It then cuts the tree at the vertical position of the pointer and highlights the cluster containing the horizontal position of the pointer. Optionally a function is applied to the index of data points contained in the cluster.

Usage

```r
## S3 method for class 'hclust'
identify(x, FUN = NULL, N = 20, MAXCLUSTER = 20, DEV.FUN = NULL, ...
```

Arguments

- `x`: an object of the type produced by `hclust`.
- `FUN`: (optional) function to be applied to the index numbers of the data points in a cluster (see ‘Details’ below).
- `N`: the maximum number of clusters to be identified.
- `MAXCLUSTER`: the maximum number of clusters that can be produced by a cut (limits the effective vertical range of the pointer).
- `DEV.FUN`: (optional) integer scalar. If specified, the corresponding graphics device is made active before `FUN` is applied.
- `...`: further arguments to `FUN`.

Details

By default clusters can be identified using the mouse and an **invisible** list of indices of the respective data points is returned.

If `FUN` is not `NULL`, then the index vector of data points is passed to this function as first argument, see the examples below. The active graphics device for `FUN` can be specified using `DEV.FUN`.

The identification process is terminated by pressing any mouse button other than the first, see also `identify`.
influence.measures
Regression Deletion Diagnostics

Description
This suite of functions can be used to compute some of the regression (leave-one-out deletion) diagnostics for linear and generalized linear models discussed in Belsley, Kuh and Welsch (1980), Cook and Weisberg (1982), etc.

Usage
influence.measures(model, infl = influence(model))

rstandard(model, ...) 
## S3 method for class 'lm'

rstandard(model, infl = lm.influence(model, do.coef = FALSE),
          sd = sqrt(deviance(model)/df.residual(model)),
          type = c("sd.1", "predictive"), ...)
## S3 method for class 'glm'
rstandard(model, infl = influence(model, do.coef = FALSE),
          type = c("deviance", "pearson"), ...)
rstudent(model, ...)  
## S3 method for class 'lm'
rstudent(model, infl = lm.influence(model, do.coef = FALSE),  
       res = infl$wt.res, ...)
## S3 method for class 'glm'
rstudent(model, infl = influence(model, do.coef = FALSE), ...)

dffits(model, infl = , res = )
dfbeta(model, ...)
## S3 method for class 'lm'
dfbeta(model, infl = lm.influence(model, do.coef = TRUE), ...)
dfbetas(model, ...)
## S3 method for class 'lm'
dfbetas(model, infl = lm.influence(model, do.coef = TRUE), ...)
covratio(model, infl = lm.influence(model, do.coef = FALSE),  
         res = weighted.residuals(model))

cooks.distance(model, ...)
## S3 method for class 'lm'
cooks.distance(model, infl = lm.influence(model, do.coef = FALSE),  
               res = weighted.residuals(model),  
               sd = sqrt(deviance(model)/df.residual(model)),  
               hat = infl$hat, ...)
## S3 method for class 'glm'
cooks.distance(model, infl = influence(model, do.coef = FALSE),  
               res = infl$pear.res,  
               dispersion = summary(model)$dispersion,  
               hat = infl$hat, ...)

hatvalues(model, ...)
## S3 method for class 'lm'
hatvalues(model, infl = lm.influence(model, do.coef = FALSE), ...)

hat(x, intercept = TRUE)

Arguments

model  an R object, typically returned by lm or glm.
infl influence structure as returned by lm.influence or influence (the latter only  
        for the glm method of rstudent and cooks.distance).
res (possibly weighted) residuals, with proper default.
sd standard deviation to use, see default.
dispersion dispersion (for glm objects) to use, see default.
hat hat values $H_{ii}$, see default.
type type of residuals for rstandard, with different options and meanings for lm and  
       glm. Can be abbreviated.
x the X or design matrix.
The primary high-level function is `influence.measures` which produces a class "infl" object tabular display showing the DFBETAS for each model variable, DFFITS, covariance ratios, Cook’s distances and the diagonal elements of the hat matrix. Cases which are influential with respect to any of these measures are marked with an asterisk.

The functions `dfbetas`, `dffits`, `covratio` and `cooks.distance` provide direct access to the corresponding diagnostic quantities. Functions `rstandard` and `rstudent` give the standardized and Studentized residuals respectively. (These re-normalize the residuals to have unit variance, using an overall and leave-one-out measure of the error variance respectively.)

Note that for multivariate `lm()` models (of class "mlm"), these functions return 3d arrays instead of matrices, or matrices instead of vectors.

Values for generalized linear models are approximations, as described in Williams (1987) (except that Cook’s distances are scaled as $F$ rather than as chi-square values). The approximations can be poor when some cases have large influence.

The optional `infl`, `res` and `sd` arguments are there to encourage the use of these direct access functions, in situations where, e.g., the underlying basic influence measures (from `lm.influence` or the generic `influence`) are already available.

Note that cases with `weights == 0` are dropped from all these functions, but that if a linear model has been fitted with `na.action = na.exclude`, suitable values are filled in for the cases excluded during fitting.

For linear models, `rstandard(*, type = "predictive")` provides leave-one-out cross validation residuals, and the “PRESS” statistic (PREdictive Sum of Squares, the same as the CV score) of model model is

\[
\text{PRESS} \leftarrow \text{sum}(rstandard(model, type="pred")^2)
\]

The function `hat()` exists mainly for S (version 2) compatibility; we recommend using `hatvalues()` instead.

Note

For `hatvalues`, `dfbeta`, and `dfbetas`, the method for linear models also works for generalized linear models.

Author(s)

Several R core team members and John Fox, originally in his ‘car’ package.

References


influence.measures


See Also

`influence` (containing `lm.influence`).

‘plotmath’ for the use of hat in plot annotation.

Examples

require(graphics)

## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)

inflm.SR <- influence.measures(lm.SR)
which(apply(inflm.SR$is.inf, 1, any))
# which observations 'are' influential
summary(inflm.SR) # only these
inflm.SR # all
plot(rstudent(lm.SR) ~ hatvalues(lm.SR)) # recommended by some
plot(lm.SR, which = 5) # an enhanced version of that via plot(<lm>)

## The 'infl' argument is not needed, but avoids recomputation:
rs <- rstandard(lm.SR)
iflSr <- influence(lm.SR)
all.equal(rs, rstandard(lm.SR, infl = iflSr), tolerance = 1e-10)
## to "see" the larger values:
1000 * round(dfbetas(lm.SR, infl = iflSr), 3)
cat("PRESS : "); (PRESS <- sum( rstandard(lm.SR, type = "predictive")^2 ))
stopifnot(all.equal(PRESS, sum( (residuals(lm.SR) / (1 - iflSr$hat))^2 )))

## Show that "PRE-residuals" == L.O.O. Crossvalidation (CV) errors:
X <- model.matrix(lm.SR)
y <- model.response(model.frame(lm.SR))
## Leave-one-out CV least-squares prediction errors (relatively fast)
rCV <- vapply(seq_len(nrow(X)), function(i)
  y[i] - X[i,] %*% .lm.fit(X[-i,], y[-i])$coefficients,
  numeric(1))
## are the same as the *faster* rstandard(*, "pred") :
stopifnot(all.equal(rCV, unname(rstandard(lm.SR, type = "predictive"))))

## Huber's data [Atkinson 1985]
X <- c(-4:0, 10)
yh <- c(2.48, .73, -.04, -1.44, -1.32, 0)
lmH <- lm(yh ~ X)
summary(lmH)
im <- influence.measures(lmH)
im
is.inf <- apply(im$iis.inf, 1, any)
plot(xh,yh, main = "Huber's data: L.S. line and influential obs.")
abline(lmH); points(xh[is.inf], yh[is.inf], pch = 20, col = 2)
## Integration of One-Dimensional Functions

### Description
Adaptive quadrature of functions of one variable over a finite or infinite interval.

### Usage
```
integrate(f, lower, upper, ..., subdivisions = 100L,
  rel.tol = .Machine$double.eps^0.25, abs.tol = rel.tol,
  stop.on.error = TRUE, keep.xy = FALSE, aux = NULL)
```

### Arguments
- **f**: an R function taking a numeric first argument and returning a numeric vector of the same length. Returning a non-finite element will generate an error.
- **lower, upper**: the limits of integration. Can be infinite.
- **...**: additional arguments to be passed to f.
- **subdivisions**: the maximum number of subintervals.
- **rel.tol**: relative accuracy requested.
- **abs.tol**: absolute accuracy requested.
- **stop.on.error**: logical. If true (the default) an error stops the function. If false some errors will give a result with a warning in the message component.
- **keep.xy**: unused. For compatibility with S.
- **aux**: unused. For compatibility with S.

### Details
Note that arguments after ... must be matched exactly.

If one or both limits are infinite, the infinite range is mapped onto a finite interval.

For a finite interval, globally adaptive interval subdivision is used in connection with extrapolation by Wynn’s Epsilon algorithm, with the basic step being Gauss–Kronrod quadrature.

**rel.tol** cannot be less than \( \max(50 \times .Machine$double.eps, 0.5 \times 10^{-28}) \) if **abs.tol** <= 0.

Note that the comments in the C source code in `src/appl/integrate.c` give more details, particularly about reasons for failure (internal error code **ier** >= 1).

In **R** versions \( \leq 3.2.x \), the first entries of **lower** and **upper** were used whereas an error is signalled now if they are not of length one.
Value

A list of class "integrate" with components

- **value**: the final estimate of the integral.
- **abs.error**: estimate of the modulus of the absolute error.
- **subdivisions**: the number of subintervals produced in the subdivision process.
- **message**: "OK" or a character string giving the error message.
- **call**: the matched call.

Note

Like all numerical integration routines, these evaluate the function on a finite set of points. If the function is approximately constant (in particular, zero) over nearly all its range it is possible that the result and error estimate may be seriously wrong.

When integrating over infinite intervals do so explicitly, rather than just using a large number as the endpoint. This increases the chance of a correct answer – any function whose integral over an infinite interval is finite must be near zero for most of that interval.

For values at a finite set of points to be a fair reflection of the behaviour of the function elsewhere, the function needs to be well-behaved, for example differentiable except perhaps for a small number of jumps or integrable singularities.

f must accept a vector of inputs and produce a vector of function evaluations at those points. The Vectorize function may be helpful to convert f to this form.

Source

Based on QUADPACK routines dqags and dqagi by R. Piessens and E. deDoncker–Kapenga, available from Netlib.

References


Examples

```r
integrate(dnorm, -1.96, 1.96)
integrate(dnorm, -Inf, Inf)

## a slowly-convergent integral
integrand <- function(x) {1/((x+1)*sqrt(x))}
integrate(integrand, lower = 0, upper = Inf)

## don’t do this if you really want the integral from 0 to Inf
integrate(integrand, lower = 0, upper = 10)
integrate(integrand, lower = 0, upper = 100000)
integrate(integrand, lower = 0, upper = 1000000, stop.on.error = FALSE)

## some functions do not handle vector input properly
f <- function(x) 2.0
try(integrate(f, 0, 1))
integrate(Vectorize(f), 0, 1) ## correct
integrate(function(x) rep(2.0, length(x)), 0, 1) ## correct
```
interaction.plot

Two-way Interaction Plot

Description

Plots the mean (or other summary) of the response for two-way combinations of factors, thereby illustrating possible interactions.

Usage

interaction.plot(x.factor, trace.factor, response, fun = mean,
                 type = c("l", "p", "b", "o", "c"), legend = TRUE,
                 trace.label = deparse1(substitute(trace.factor)),
                 fixed = FALSE,
                 xlab = deparse1(substitute(x.factor)),
                 ylab = ylabel,
                 ylim = range(cells, na.rm = TRUE),
                 lty = nc:1, col = 1, pch = c(1:9, 0, letters),
                 xpd = NULL, leg.bg = par("bg"), leg.bty = "n",
                 xtick = FALSE, xaxt = par("xaxt"), axes = TRUE,
                 ...)
interaction.plot

col  the color to be used for plotting.
pch  a vector of plotting symbols or characters, with sensible default.
xpd  determines clipping behaviour for the legend used, see par(xpd). Per default, the legend is not clipped at the figure border.
leg.bg, leg.bty  arguments passed to legend().
xtick  logical. Should tick marks be used on the x axis?
xaxt, axes, ... graphics parameters to be passed to the plotting routines.

Details

By default the levels of x.factor are plotted on the x axis in their given order, with extra space on the right for the legend (if specified). If x.factor is an ordered factor and the levels are numeric, these numeric values are used for the x axis.

The response and hence its summary can contain missing values. If so, the missing values and the line segments joining them are omitted from the plot (and this can be somewhat disconcerting). The graphics parameters xlab, ylab, ylim, lty, col and pch are given suitable defaults (and xlim and xaxs are set and cannot be overridden). The defaults are to cycle through the line types, use the foreground colour, and to use the symbols 1:9, 0, and the small letters to plot the traces.

Note

Some of the argument names and the precise behaviour are chosen for S-compatibility.

References


Examples

require(graphics)

with(ToothGrowth, {
  interaction.plot(dose, supp, len, fixed = TRUE)
  dose <- ordered(dose)
  interaction.plot(dose, supp, len, fixed = TRUE,
      col = 2:3, leg.bty = "o", xtick = TRUE)
  interaction.plot(dose, supp, len, fixed = TRUE, col = 2:3, type = "p")
})

with(OrchardSprays, {
  interaction.plot(treatment, rowpos, decrease)
  interaction.plot(rowpos, treatment, decrease, cex.axis = 0.8)
  ## order the rows by their mean effect
  rowpos <- factor(rowpos,
      levels = sort.list(tapply(decrease, rowpos, mean)))
  interaction.plot(rowpos, treatment, decrease, col = 2:9, lty = 1)
})
The Interquartile Range

**Description**
computes interquartile range of the \( x \) values.

**Usage**
\[
\text{IQR}(x, \text{na.rm} = \text{FALSE}, \text{type} = 7)
\]

**Arguments**
- \( x \) a numeric vector.
- \( \text{na.rm} \) logical. Should missing values be removed?
- \( \text{type} \) an integer selecting one of the many quantile algorithms, see `quantile`.

**Details**
Note that this function computes the quartiles using the `quantile` function rather than following Tukey’s recommendations, i.e., \( \text{IQR}(x) = \text{quantile}(x, 3/4) - \text{quantile}(x, 1/4) \).

For normally \( N(m, 1) \) distributed \( X \), the expected value of \( \text{IQR}(X) \) is \( 2 \times \text{qnorm}(3/4) = 1.3490 \), i.e., for a normal-consistent estimate of the standard deviation, use \( \text{IQR}(x) / 1.349 \).

**References**

**See Also**
- `fivenum`, `mad` which is more robust, `range`, `quantile`.

**Examples**
\[
\text{IQR(rivers)}
\]
is.empty.model  Test if a Model’s Formula is Empty

Description

R’s formula notation allows models with no intercept and no predictors. These require special handling internally. is.empty.model() checks whether an object describes an empty model.

Usage

is.empty.model(x)

Arguments

x  A terms object or an object with a terms method.

Value

TRUE if the model is empty

See Also

lm, glm

Examples

y <- rnorm(20)
is.empty.model(y ~ 0)
is.empty.model(y ~ -1)
is.empty.model(lm(y ~ 0))

isoreg  Isotonic / Monotone Regression

Description

Compute the isotonic (monotonely increasing nonparametric) least squares regression which is piecewise constant.

Usage

isoreg(x, y = NULL)

Arguments

x, y  coordinate vectors of the regression points. Alternatively a single plotting structure can be specified: see xy.coords. The y values, and even sum(y) must be finite, currently.
Details
The algorithm determines the convex minorant \( m(x) \) of the cumulative data (i.e., \( \text{cumsum}(y) \)) which is piecewise linear and the result is \( m'(x) \), a step function with level changes at locations where the convex \( m(x) \) touches the cumulative data polygon and changes slope. 
\texttt{as.stepfun()} returns a \texttt{stepfun} object which can be more parsimonious.

Value
\texttt{isoreg()} returns an object of class \texttt{isoreg} which is basically a list with components
- \texttt{x} original (constructed) abscissa values \( x \).
- \texttt{y} corresponding \( y \) values.
- \texttt{yf} fitted values corresponding to ordered \( x \) values.
- \texttt{yc} cumulative \( y \) values corresponding to ordered \( x \) values.
- \texttt{iKnots} integer vector giving indices where the fitted curve jumps, i.e., where the convex minorant has kinks.
- \texttt{isOrd} logical indicating if original \( x \) values were ordered increasingly already.
- \texttt{ord} if(!isOrd): integer permutation \texttt{order(x)} of original \( x \).
- \texttt{call} the \texttt{call} to \texttt{isoreg()} used.

Note
The code should be improved to accept \texttt{weights} additionally and solve the corresponding weighted least squares problem.
‘Patches are welcome!’

References

See Also
the plotting method \texttt{plot.isoreg} with more examples; \texttt{isoMDS()} from the \texttt{MASS} package internally uses isotonic regression.

Examples
\begin{verbatim}
require(graphics)

(ir <- isoreg(c(1,0,4,3,3,5,4,2,0)))
plot(ir, plot.type = "row")

(ir3 <- isoreg(y3 <- c(1,0,4,3,3,5,4,2,3))) # last "3", not "0"
(fi3 <- as.stepfun(ir3))

(ir4 <- isoreg(1:10, y4 <- c(5, 9, 1:2, 5:8, 3, 8)))
cat(sprintf("R^2 = %5.2f\n",
  1 - sum(residuals(ir4)^2) / ((10-1)*var(y4))))

## If you are interested in the knots alone:
\end{verbatim}
## Example of unordered x[] with ties:
```r
x <- sample((0:30)/8)
y <- exp(x)
x. <- round(x) # ties!
plot(m <- isoreg(x., y))
stopifnot(all.equal(with(m, yf[iKnots]),
as.vector(tapply(y, x., mean))))
```

---

**KalmanLike**

**Kalman Filtering**

### Description

Use Kalman Filtering to find the (Gaussian) log-likelihood, or for forecasting or smoothing.

### Usage

```r
KalmanLike(y, mod, nit = 0L, update = FALSE)
KalmanRun(y, mod, nit = 0L, update = FALSE)
KalmanSmooth(y, mod, nit = 0L)
KalmanForecast(n.ahead = 10L, mod, update = FALSE)
makeARIMA(phi, theta, Delta, kappa = 1e6,
          SSinit = c("Gardner1980", "Rossignol2011"),
          tol = .Machine$double.eps)
```

### Arguments

- **y**: a univariate time series.
- **mod**: a list describing the state-space model: see ‘Details’.
- **nit**: the time at which the initialization is computed. nit = 0L implies that the initialization is for a one-step prediction, so \(P_n\) should not be computed at the first step.
- **update**: if TRUE the update mod object will be returned as attribute "mod" of the result.
- **n.ahead**: the number of steps ahead for which prediction is required.
- **phi**, **theta**: numeric vectors of length \(\geq 0\) giving AR and MA parameters.
- **Delta**: vector of differencing coefficients, so an ARMA model is fitted to \(y[t] - Delta[1]y[t-1] - \ldots\).
- **kappa**: the prior variance (as a multiple of the innovations variance) for the past observations in a differenced model.
- **SSinit**: a string specifying the algorithm to compute the \(P_n\) part of the state-space initialization; see ‘Details’.
- **tol**: tolerance eventually passed to `solve.default` when SSinit = "Rossignol2011".
Details

These functions work with a general univariate state-space model with state vector \( a \), transitions \( a \leftarrow T a + R e \), \( e \sim \mathcal{N}(0, \kappa Q) \) and observation equation \( y = Z a + \eta a \), \( \eta \sim \mathcal{N}(0, \kappa h) \).

The likelihood is a profile likelihood after estimation of \( \kappa \).

The model is specified as a list with at least components

- \( T \) the transition matrix
- \( Z \) the observation coefficients
- \( h \) the observation variance
- \( V \) ‘RQR’
- \( a \) the current state estimate
- \( P \) the current estimate of the state uncertainty matrix \( Q \)
- \( P_n \) the estimate at time \( t - 1 \) of the state uncertainty matrix \( Q \) (not updated by KalmanForecast).

KalmanSmooth is the workhorse function for \texttt{tsSmooth}.

\texttt{makeARIMA} constructs the state-space model for an ARIMA model, see also \texttt{arima}.

The state-space initialization has used Gardner \textit{et al}’s method (\texttt{SSinit = "Gardner1980"}), as only method for years. However, that suffers sometimes from deficiencies when close to non-stationarity. For this reason, it may be replaced as default in the future and only kept for reproducibility reasons. Explicit specification of \texttt{SSinit} is therefore recommended, notably also in \texttt{arima()}. The "Rossignol2011" method has been proposed and partly documented by Raphael Rossignol, Univ. Grenoble, on 2011-09-20 (see PR#14682, below), and later been ported to C by Matwey V. Kornilov. It computes the covariance matrix of \( (X_{t-1}, ..., X_{t-p}, Z_t, ..., Z_{t-q}) \) by the method of difference equations (page 93 of Brockwell and Davis), apparently suggested by a referee of Gardner \textit{et al} (see p.314 of their paper).

Value

For \texttt{KalmanLike}, a list with components \texttt{Lik} (the log-likelihood less some constants) and \texttt{s2}, the estimate of \( \kappa \).

For \texttt{KalmanRun}, a list with components \texttt{values}, a vector of length 2 giving the output of \texttt{KalmanLike}, \texttt{resid} (the residuals) and \texttt{states}, the contemporaneous state estimates, a matrix with one row for each observation time.

For \texttt{KalmanSmooth}, a list with two components. Component \texttt{smooth} is a \( n \) by \( p \) matrix of state estimates based on all the observations, with one row for each time. Component \texttt{var} is a \( n \) by \( p \) by \( p \) array of variance matrices.

For \texttt{KalmanForecast}, a list with components \texttt{pred}, the predictions, and \texttt{var}, the unscaled variances of the prediction errors (to be multiplied by \texttt{s2}).

For \texttt{makeARIMA}, a model list including components for its arguments.

Warning

These functions are designed to be called from other functions which check the validity of the arguments passed, so very little checking is done.
References


See Also

*arima, StructTS, tsSmooth.*

Examples

```r
## an ARIMA fit
fit3 <- arima(presidents, c(3, 0, 0))
predict(fit3, 12)
## reconstruct this
pr <- KalmanForecast(12, fit3$model)
pr$pred + fit3$coef[4]
## and now do it year by year
mod <- fit3$model
for(y in 1:3) {
  pr <- KalmanForecast(4, mod, TRUE)
  print(list(pred = pr$pred + fit3$coef["intercept"],
            se = sqrt(pr$var * fit3$sigma2)))
  mod <- attr(pr, "mod")
}
```

---

**kernapply**

*Apply Smoothing Kernel*

**Description**

kernapply computes the convolution between an input sequence and a specific kernel.

**Usage**

```r
kernapply(x, ...)
```

## Default S3 method:
kernapply(x, k, circular = FALSE, ...)

## S3 method for class 'ts'
kernapply(x, k, circular = FALSE, ...)

## S3 method for class 'vector'
kernapply(x, k, circular = FALSE, ...)

## S3 method for class 'tskernel'
kernapply(x, k, ...)

## S3 method for class 'tskernel'
kernapply(x, k, ...)

```
**Arguments**

- **x**: an input vector, matrix, time series or kernel to be smoothed.
- **k**: smoothing "tskernel" object.
- **circular**: a logical indicating whether the input sequence to be smoothed is treated as circular, i.e., periodic.
- `...`: arguments passed to or from other methods.

**Value**

A smoothed version of the input sequence.

**Note**

This uses `fft` to perform the convolution, so is fastest when `NROW(x)` is a power of 2 or some other highly composite integer.

**Author(s)**

A. Trapletti

**See Also**

- `kernel`, `convolve`, `filter`, `spectrum`

**Examples**

```r
## see 'kernel' for examples
```

---

**Description**

The "tskernel" class is designed to represent discrete symmetric normalized smoothing kernels. These kernels can be used to smooth vectors, matrices, or time series objects. There are `print`, `plot` and `[` methods for these kernel objects.

**Usage**

```r
kernel(coef, m = 2, r, name)
df.kernel(k)
bandwidth.kernel(k)
is.tskernel(k)
```

```r
## S3 method for class 'tskernel'
plot(x, type = "h", xlab = "k", ylab = "W[k]", main = attr(x,"name"), ...)
```
Arguments

- **coef**: the upper half of the smoothing kernel coefficients (including coefficient zero) or the name of a kernel (currently "daniell", "dirichlet", "fejer" or "modified.daniell").
- **m**: the kernel dimension(s) if coef is a name. When m has length larger than one, it means the convolution of kernels of dimension m[j], for j in 1:length(m). Currently this is supported only for the named "*daniell" kernels.
- **name**: the name the kernel will be called.
- **r**: the kernel order for a Fejer kernel.
- **k, x**: a "tskernel" object.
- **type, xlab, ylab, main, ...**: arguments passed to `plot.default`.

Details

`kernel` is used to construct a general kernel or named specific kernels. The modified Daniell kernel halves the end coefficients (as used by S-PLUS).

The `[method allows natural indexing of kernel objects with indices in (-m) : m. The normalization is such that for k <- kernel(*), sum(k[-k$m : k$m]) is one.

`df.kernel` returns the 'equivalent degrees of freedom' of a smoothing kernel as defined in Brockwell and Davis (1991), page 362, and `bandwidth.kernel` returns the equivalent bandwidth as defined in Bloomfield (1976), p. 201, with a continuity correction.

Value

`kernel()` returns an object of class "tskernel" which is basically a list with the two components `coef` and the kernel dimension `m`. An additional attribute is "name".

Author(s)

A. Trapletti; modifications by B.D. Ripley

References


See Also

`kernapply`

Examples

```r
require(graphics)

## Demonstrate a simple trading strategy for the financial time series German stock index DAX.
x <- EuStockMarkets[,1]
k1 <- kernel("daniell", 50) # a long moving average
k2 <- kernel("daniell", 10) # and a short one
```
plot(k1)
plot(k2)
x1 <- kernapply(x, k1)
x2 <- kernapply(x, k2)
plot(x)
lines(x1, col = "red")  # go long if the short crosses the long upwards
lines(x2, col = "green")  # and go short otherwise

## More interesting kernels
kd <- kernel("daniell", c(3, 3))
kd # note the unusual indexing
kd[-2:2]
plot(kernel("fejer", 100, r = 6))
plot(kernel("modified.daniell", c(7,5,3)))

# Reproduce example 10.4.3 from Brockwell and Davis (1991)
spectrum(sunspot.year, kernel = kernel("daniell", c(11,7,3)), log = "no")

---

**kmeans**

*K-Means Clustering*

**Description**

Perform k-means clustering on a data matrix.

**Usage**

```r
kmeans(x, centers, iter.max = 10, nstart = 1,
algorithm = c("Hartigan-Wong", "Lloyd", "Forgy",
"MacQueen"), trace = FALSE)
```

## S3 method for class 'kmeans'

```r
fitted(object, method = c("centers", "classes"), ...)
```

**Arguments**

- **x** numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns).
- **centers** either the number of clusters, say \( k \), or a set of initial (distinct) cluster centres. If a number, a random set of (distinct) rows in \( x \) is chosen as the initial centres.
- **iter.max** the maximum number of iterations allowed.
- **nstart** if centers is a number, how many random sets should be chosen?
- **algorithm** character: may be abbreviated. Note that "Lloyd" and "Forgy" are alternative names for one algorithm.
- **object** an R object of class "kmeans", typically the result ob of ob <- kmeans(..).
- **method** character: may be abbreviated. "centers" causes fitted to return cluster centres (one for each input point) and "classes" causes fitted to return a vector of class assignments.
- **trace** logical or integer number, currently only used in the default method ("Hartigan-Wong"): if positive (or true), tracing information on the progress of the algorithm is produced. Higher values may produce more tracing information.
- **...** not used.
Details

The data given by \( x \) are clustered by the \( k \)-means method, which aims to partition the points into \( k \) groups such that the sum of squares from points to the assigned cluster centres is minimized. At the minimum, all cluster centres are at the mean of their Voronoi sets (the set of data points which are nearest to the cluster centre).

The algorithm of Hartigan and Wong (1979) is used by default. Note that some authors use \( k \)-means to refer to a specific algorithm rather than the general method: most commonly the algorithm given by MacQueen (1967) but sometimes that given by Lloyd (1957) andForgy (1965). The Hartigan–Wong algorithm generally does a better job than either of those, but trying several random starts (\( n_{\text{start}} > 1 \)) is often recommended. In rare cases, when some of the points (rows of \( x \)) are extremely close, the algorithm may not converge in the “Quick-Transfer” stage, signalling a warning (and returning \( \text{ifault} = 4 \)). Slight rounding of the data may be advisable in that case.

For ease of programmatic exploration, \( k = 1 \) is allowed, notably returning the center and \( \text{withinss} \).

Except for the Lloyd–Forgy method, \( k \) clusters will always be returned if a number is specified. If an initial matrix of centres is supplied, it is possible that no point will be closest to one or more centres, which is currently an error for the Hartigan–Wong method.

Value

\( \text{kmeans} \) returns an object of class "kmeans" which has a print and a fitted method. It is a list with at least the following components:

- \( \text{cluster} \): A vector of integers (from 1:\( k \)) indicating the cluster to which each point is allocated.
- \( \text{centers} \): A matrix of cluster centres.
- \( \text{totss} \): The total sum of squares.
- \( \text{withinss} \): Vector of within-cluster sum of squares, one component per cluster.
- \( \text{tot.withinss} \): Total within-cluster sum of squares, i.e. \( \text{sum(withinss)} \).
- \( \text{betweenss} \): The between-cluster sum of squares, i.e. \( \text{totss-tot.withinss} \).
- \( \text{size} \): The number of points in each cluster.
- \( \text{iter} \): The number of (outer) iterations.
- \( \text{ifault} \): Integer: indicator of a possible algorithm problem – for experts.

Note

The clusters are numbered in the returned object, but they are a set and no ordering is implied. (Their apparent ordering may differ by platform.)

References


Examples

```r
require(graphics)

# a 2-dimensional example
x <- rbind(matrix(rnorm(100, sd = 0.3), ncol = 2),
          matrix(rnorm(100, mean = 1, sd = 0.3), ncol = 2))
colnames(x) <- c("x", "y")
(cl <- kmeans(x, 2))
plot(x, col = cl$cluster)
points(cl$centers, col = 1:2, pch = 8, cex = 2)

# sum of squares
ss <- function(x) sum(scale(x, scale = FALSE)^2)

## cluster centers "fitted" to each obs.:
fitted.x <- fitted(cl); head(fitted.x)
resid.x <- x - fitted(cl)

## Equalities : ----------------------------------
cbind(cl[c("betweens", "tot.withinss", "totss")], # the same two columns
c(ss(fitted.x), ss(resid.x), ss(x))
stopifnot(all.equal(cl$totss, ss(x)),
          all.equal(cl$tot.withinss, ss(resid.x)),
          ## these three are the same:
          all.equal(cl$betweens, ss(fitted.x)),
          all.equal(cl$betweens, cl$totss - cl$tot.withinss),
          ## and hence also
          all.equal(ss(x), ss(fitted.x) + ss(resid.x))
)

kmeans(x,1)$withinss # trivial one-cluster, (its W.SS == ss(x))

## random starts do help here with too many clusters
## (and are often recommended anyway!):
## The ordering of the clusters may be platform-dependent.
## IGNORE_RDIFF_BEGIN
(cl <- kmeans(x, 5, nstart = 25))
## IGNORE_RDIFF_END
plot(x, col = cl$cluster)
points(cl$centers, col = 1:5, pch = 8)
```

---

**kruskal.test**  

*Kruskal-Wallis Rank Sum Test*

**Description**

Performs a Kruskal-Wallis rank sum test.

**Usage**

```r
kruskal.test(x, ...)
```

## Default S3 method:
```
kruskal.test(x, g, ...)
```
kruskal.test

## S3 method for class 'formula'
kruskal.test(formula, data, subset, na.action, ...)

Arguments

x a numeric vector of data values, or a list of numeric data vectors. Non-numeric elements of a list will be coerced, with a warning.
g a vector or factor object giving the group for the corresponding elements of x. Ignored with a warning if x is a list.
formula a formula of the form response ~ group where response gives the data values and group a vector or factor of the corresponding groups.
data an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset an optional vector specifying a subset of observations to be used.
na.action a function which indicates what should happen when the data contain NAs. Defaults togetOption("na.action").
... further arguments to be passed to or from methods.

Details

kruskal.test performs a Kruskal-Wallis rank sum test of the null that the location parameters of the distribution of x are the same in each group (sample). The alternative is that they differ in at least one.

If x is a list, its elements are taken as the samples to be compared, and hence have to be numeric data vectors. In this case, g is ignored, and one can simply use kruskal.test(x) to perform the test. If the samples are not yet contained in a list, use kruskal.test(list(x, ...)).

Otherwise, x must be a numeric data vector, and g must be a vector or factor object of the same length as x giving the group for the corresponding elements of x.

Value

A list with class "htest" containing the following components:

statistic the Kruskal-Wallis rank sum statistic.
parameter the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value the p-value of the test.
method the character string "Kruskal-Wallis rank sum test".
data.name a character string giving the names of the data.

References

See Also

The Wilcoxon rank sum test (**wilcox.test**) as the special case for two samples; **lm** together with **anova** for performing one-way location analysis under normality assumptions; with Student’s t test (**t.test**) as the special case for two samples. **wilcox.test** in package **coin** for exact, asymptotic and Monte Carlo conditional p-values, including in the presence of ties.

Examples

```r
## Hollander & Wolfe (1973), 116.
## Mucociliary efficiency from the rate of removal of dust in normal
## subjects, subjects with obstructive airway disease, and subjects
## with asbestosis.
x <- c(2.9, 3.0, 2.5, 2.6, 3.2) # normal subjects
y <- c(3.8, 2.7, 4.0, 2.4) # with obstructive airway disease
z <- c(2.8, 3.4, 3.7, 2.2, 2.0) # with asbestosis
kruskal.test(list(x, y, z))
## Equivalently,
x <- c(x, y, z)
g <- factor(rep(1:3, c(5, 4, 5)),
labels = c("Normal subjects",
"Subjects with obstructive airway disease",
"Subjects with asbestosis"))
kruskal.test(x, g)
## Formula interface.
require(graphics)
boxplot(Ozone ~ Month, data = airquality)
kruskal.test(Ozone ~ Month, data = airquality)
```

ks.test

Kolmogorov-Smirnov Tests

Description

Perform a one- or two-sample Kolmogorov-Smirnov test.

Usage

```r
ks.test(x, ...)  
## Default S3 method:
ks.test(x, y, ...,
alternative = c("two.sided", "less", "greater"),
exact = NULL, simulate.p.value = FALSE, B = 2000)
## S3 method for class 'formula'
ks.test(formula, data, subset, na.action, ...)
```

Arguments

- **x**
  - a numeric vector of data values.
ks.test

y
   either a numeric vector of data values, or a character string naming a cumulative
distribution function or an actual cumulative distribution function such as pnorm.
Only continuous CDFs are valid.

... for the default method, parameters of the distribution specified (as a character
string) by y. Otherwise, further arguments to be passed to or from methods.

alternative indicates the alternative hypothesis and must be one of "two.sided" (default),
"less", or "greater". You can specify just the initial letter of the value, but
the argument name must be given in full. See 'Details' for the meanings of the
possible values.

exact NULL or a logical indicating whether an exact p-value should be computed. See
'Details' for the meaning of NULL.

simulate.p.value a logical indicating whether to compute p-values by Monte Carlo simulation.

B an integer specifying the number of replicates used in the Monte Carlo test.

formula a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data
values and rhs either 1 for a one-sample test or a factor with two levels giving
the corresponding groups for a two-sample test.

data an optional matrix or data frame (or similar: see model.frame) containing
the variables in the formula formula. By default the variables are taken from
environment(formula).

subset an optional vector specifying a subset of observations to be used.

na.action a function which indicates what should happen when the data contain NAs. De-
faults togetOption("na.action").

Details

If y is numeric, a two-sample (Smirnov) test of the null hypothesis that x and y were drawn from
the same continuous distribution is performed.

Alternatively, y can be a character string naming a continuous (cumulative) distribution function,
or such a function. In this case, a one-sample (Kolmogorov) test is carried out of the null that the
distribution function which generated x is distribution y with parameters specified by ....

The presence of ties always generates a warning, since continuous distributions do not generate
them. If the ties arose from rounding the tests may be approximately valid, but even modest amounts
of rounding can have a significant effect on the calculated statistic.

Missing values are silently omitted from x and (in the two-sample case) y.

The possible values "two.sided", "less" and "greater" of alternative specify the null hy-
pothesis that the true distribution function of x is equal to, not less than or not greater than
the hypothesized distribution function (one-sample case) or the distribution function of y (two-
sample case), respectively. This is a comparison of cumulative distribution functions, and the test
statistic is the maximum difference in value, with the statistic in the "greater" alternative being
\[ D^+ = \max_u [F_x(u) - F_y(u)] \]. Thus in the two-sample case alternative = "greater" includes
distributions for which x is stochastically smaller than y (the CDF of x lies above and hence to the
left of that for y), in contrast to t.test or wilcox.test.

Exact p-values are not available for the one-sample case in the presence of ties. If exact = NULL
(the default), an exact p-value is computed if the sample size is less than 100 in the one-sample case
and there are no ties, and if the product of the sample sizes is less than 10000 in the two-sample
case, with or without ties (using the algorithm described in Schröer and Trenkler, 1995). Otherwise,
asymptotic distributions are used whose approximations may be inaccurate in small samples. In the
one-sample two-sided case, exact p-values are obtained as described in Marsaglia, Tsang & Wang (2003) (but not using the optional approximation in the right tail, so this can be slow for small p-values). The formula of Birnbaum & Tingey (1951) is used for the one-sample one-sided case.

If a one-sample test is used, the parameters specified in . . . must be pre-specified and not estimated from the data. There is some more refined distribution theory for the KS test with estimated parameters (see Durbin, 1973), but that is not implemented in ks.test.

Value

A list inheriting from classes "ks.test" and "htest" containing the following components:

- statistic: the value of the test statistic.
- p.value: the p-value of the test.
- alternative: a character string describing the alternative hypothesis.
- method: a character string indicating what type of test was performed.
- data.name: a character string giving the name(s) of the data.

Source


Exact distributions for the two-sample (Smirnov) test are computed by the algorithm proposed Schröer (1991) and Schröer & Trenkler (1995).

References


See Also

- psmirnov.
- shapiro.test which performs the Shapiro-Wilk test for normality.
Examples

```r
require("graphics")
x <- rnorm(50)
y <- runif(30)
# Do x and y come from the same distribution?
ks.test(x, y)
# Does x come from a shifted gamma distribution with shape 3 and rate 2?
ks.test(x+2, "pgamma", 3, 2) # two-sided, exact
ks.test(x+2, "pgamma", 3, 2, exact = FALSE)
ks.test(x+2, "pgamma", 3, 2, alternative = "gr")

# test if x is stochastically larger than x2
x2 <- rnorm(50, -1)
plot(ecdf(x), xlim = range(c(x, x2)))
plot(ecdf(x2), add = TRUE, lty = "dashed")
t.test(x, x2, alternative = "g")
wilcox.test(x, x2, alternative = "g")
ks.test(x, x2, alternative = "l")

# with ties, example from Schröer and Trenkler (1995)
# D = 3 / 7, p = 0.2424242
ks.test(c(1, 2, 2, 3, 3), c(1, 2, 3, 3, 4, 5, 6), exact = TRUE)

# formula interface, see ?wilcox.test
ks.test(Ozone ~ Month, data = airquality, 
  subset = Month %in% c(5, 8))
```

ksmooth

Kernel Regression Smoother

Description

The Nadaraya–Watson kernel regression estimate.

Usage

```r
ksmooth(x, y, kernel = c("box", "normal"), bandwidth = 0.5,
  range.x = range(x),
  n.points = max(100L, length(x)), x.points)
```

Arguments

- **x**: input x values. Long vectors are supported.
- **y**: input y values. Long vectors are supported.
- **kernel**: the kernel to be used. Can be abbreviated.
- **bandwidth**: the bandwidth. The kernels are scaled so that their quartiles (viewed as probability densities) are at ±0.25*bandwidth.
- **range.x**: the range of points to be covered in the output.
- **n.points**: the number of points at which to evaluate the fit.
- **x.points**: points at which to evaluate the smoothed fit. If missing, n.points are chosen uniformly to cover range.x. Long vectors are supported.
Value
A list with components

x values at which the smoothed fit is evaluated. Guaranteed to be in increasing order.
y fitted values corresponding to x.

Note
This function was implemented for compatibility with S, although it is nowhere near as slow as the S function. Better kernel smoothers are available in other packages such as KernSmooth.

Examples
require(graphics)

with(cars, {
  plot(speed, dist)
  lines(ksmooth(speed, dist, "normal", bandwidth = 2), col = 2)
  lines(ksmooth(speed, dist, "normal", bandwidth = 5), col = 3)
})

lag
Lag a Time Series

Description
Compute a lagged version of a time series, shifting the time base back by a given number of observations.

lag is a generic function; this page documents its default method.

Usage
lag(x, ...)

## Default S3 method:
lag(x, k = 1, ...)

Arguments

x A vector or matrix or univariate or multivariate time series
k The number of lags (in units of observations).
... further arguments to be passed to or from methods.

Details
Vector or matrix arguments x are given a tsp attribute via hasTsp.

Value
A time series object with the same class as x.
Note

Note the sign of k: a series lagged by a positive k starts earlier.

References


See Also
diff, deltat

Examples

\[
\text{lag(ldeaths, 12) } \# \text{ starts one year earlier}
\]

\[
\text{lag.plot}
\]

**Time Series Lag Plots**

Description

Plot time series against lagged versions of themselves. Helps visualizing ‘auto-dependence’ even when auto-correlations vanish.

Usage

```
lag.plot(x, lags = 1, layout = NULL, set.lags = 1:lags,
        main = NULL, asp = 1,
        diag = TRUE, diag.col = "gray", type = "p", oma = NULL,
        ask = NULL, do.lines = (n <= 150), labels = do.lines,
        ...)  
```

Arguments

- **x**: time-series (univariate or multivariate)
- **lags**: number of lag plots desired, see arg `set.lags`.
- **layout**: the layout of multiple plots, basically the `mfrow` `par()` argument. The default uses about a square layout (see `n2mfrow`) such that all plots are on one page.
- **set.lags**: vector of positive integers allowing specification of the set of lags used; defaults to 1:lags.
- **main**: character with a main header title to be done on the top of each page.
- **asp**: Aspect ratio to be fixed, see `plot.default`.
- **diag**: logical indicating if the x=y diagonal should be drawn.
- **diag.col**: color to be used for the diagonal if(diag).
- **type**: plot type to be used, but see `plot.ts` about its restricted meaning.
- **oma**: outer margins, see `par`.
- **ask**: logical or NULL; if true, the user is asked to confirm before a new page is started.
- **do.lines**: logical indicating if lines should be drawn.
logical indicating if labels should be used.

Further arguments to `plot.ts`. Several graphical parameters are set in this function and so cannot be changed: these include `xlab`, `ylab`, `mgp`, `col.lab` and `font.lab`: this also applies to the arguments `xy.labels` and `xy.lines`.

Details

If just one plot is produced, this is a conventional plot. If more than one plot is to be produced, `par(mfrow)` and several other graphics parameters will be set, so it is not (easily) possible to mix such lag plots with other plots on the same page.

If `ask = NULL`, `par(ask = TRUE)` will be called if more than one page of plots is to be produced and the device is interactive.

Note

It is more flexible and has different default behaviour than the S version. We use `main` instead of `head` for internal consistency.

Author(s)

Martin Maechler

See Also

`plot.ts` which is the basic work horse.

Examples

```r
require(graphics)

lag.plot(nhtemp, 8, diag.col = "forest green")
lag.plot(nhtemp, 5, main = "Average Temperatures in New Haven")
## ask defaults to TRUE when we have more than one page:
lag.plot(nhtemp, 6, layout = c(2,1), asp = NA,
       main = "New Haven Temperatures", col.main = "blue")

## Multivariate (but non-stationary! ...)
lag.plot(freeny.x, lags = 3)

## no lines for long series :
lag.plot(sqrt(sunspots), set.lags = c(1:4, 9:12), pch = ".", col = "gold")
```

Robust Line Fitting

Description

Fit a line robustly as recommended in Exploratory Data Analysis.

Currently by default (iter = 1) the initial median-median line is not iterated (as opposed to Tukey’s “resistant line” in the references).
Usage

line(x, y, iter = 1)

Arguments

x, y the arguments can be any way of specifying x-y pairs. See \texttt{xy.coords}.
iter positive integer specifying the number of “polishing” iterations. Note that this was hard coded to 1 in R versions before 3.5.0, and more importantly that such simple iterations may not converge, see Siegel’s 9-point example.

Details

Cases with missing values are omitted.

Contrary to the references where the data is split in three (almost) equally sized groups with symmetric sizes depending on \( n \) and \( n \mod 3 \) and computes medians inside each group, the \texttt{line()} code splits into three groups using all observations with \( x[.] <= q1 \) and \( x[.] >= q2 \), where \( q1, q2 \) are (a kind of) quantiles for probabilities \( p = 1/3 \) and \( p = 2/3 \) of the form \( (x[j1]+x[j2])/2 \) where \( j1 = \text{floor}(p*(n-1)) \) and \( j2 = \text{ceiling}(p(n-1)) \), \( n = \text{length}(x) \).

Long vectors are not supported yet.

Value

An object of class "tukeyline".

Methods are available for the generic functions \texttt{coef}, \texttt{residuals}, \texttt{fitted}, and \texttt{print}.

References


See Also

\texttt{lm}.

There are alternatives for robust linear regression more robust and more (statistically) efficient, see \texttt{rlm()} from \texttt{MASS}, or \texttt{lmrob()} from \texttt{robustbase}.

Examples

\begin{verbatim}
require(graphics)
plot(cars)
(z <- line(cars))
abline(coef(z))
## Tukey-Anscombe Plot :
plot(residuals(z) ~ fitted(z), main = deparse(z$call))
\end{verbatim}
## Andrew Siegel's pathological 9-point data, y-values multiplied by 3:

d.AS <- data.frame(x = c(-4:3, 12), y = 3*c(rep(0,6), -5, 5, 1))
cAS <- with(d.AS, t(sapply(1:10, 
   function(it) line(x,y, iter=it)$coefficients)))
dimnames(cAS) <- list(paste("it =", format(1:10)), c("intercept", "slope"))
cAS

## iterations started to oscillate, repeating iteration 7,8 indefinitely

---

### listof

**A Class for Lists of (Parts of) Model Fits**

**Description**

Class "listof" is used by `aov` and the "lm" method of `alias` for lists of model fits or parts thereof. It is simply a list with an assigned class to control the way methods, especially printing, act on it.

It has a `coef` method in this package (which returns an object of this class), and `[` and `print` methods in package `base`.

---

### lm

**Fitting Linear Models**

**Description**

`lm` is used to fit linear models, including multivariate ones. It can be used to carry out regression, single stratum analysis of variance and analysis of covariance (although `aov` may provide a more convenient interface for these).

**Usage**

```r
lm(formula, data, subset, weights, na.action, 
   method = "qr", model = TRUE, x = FALSE, y = FALSE, qr = TRUE, 
   singular.ok = TRUE, contrasts = NULL, offset, ...)
```

```r
## S3 method for class 'lm'
print(x, digits = max(3L, getOption("digits") - 3L), ...)
```

**Arguments**

- `formula`: an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.

- `data`: an optional data frame, list or environment (or object coercible by `as.data.frame` to a data frame) containing the variables in the model. If not found in data, the variables are taken from `environment(formula)`, typically the environment from which `lm` is called.

- `subset`: an optional vector specifying a subset of observations to be used in the fitting process. (See additional details about how this argument interacts with data-dependent bases in the 'Details' section of the `model.frame` documentation.)
weights  an optional vector of weights to be used in the fitting process. Should be NULL or a numeric vector. If non-NULL, weighted least squares is used with weights (that is, minimizing \( \text{sum}(w*e^2) \)); otherwise ordinary least squares is used. See also ‘Details’.

na.action  a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The ‘factory-fresh’ default is na.omit. Another possible value is NULL, no action. Value na.exclude can be useful.

method  the method to be used; for fitting, currently only method = "qr" is supported; method = "model.frame" returns the model frame (the same as with model = TRUE, see below).

model, x, y, qr  logicals. If TRUE the corresponding components of the fit (the model frame, the model matrix, the response, the QR decomposition) are returned.

singular.ok  logical. If FALSE (the default in S but not in R) a singular fit is an error.

contrasts  an optional list. See the contrasts.arg of model.matrix.default.

offset  this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector or matrix of extents matching those of the response. One or more offset terms can be included in the formula instead or as well, and if more than one are specified their sum is used. See model.offset.

...  For lm(): additional arguments to be passed to the low level regression fitting functions (see below).

digits  the number of significant digits to be passed to format(coef(x),..) when print()ing.

Details

Models for \( \text{lm} \) are specified symbolically. A typical model has the form response ~ terms where response is the (numeric) response vector and terms is a series of terms which specifies a linear predictor for response. A terms specification of the form first + second indicates all the terms in first together with all the terms in second with duplicates removed. A specification of the form first:second indicates the set of terms obtained by taking the interactions of all terms in first with all terms in second. The specification first*second indicates the cross of first and second. This is the same as first + second + first:second.

If the formula includes an offset, this is evaluated and subtracted from the response.

If response is a matrix a linear model is fitted separately by least-squares to each column of the matrix and the result inherits from "mlm" ("multivariate linear model").

See model.matrix for some further details. The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula (see aov and demo(glm.vr) for an example).

A formula has an implied intercept term. To remove this use either y ~ x - 1 or y ~ 0 + x. See formula for more details of allowed formulae.

Non-NULL weights can be used to indicate that different observations have different variances (with the values in weights being inversely proportional to the variances); or equivalently, when the elements of weights are positive integers \( w_i \), that each response \( y_i \) is the mean of \( w_i \) unit-weight observations (including the case that there are \( w_i \) observations equal to \( y_i \) and the data have been summarized). However, in the latter case, notice that within-group variation is not used. Therefore, the sigma estimate and residual degrees of freedom may be suboptimal; in the case of replication
weights, even wrong. Hence, standard errors and analysis of variance tables should be treated with care.

lm calls the lower level functions lm.fit, etc, see below, for the actual numerical computations. For programming only, you may consider doing likewise.

All of weights, subset and offset are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula.

Value

lm returns an object of class "lm" or for multivariate (‘multiple’) responses of class c("mlm", "lm").

The functions summary and anova are used to obtain and print a summary and analysis of variance table of the results. The generic accessor functions coefficients, effects, fitted.values and residuals extract various useful features of the value returned by lm.

An object of class "lm" is a list containing at least the following components:

coefficients a named vector of coefficients
residuals the residuals, that is response minus fitted values.
fitted.values the fitted mean values.
rank the numeric rank of the fitted linear model.
weights (only for weighted fits) the specified weights.
df.residual the residual degrees of freedom.
call the matched call.
terms the terms object used.
contrasts (only where relevant) the contrasts used.
xlevels (only where relevant) a record of the levels of the factors used in fitting.
offset the offset used (missing if none were used).
y if requested, the response used.
x if requested, the model matrix used.
model if requested (the default), the model frame used.
na.action (where relevant) information returned by model.frame on the special handling of NAs.

In addition, non-null fits will have components assign, effects and (unless not requested) qr relating to the linear fit, for use by extractor functions such as summary and effects.

Using time series

Considerable care is needed when using lm with time series.

Unless na.action = NULL, the time series attributes are stripped from the variables before the regression is done. (This is necessary as omitting NAs would invalidate the time series attributes, and if NAs are omitted in the middle of the series the result would no longer be a regular time series.)

Even if the time series attributes are retained, they are not used to line up series, so that the time shift of a lagged or differenced regressor would be ignored. It is good practice to prepare a data argument by ts.intersect(..., dframe = TRUE), then apply a suitable na.action to that data frame and call lm with na.action = NULL so that residuals and fitted values are time series.
**lm**

**Author(s)**

The design was inspired by the S function of the same name described in Chambers (1992). The implementation of model formula by Ross Ihaka was based on Wilkinson & Rogers (1973).

**References**


**See Also**

`summary.lm` for more detailed summaries and `anova.lm` for the ANOVA table; `aov` for a different interface.

The generic functions `coef`, `effects`, `residuals`, `fitted`, `vcov`,

`predict.lm` (via `predict`) for prediction, including confidence and prediction intervals; `confint` for confidence intervals of parameters.

`lm.influence` for regression diagnostics, and `glm` for **generalized** linear models.

The underlying low level functions, `lm.fit` for plain, and `lm.wfit` for weighted regression fitting.

More `lm()` examples are available e.g., in `anscombe`, `attitude`, `freeny`, `LifeCycleSavings`, `longley`, `stackloss`, `swiss`.

`biglm` in package `biglm` for an alternative way to fit linear models to large datasets (especially those with many cases).

**Examples**

```r
require(graphics)
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2, 10, 20, labels = c("Ctl","Trt"))
weight <- c(ctl, trt)
fm.D9 <- lm(weight ~ group)
fm.D90 <- lm(weight ~ group - 1) # omitting intercept
anova(fm.D9)
summary(fm.D90)
plot(fm.D9, las = 1) # Residuals, Fitted, ... 
par(opar)
```

### less simple examples in "See Also" above
Fitter Functions for Linear Models

Description
These are the basic computing engines called by \texttt{lm} used to fit linear models. These should usually not be used directly unless by experienced users. \texttt{.lm.fit()} is a bare-bones wrapper to the innermost QR-based C code, on which \texttt{glm.fit} and \texttt{lsfit} are also based, for even more experienced users.

Usage
\begin{verbatim}
lm.fit (x, y, offset = NULL, method = "qr", tol = 1e-7, singular.ok = TRUE, ...)
lm.wfit(x, y, w, offset = NULL, method = "qr", tol = 1e-7, singular.ok = TRUE, ...)
.lm.fit(x, y, tol = 1e-7)
\end{verbatim}

Arguments
\begin{itemize}
\item \texttt{x} design matrix of dimension \(n \times p\).
\item \texttt{y} vector of observations of length \(n\), or a matrix with \(n\) rows.
\item \texttt{w} vector of weights (length \(n\)) to be used in the fitting process for the \texttt{wfit} functions. Weighted least squares is used with weights \(w\), i.e., \(\sum(w \times e^2)\) is minimized.
\item \texttt{offset} (numeric of length \(n\)). This can be used to specify an \textit{a priori} known component to be included in the linear predictor during fitting.
\item \texttt{method} currently, only \texttt{method = "qr"} is supported.
\item \texttt{tol} tolerance for the \texttt{qr} decomposition. Default is 1e-7.
\item \texttt{singular.ok} logical. If \texttt{FALSE}, a singular model is an error.
\item \texttt{...} currently disregarded.
\end{itemize}

Details
If \(y\) is a matrix, \texttt{offset} can be a numeric matrix of the same dimensions, in which case each column is applied to the corresponding column of \(y\).

Value
\begin{verbatim}
a list with components (for \texttt{lm.fit} and \texttt{lm.wfit})
coefficients \(p\) vector
residuals \(n\) vector or matrix
fitted.values \(n\) vector or matrix
effects \(n\) vector of orthogonal single-df effects. The first rank of them correspond to non-aliased coefficients, and are named accordingly.
\end{verbatim}
weights
rank
df.residual
qr

Fits without any columns or non-zero weights do not have the effects and qr components.

See Also

lm which you should use for linear least squares regression, unless you know better.

Examples

require(utils)
set.seed(129)

n <- 7 ; p <- 2
X <- matrix(rnorm(n * p), n, p) # no intercept!
y <- rnorm(n)
w <- rnorm(n)^2

str(lmw <- lm.wfit(x = X, y = y, w = w))
str(lm. <- lm.fit (x = X, y = y))

if(require("microbenchmark")) {
  mb <- microbenchmark(lm(y~X), lm.fit(X,y), .lm.fit(X,y))
  print(mb)
  boxplot(mb, notch=TRUE)
}

Description

This function provides the basic quantities which are used in forming a wide variety of diagnostics for checking the quality of regression fits.

Usage

influence(model, ...)
## S3 method for class 'lm'
influence(model, do.coef = TRUE, ...)
## S3 method for class 'glm'
influence(model, do.coef = TRUE, ...)

lm.influence(model, do.coef = TRUE)
Arguments

model an object as returned by \texttt{lm} or \texttt{glm}.
do.coef logical indicating if the changed coefficients (see below) are desired. These need $O(n^2p)$ computing time.

... further arguments passed to or from other methods.

Details

The \texttt{influence.measures()} and other functions listed in \texttt{See Also} provide a more user oriented way of computing a variety of regression diagnostics. These all build on \texttt{lm.influence}. Note that for GLMs (other than the Gaussian family with identity link) these are based on one-step approximations which may be inadequate if a case has high influence.

An attempt is made to ensure that computed hat values that are probably one are treated as one, and the corresponding rows in \texttt{sigma} and \texttt{coefficients} are \texttt{NaN}. (Dropping such a case would normally result in a variable being dropped, so it is not possible to give simple drop-one diagnostics.)

\texttt{na.resid} is applied to the results and so will fill in with NAs it the fit had \texttt{na.action = na.exclude}.

Value

A list containing the following components of the same length or number of rows $n$, which is the number of non-zero weights. Cases omitted in the fit are omitted unless a \texttt{na.action} method was used (such as \texttt{na.exclude}) which restores them.

- \texttt{hat} a vector containing the diagonal of the ‘hat’ matrix.
- \texttt{coefficients} (unless \texttt{do.coef} is false) a matrix whose $i$-th row contains the change in the estimated coefficients which results when the $i$-th case is dropped from the regression. Note that aliased coefficients are not included in the matrix.
- \texttt{sigma} a vector whose $i$-th element contains the estimate of the residual standard deviation obtained when the $i$-th case is dropped from the regression. (The approximations needed for GLMs can result in this being \texttt{NaN}.)
- \texttt{wt.res} a vector of weighted (or for class \texttt{glm} rather \texttt{deviance}) residuals.

Note

The \texttt{coefficients} returned by the \texttt{R} version of \texttt{lm.influence} differ from those computed by \texttt{S}. Rather than returning the coefficients which result from dropping each case, we return the changes in the coefficients. This is more directly useful in many diagnostic measures. Since these need $O(np^2)$ computing time, they can be omitted by \texttt{do.coef = FALSE}.

Note that cases with weights == 0 are \texttt{dropped} (contrary to the situation in \texttt{S}).

If a model has been fitted with \texttt{na.action = na.exclude} (see \texttt{na.exclude}), cases excluded in the fit are considered here.

References

See the list in the documentation for \texttt{influence.measures}.

See Also

`summary.lm` for `summary` and related methods;
`influence.measures`,
`hat` for the hat matrix diagonals,
`dfbetas`, `dffits`, `covratio`, `cooks.distance`, `lm`.

Examples

```r
## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
summary(lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi,
data = LifeCycleSavings),
correlation = TRUE)
utils::str(lmI <- lm.influence(lm.SR))
```

```r
## For more "user level" examples, use example(influence.measures)
```

---

**lm.summaries**

**Accessing Linear Model Fits**

Description

All these functions are methods for class "lm" objects.

Usage

```r
## S3 method for class 'lm'
family(object, ...)

## S3 method for class 'lm'
formula(x, ...)

## S3 method for class 'lm'
residuals(object, type = c("working", "response", "deviance", "pearson", "partial"),
          ...)

## S3 method for class 'lm'
labels(object, ...)
```

Arguments

- `object, x` an object inheriting from class `lm`, usually the result of a call to `lm` or `aov`.
- `...` further arguments passed to or from other methods.
- `type` the type of residuals which should be returned. Can be abbreviated.
Details

The generic accessor functions coef, effects, fitted and residuals can be used to extract various useful features of the value returned by `lm`.

The working and response residuals are `observed - fitted`. The deviance and Pearson residuals are weighted residuals, scaled by the square root of the weights used in fitting. The `partial residuals` are a matrix with each column formed by omitting a term from the model. In all these, zero weight cases are never omitted (as opposed to the standardized `rstudent` residuals, and the `weighted.residuals`).

How residuals treats cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear, with residual value `NA`. See also `naresid`.

The "lm" method for generic `labels` returns the term labels for estimable terms, that is the names of the terms with at least one estimable coefficient.

References


See Also

The model fitting function `lm`, `anova.lm`, `coef`, `deviance`, `df.residual`, `effects`, `fitted`, `glm` for generalized linear models, `influence` (etc on that page) for regression diagnostics, `weighted.residuals`, `residuals`, `residuals.glm`, `summary.lm`, `weights`.

`influence.measures` for deletion diagnostics, including standardized (`rstandard`) and studentized (rstudent) residuals.

Examples

```r
##-- Continuing the lm(.), example:
coef(lm.D90)  # the bare coefficients

## The 2 basic regression diagnostic plots [plot.lm(.) is preferred]
plot(resid(lm.D90), fitted(lm.D90))  # Tukey-Anscombe's
abline(h = 0, lty = 2, col = "gray")

qqnorm(residuals(lm.D90))
```

loadings

Print Loadings in Factor Analysis

Description

Extract or print loadings in factor analysis (or principal components analysis).
Usage

loadings(x, ...)

## S3 method for class 'loadings'
print(x, digits = 3, cutoff = 0.1, sort = FALSE, ...)

## S3 method for class 'factanal'
print(x, digits = 3, ...)

Arguments

x an object of class "factanal" or "princomp" or the loadings component of such an object.
digits number of decimal places to use in printing uniquenesses and loadings.
cutoff loadings smaller than this (in absolute value) are suppressed.
sort logical. If true, the variables are sorted by their importance on each factor. Each variable with any loading larger than 0.5 (in modulus) is assigned to the factor with the largest loading, and the variables are printed in the order of the factor they are assigned to, then those unassigned.
...

... further arguments for other methods, ignored for loadings.

Details

'Loadings' is a term from factor analysis, but because factor analysis and principal component analysis (PCA) are often conflated in the social science literature, it was used for PCA by SPSS and hence by princomp in S-PLUS to help SPSS users. Small loadings are conventionally not printed (replaced by spaces), to draw the eye to the pattern of the larger loadings. The print method for class "factanal" calls the "loadings" method to print the loadings, and so passes down arguments such as cutoff and sort. The signs of the loadings vectors are arbitrary for both factor analysis and PCA.

Note

There are other functions called loadings in contributed packages which are S3 or S4 generic: the ... argument is to make it easier for this one to become a default method.

See Also

factanal, princomp

-----------------------------------------------------------------------------------

loess Local Polynomial Regression Fitting

Description

Fit a polynomial surface determined by one or more numerical predictors, using local fitting.
Usage

loess(formula, data, weights, subset, na.action, model = FALSE,
span = 0.75, enp.target, degree = 2,
parametric = FALSE, drop.square = FALSE, normalize = TRUE,
family = c("gaussian", "symmetric"),
method = c("loess", "model.frame"),
control = loess.control(...), ...)

Arguments

formula a formula specifying the numeric response and one to four numeric predictors
(best specified via an interaction, but can also be specified additively). Will be coerced
to a formula if necessary.
data an optional data frame, list or environment (or object coercible by
as.data.frame to a data frame) containing the variables in the model. If not found in
data, the variables are taken from environment(formula), typically
the environment from which loess is called.
weights optional weights for each case.
subset an optional specification of a subset of the data to be used.
na.action the action to be taken with missing values in the response or predictors. The
default is given by getOption("na.action").
model should the model frame be returned?
span the parameter \( \alpha \) which controls the degree of smoothing.
enp.target an alternative way to specify span, as the approximate equivalent number of
parameters to be used.
degree the degree of the polynomials to be used, normally 1 or 2. (Degree 0 is also
allowed, but see the 'Note'.)
parametric should any terms be fitted globally rather than locally? Terms can be specified
by name, number or as a logical vector of the same length as the number of
predictors.
drop.square for fits with more than one predictor and degree = 2, should the quadratic term
be dropped for particular predictors? Terms are specified in the same way as for
parametric.
normalize should the predictors be normalized to a common scale if there is more than
one? The normalization used is to set the 10% trimmed standard deviation to one. Set to false for spatial coordinate predictors and others known to be on a
common scale.
family if "gaussian" fitting is by least-squares, and if "symmetric" a re-descending
M estimator is used with Tukey’s biweight function. Can be abbreviated.
method fit the model or just extract the model frame. Can be abbreviated.
control control parameters: see loess.control.
... control parameters can also be supplied directly (if control is not specified).

Details

Fitting is done locally. That is, for the fit at point \( x \), the fit is made using points in a neighbourhood
of \( x \), weighted by their distance from \( x \) (with differences in 'parametric' variables being ignored
when computing the distance). The size of the neighbourhood is controlled by \( \alpha \) (set by span or
loess

For \( \alpha < 1 \), the neighbourhood includes proportion \( \alpha \) of the points, and these have tricubic weighting (proportional to \( (1 - \text{dist}/\text{maxdist})^3 \)). For \( \alpha > 1 \), all points are used, with the ‘maximum distance’ assumed to be \( \alpha^{1/\rho} \) times the actual maximum distance for \( \rho \) explanatory variables.

For the default family, fitting is by (weighted) least squares. For family="symmetric" a few iterations of an M-estimation procedure with Tukey’s biweight are used. Be aware that as the initial value is the least-squares fit, this need not be a very resistant fit.

It can be important to tune the control list to achieve acceptable speed. See `loess.control` for details.

Value

An object of class "loess".

Note

As this is based on cloess, it is similar to but not identical to the loess function of S. In particular, conditioning is not implemented.

The memory usage of this implementation of loess is roughly quadratic in the number of points, with 1000 points taking about 10Mb.

degree = 0, local constant fitting, is allowed in this implementation but not documented in the reference. It seems very little tested, so use with caution.

Author(s)

B. D. Ripley, based on the cloess package of Cleveland, Grosse and Shyu.

Source

The 1998 version of cloess package of Cleveland, Grosse and Shyu. A later version is available as cloess at https://netlib.org/a/.

References


See Also

`loess.control`, `predict.loess`, `lowess`, the ancestor of loess (with different defaults!).

Examples

cars.lo <- loess(dist ~ speed, cars)
predict(cars.lo, data.frame(speed = seq(5, 30, 1)), se = TRUE) # to allow extrapolation
cars.lo2 <- loess(dist ~ speed, cars, control = loess.control(surface = "direct"))
predict(cars.lo2, data.frame(speed = seq(5, 30, 1)), se = TRUE)
loess.control  

Set Parameters for Loess

Description

Set control parameters for loess fits.

Usage

loess.control(surface = c("interpolate", "direct"),
               statistics = c("approximate", "exact", "none"),
               trace.hat = c("exact", "approximate"),
               cell = 0.2, iterations = 4, iterTrace = FALSE, ...)

Arguments

- **surface**: should the fitted surface be computed exactly ("direct") or via interpolation from a kd tree? Can be abbreviated.
- **statistics**: should the statistics be computed exactly, approximately or not at all? Exact computation can be very slow. Can be abbreviated.
- **trace.hat**: Only for the (default) case (surface = "interpolate", statistics = "approximate"): should the trace of the smoother matrix be computed exactly or approximately? It is recommended to use the approximation for more than about 1000 data points. Can be abbreviated.
- **cell**: if interpolation is used this controls the accuracy of the approximation via the maximum number of points in a cell in the kd tree. Cells with more than $\text{floor}(n*\text{span}*\text{cell})$ points are subdivided.
- **iterations**: the number of iterations used in robust fitting, i.e. only if family is "symmetric".
- **iterTrace**: logical (or integer) determining if tracing information during the robust iterations (iterations $\geq$ 2) is produced.
- **...**: further arguments which are ignored.

Value

A list with components

- **surface**
- **statistics**
- **trace.hat**
- **cell**
- **iterations**
- **iterTrace**

with meanings as explained under ‘Arguments’.

See Also

loess
**Logistic**

**The Logistic Distribution**

**Description**
Density, distribution function, quantile function and random generation for the logistic distribution with parameters location and scale.

**Usage**
- `dlogis(x, location = 0, scale = 1, log = FALSE)`
- `plogis(q, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)`
- `qlogis(p, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)`
- `rlogis(n, location = 0, scale = 1)`

**Arguments**
- `x`, `q`: vector of quantiles.
- `p`: vector of probabilities.
- `n`: number of observations. If `length(n) > 1`, the length is taken to be the number required.
- `location`, `scale`: location and scale parameters.
- `log`, `log.p`: logical; if TRUE, probabilities `p` are given as `log(p)`.
- `lower.tail`: logical; if TRUE (default), probabilities are `P[X ≤ x]`, otherwise, `P[X > x]`.

**Details**
If `location` or `scale` are omitted, they assume the default values of 0 and 1 respectively.

The Logistic distribution with location = $\mu$ and scale = $\sigma$ has distribution function

$$F(x) = \frac{1}{1 + e^{-(x-\mu)/\sigma}}$$

and density

$$f(x) = \frac{1}{\sigma} \frac{e^{(x-\mu)/\sigma}}{(1 + e^{(x-\mu)/\sigma})^2}$$

It is a long-tailed distribution with mean $\mu$ and variance $\pi^2 / 3\sigma^2$.

**Value**
- `dlogis` gives the density, `plogis` gives the distribution function, `qlogis` gives the quantile function, and `rlogis` generates random deviates.

The length of the result is determined by `n` for `rlogis`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.
Note

qlogis(p) is the same as the well known 'logit' function, \( \text{logit}(p) = \log p / (1 - p) \), and \( \text{plogis}(x) \) has consequently been called the 'inverse logit'.

The distribution function is a rescaled hyperbolic tangent, \( \text{plogis}(x) = (1 + \tanh(x/2))/2 \), and it is called a sigmoid function in contexts such as neural networks.

Source

[dpq]logis are calculated directly from the definitions.

rlogis uses inversion.

References


See Also

Distributions for other standard distributions.

Examples

```r
var(rlogis(4000, 0, scale = 5)) # approximately (+/- 3)
pi^2/3 * 5^2
```

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which have methods for this function include: "glm", "lm", "nls" and "Arima". Packages contain methods for other classes, such as "fitdistr", "negbin" and "polr" in package MASS, "multinom" in package nnet and "gls", "gnls" "lme" and others in package nlme.

Usage

```r
logLik(object, ...)  # logLik(object, REML = FALSE, ...)
```

Arguments

- `object` any object from which a log-likelihood value, or a contribution to a log-likelihood value, can be extracted.
- `...` some methods for this generic function require additional arguments.
- `REML` an optional logical value. If TRUE the restricted log-likelihood is returned, else, if FALSE, the log-likelihood is returned. Defaults to FALSE.
**Details**

`logLik` is most commonly used for a model fitted by maximum likelihood, and some uses, e.g. by `AIC`, assume this. So care is needed where other fit criteria have been used, for example REML (the default for "lme").

For a "glm" fit the `family` does not have to specify how to calculate the log-likelihood, so this is based on using the family’s `aic()` function to compute the AIC. For the `gaussian`, `Gamma` and `inverse.gaussian` families it assumed that the dispersion of the GLM is estimated and has been counted as a parameter in the AIC value, and for all other families it is assumed that the dispersion is known. Note that this procedure does not give the maximized likelihood for "glm" fits from the Gamma and inverse gaussian families, as the estimate of dispersion used is not the MLE.

For "lm" fits it is assumed that the scale has been estimated (by maximum likelihood or REML), and all the constants in the log-likelihood are included. That method is only applicable to single-response fits.

**Value**

Returns an object of class `logLik`. This is a number with at least one attribute, "df" (degrees of freedom), giving the number of (estimated) parameters in the model.

There is a simple print method for "logLik" objects.

There may be other attributes depending on the method used: see the appropriate documentation. One that is used by several methods is "nobs", the number of observations used in estimation (after the restrictions if `REML = TRUE`).

**Author(s)**

José Pinheiro and Douglas Bates

**References**

For `logLik.lm`:


**See Also**

`logLik.gls`, `logLik.lme`, in package `nlme`, etc.

`AIC`

**Examples**

```r
x <- 1:5
lmx <- lm(x ~ 1)
logLik(lmx) # using print.logLik() method
utils::str(logLik(lmx))

## lm method
(fm1 <- lm(rating ~ ., data = attitude))
logLik(fm1)
logLik(fm1, REML = TRUE)

utils::data(Orthodont, package = "nlme")
fm1 <- lm(distance ~ Sex * age, Orthodont)
```
Description

\texttt{loglin} is used to fit log-linear models to multidimensional contingency tables by Iterative Proportional Fitting.

Usage

\texttt{loglin(table, margin, start = rep(1, length(table)), fit = FALSE, eps = 0.1, iter = 20, param = FALSE, print = TRUE)}

Arguments

table: a contingency table to be fit, typically the output from \texttt{table}.

margin: a list of vectors with the marginal totals to be fit. (Hierarchical) log-linear models can be specified in terms of these marginal totals which give the ‘maximal’ factor subsets contained in the model. For example, in a three-factor model, \texttt{list(c(1, 2), c(1, 3))} specifies a model which contains parameters for the grand mean, each factor, and the 1-2 and 1-3 interactions, respectively (but no 2-3 or 1-2-3 interaction), i.e., a model where factors 2 and 3 are independent conditional on factor 1 (sometimes represented as ‘[12][13]’). The names of factors (i.e., \texttt{names(dimnames(table))}) may be used rather than numeric indices.

start: a starting estimate for the fitted table. This optional argument is important for incomplete tables with structural zeros in \texttt{table} which should be preserved in the fit. In this case, the corresponding entries in \texttt{start} should be zero and the others can be taken as one.

fit: a logical indicating whether the fitted values should be returned.

esps: maximum deviation allowed between observed and fitted margins.

iter: maximum number of iterations.

param: a logical indicating whether the parameter values should be returned.

print: a logical. If \texttt{TRUE}, the number of iterations and the final deviation are printed.

Details

The Iterative Proportional Fitting algorithm as presented in Haberman (1972) is used for fitting the model. At most \texttt{iter} iterations are performed, convergence is taken to occur when the maximum deviation between observed and fitted margins is less than \texttt{eps}. All internal computations are done in double precision; there is no limit on the number of factors (the dimension of the table) in the model.

Assuming that there are no structural zeros, both the Likelihood Ratio Test and Pearson test statistics have an asymptotic chi-squared distribution with \texttt{df} degrees of freedom.
Note that the IPF steps are applied to the factors in the order given in margin. Hence if the model is decomposable and the order given in margin is a running intersection property ordering then IPF will converge in one iteration.

Package MASS contains loglm, a front-end to loglin which allows the log-linear model to be specified and fitted in a formula-based manner similar to that of other fitting functions such as lm or glm.

Value

A list with the following components.

- lrt: the Likelihood Ratio Test statistic.
- pearson: the Pearson test statistic (X-squared).
- df: the degrees of freedom for the fitted model. There is no adjustment for structural zeros.
- margin: list of the margins that were fit. Basically the same as the input margin, but with numbers replaced by names where possible.
- fit: An array like table containing the fitted values. Only returned if fit is TRUE.
- param: A list containing the estimated parameters of the model. The ‘standard’ constraints of zero marginal sums (e.g., zero row and column sums for a two factor parameter) are employed. Only returned if param is TRUE.

Author(s)

Kurt Hornik

References


See Also

table.
loglm in package MASS for a user-friendly wrapper.
glm for another way to fit log-linear models.

Examples

```r
### Model of joint independence of sex from hair and eye color.
fm <- loglin(HairEyeColor, list(c(1, 2), c(1, 3), c(2, 3)))
fm
1 - pchisq(fm$lrt, fm$df)
### Model with no three-factor interactions fits well.
```
The Log Normal Distribution

Description
Density, distribution function, quantile function and random generation for the log normal distribution whose logarithm has mean equal to meanlog and standard deviation equal to sdlog.

Usage

\begin{align*}
dlnorm(x, \text{meanlog} = 0, \text{sdlog} = 1, \text{log} = \text{FALSE}) \\
plnorm(q, \text{meanlog} = 0, \text{sdlog} = 1, \text{lower.tail} = \text{TRUE}, \text{log.p} = \text{FALSE}) \\
qlnorm(p, \text{meanlog} = 0, \text{sdlog} = 1, \text{lower.tail} = \text{TRUE}, \text{log.p} = \text{FALSE}) \\
rlnorm(n, \text{meanlog} = 0, \text{sdlog} = 1)
\end{align*}

Arguments

- \(x, q\): vector of quantiles.
- \(p\): vector of probabilities.
- \(n\): number of observations. If \(\text{length}(n) > 1\), the length is taken to be the number required.
- \(\text{meanlog}, \text{sdlog}\): mean and standard deviation of the distribution on the log scale with default values of 0 and 1 respectively.
- \(\text{log}, \text{log.p}\): logical; if TRUE, probabilities \(p\) are given as \(\log(p)\).
- \(\text{lower.tail}\): logical; if TRUE (default), probabilities are \(P[X \leq x]\), otherwise, \(P[X > x]\).

Details
The log normal distribution has density
\[f(x) = \frac{1}{\sqrt{2\pi}\sigma x} e^{-(\log(x) - \mu)^2 / 2\sigma^2}\]
where \(\mu\) and \(\sigma\) are the mean and standard deviation of the logarithm. The mean is \(E(X) = e^{\mu + 1/2\sigma^2}\), the median is \(\text{med}(X) = e^{\mu}\), and the variance \(\text{Var}(X) = e^{2\mu + \sigma^2}(e^{\sigma^2} - 1)\) and hence the coefficient of variation is \(\sqrt{e^{\sigma^2} - 1}\) which is approximately \(\sigma\) when that is small (e.g., \(\sigma < 1/2\)).

Value
\(\text{dlnorm}\) gives the density, \(\text{plnorm}\) gives the distribution function, \(\text{qlnorm}\) gives the quantile function, and \(\text{rlnorm}\) generates random deviates.

The length of the result is determined by \(n\) for \(\text{rlnorm}\), and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than \(n\) are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note
The cumulative hazard \(H(t) = -\log(1 - F(t))\) is \(-\text{plnorm}(t, r, \text{lower} = \text{FALSE}, \text{log} = \text{TRUE})\).
lowess

Source
dlnorm is calculated from the definition (in ‘Details’). \( \text{lnorm} \) are based on the relationship to the normal.
Consequently, they model a single point mass at \( \exp(\text{meanLog}) \) for the boundary case \( \text{sdLog} = 0 \).

References

See Also
Distributions for other standard distributions, including dnorm for the normal distribution.

Examples
dlnorm(1) == dnorm(0)

---

lowess        Scatter Plot Smoothing

Description
This function performs the computations for the LOWESS smoother which uses locally-weighted polynomial regression (see the references).

Usage
lowess(x, y = NULL, f = 2/3, iter = 3, delta = 0.01 * diff(range(x)))

Arguments

- **x, y** vectors giving the coordinates of the points in the scatter plot. Alternatively a single plotting structure can be specified – see \texttt{xy.coords}.
- **f** the smoother span. This gives the proportion of points in the plot which influence the smooth at each value. Larger values give more smoothness.
- **iter** the number of ‘robustifying’ iterations which should be performed. Using smaller values of iter will make \texttt{lowess} run faster.
- **delta** See ‘Details’. Defaults to 1/100th of the range of \( x \).
Details

`lowess` is defined by a complex algorithm, the Ratfor original of which (by W. S. Cleveland) can be found in the `R` sources as file `src/library/stats/src/lowess.doc`. Normally a local linear polynomial fit is used, but under some circumstances (see the file) a local constant fit can be used. ‘Local’ is defined by the distance to the floor\((f*n)\)th nearest neighbour, and tricubic weighting is used for \(x\) which fall within the neighbourhood.

The initial fit is done using weighted least squares. If `iter > 0`, further weighted fits are done using the product of the weights from the proximity of the \(x\) values and case weights derived from the residuals at the previous iteration. Specifically, the case weight is Tukey’s biweight, with cutoff 6 times the MAD of the residuals. (The current `R` implementation differs from the original in stopping iteration if the MAD is effectively zero since the algorithm is highly unstable in that case.)

delta is used to speed up computation: instead of computing the local polynomial fit at each data point it is not computed for points within \(\delta\) of the last computed point, and linear interpolation is used to fill in the fitted values for the skipped points.

Value

`lowess` returns a list containing components `x` and `y` which give the coordinates of the smooth. The smooth can be added to a plot of the original points with the function `lines`: see the examples.

References


See Also

`loess`, a newer formula based version of `lowess` (with different defaults!).

Examples

```r
require(graphics)

plot(cars, main = "lowess(cars)")
lines(lowess(cars), col = 2)
lines(lowess(cars, f = .2), col = 3)
legend(5, 120, c(paste("f = ", c("2/3", ".2"))), lty = 1, col = 2:3)
```

`ls.diag`  
Compute Diagnostics for `lsfit` Regression Results

Description

Computes basic statistics, including standard errors, t- and p-values for the regression coefficients.
Usage

ls.diag(ls.out)

Arguments

ls.out Typically the result of lsfit()

Value

A list with the following numeric components.

- **std.dev** The standard deviation of the errors, an estimate of \( \sigma \).
- **hat** diagonal entries \( h_{ii} \) of the hat matrix \( H \)
- **std.res** standardized residuals
- **stud.res** studentized residuals
- **cooks** Cook's distances
- **dfits** DFITS statistics
- **correlation** correlation matrix
- **std.err** standard errors of the regression coefficients
- **cov.scaled** Scaled covariance matrix of the coefficients
- **cov.unscaled** Unscaled covariance matrix of the coefficients

References


See Also

hat for the hat matrix diagonals, ls.print, lm.influence, summary.lm, anova.

Examples

```r
##-- Using the same data as the lm(.) example:
lsD9 <- lsfit(x = as.numeric(gl(2, 10, 20)), y = weight)
dlsD9 <- ls.diag(lsD9)
utils::str(dlsD9, give.attr = FALSE)
abs(1 - sum(dlsD9$hat) / 2) < 10*.Machine$double.eps # sum(h.ii) = p
plot(dlsD9$hat, dlsD9$stud.res, xlim = c(0, 0.11))
abline(h = 0, lty = 2, col = "lightgray")
```
ls.print  

Print lsfit Regression Results

Description

Computes basic statistics, including standard errors, t- and p-values for the regression coefficients and prints them if print.it is TRUE.

Usage

ls.print(ls.out, digits = 4, print.it = TRUE)

Arguments

- **ls.out**: Typically the result of `lsfit()`
- **digits**: The number of significant digits used for printing
- **print.it**: a logical indicating whether the result should also be printed

Value

A list with the components

- **summary**: The ANOVA table of the regression
- **coef.table**: matrix with regression coefficients, standard errors, t- and p-values

Note

Usually you would use `summary(lm(...))` and `anova(lm(...))` to obtain similar output.

See Also

`ls.diag`, `lsfit`, also for examples; `lm`, `lm.influence` which usually are preferable.

lsfit  

Find the Least Squares Fit

Description

The least squares estimate of $\beta$ in the model

$$Y = X\beta + \epsilon$$

is found.

Usage

`lsfit(x, y, wt = NULL, intercept = TRUE, tolerance = 1e-07, yname = NULL)`
Arguments

x  a matrix whose rows correspond to cases and whose columns correspond to variables.
y  the responses, possibly a matrix if you want to fit multiple left hand sides.
wt  an optional vector of weights for performing weighted least squares.
intercept  whether or not an intercept term should be used.
tolerance  the tolerance to be used in the matrix decomposition.
yname  names to be used for the response variables.

Details

If weights are specified then a weighted least squares is performed with the weight given to the \( j \)th case specified by the \( j \)th entry in \( wt \).

If any observation has a missing value in any field, that observation is removed before the analysis is carried out. This can be quite inefficient if there is a lot of missing data.

The implementation is via a modification of the LINPACK subroutines which allow for multiple left-hand sides.

Value

A list with the following named components:

coeff  the least squares estimates of the coefficients in the model (\( \beta \) as stated above).
residuals  residuals from the fit.
intercept  indicates whether an intercept was fitted.
qr  the QR decomposition of the design matrix.

References


See Also

lm which usually is preferable: ls.print, ls.diag.

Examples

```r
##-- Using the same data as the lm(.) example:
lsD9 <- lsfit(x = unclass(gl(2, 10)), y = weight)
ls.print(lsD9)
```
Description

Compute the median absolute deviation, i.e., the (lo-/hi-) median of the absolute deviations from the median, and (by default) adjust by a factor for asymptotically normal consistency.

Usage

\[ \text{mad}(x, \text{center} = \text{median}(x), \text{constant} = 1.4826, \text{na.rm} = \text{FALSE}, \text{low} = \text{FALSE}, \text{high} = \text{FALSE}) \]

Arguments

- **x**: a numeric vector.
- **center**: Optionally, the centre: defaults to the median.
- **constant**: scale factor.
- **na.rm**: if TRUE then NA values are stripped from x before computation takes place.
- **low**: if TRUE, compute the ‘lo-median’, i.e., for even sample size, do not average the two middle values, but take the smaller one.
- **high**: if TRUE, compute the ‘hi-median’, i.e., take the larger of the two middle values for even sample size.

Details

The actual value calculated is \( \text{constant} \times \text{cMedian}(\text{abs}(x - \text{center})) \) with the default value of center being median(x), and cMedian being the usual, the ‘low’ or ‘high’ median, see the arguments description for low and high above.

In the case of \( n = 1 \) non-missing values and default center, the result is 0, consistent with “no deviation from the center”.

The default constant = 1.4826 (approximately \( 1/\Phi^{-1}(3/4) = 1/qnorm(3/4) \)) ensures consistency, i.e.,

\[ E[\text{mad}(X_1, \ldots, X_n)] = \sigma \]

for \( X_i \) distributed as \( N(\mu, \sigma^2) \) and large \( n \).

If na.rm is TRUE then NA values are stripped from x before computation takes place. If this is not done then an NA value in x will cause mad to return NA.

See Also

- IQR which is simpler but less robust, median, var.
Examples

```r
mad(c(1:9))
print(mad(c(1:9), constant = 1)) ==
mad(c(1:8, 100), constant = 1) # = 2 ; TRUE
x <- c(1,2,3,5,7,8)
sort(abs(x - median(x)))
c(mad(x, constant = 1),
mad(x, constant = 1, low = TRUE),
mad(x, constant = 1, high = TRUE))
```

---

**mahalanobis**

**Mahalanobis Distance**

**Description**

Returns the squared Mahalanobis distance of all rows in `x` and the vector `μ = center` with respect to `Σ = cov`. This is (for vector `x`) defined as

\[ D^2 = (x - \mu)'\Sigma^{-1}(x - \mu) \]

**Usage**

`mahalanobis(x, center, cov, inverted = FALSE, ...)`

**Arguments**

- `x` vector or matrix of data with, say, `p` columns.
- `center` mean vector of the distribution or second data vector of length `p` or recyclable to that length. If set to `FALSE`, the centering step is skipped.
- `cov` covariance matrix (`p × p`) of the distribution.
- `inverted` logical. If `TRUE`, `cov` is supposed to contain the inverse of the covariance matrix.
- `...` passed to `solve` for computing the inverse of the covariance matrix (if `inverted` is false).

**See Also**

`cov`, `var`

**Examples**

```r
require(graphics)
ma <- cbind(1:6, 1:3)
(S <- var(ma))
mahalanobis(c(0, 0), 1:2, S)
x <- matrix(rnorm(100*3), ncol = 3)
stopifnot(mahalanobis(x, 0, diag(ncol(x))) == rowSums(x*x))
  # Here, D^2 = usual squared Euclidean distances
Sx <- cov(x)
D2 <- mahalanobis(x, colMeans(x), Sx)
```
plot(density(D2, bw = 0.5),
     main="Squared Mahalanobis distances, n=100, p=3") ; rug(D2)
qqplot(qchisq(ppoints(100), df = 3), D2,
     main = expression("Q-Q plot of Mahalanobis" * ~D^2 *
                      " vs. quantiles of" * ~ chi[3]^2))
abline(0, 1, col = 'gray')

---

**make.link**  
Create a Link for GLM Families

**Description**

This function is used with the `family` functions in `glm()`. Given the name of a link, it returns a link function, an inverse link function, the derivative $d\mu/d\eta$ and a function for domain checking.

**Usage**

```r
make.link(link)
```

**Arguments**

- `link` character; one of "logit", "probit", "cauchit", "cloglog", "identity", "log", "sqrt", "1/mu^2", "inverse".

**Value**

A object of class "link-glm", a list with components

- `linkfun` Link function function($\mu$
- `linkinv` Inverse link function function($\eta$
- `mu.eta` Derivative function($\eta$) $d\mu/d\eta$
- `valideta` function($\eta$){ TRUE if $\eta$ is in the domain of `linkinv` }
- `name` a name to be used for the link

**See Also**

`power`, `glm`, `family`.

**Examples**

```r
utils::str(make.link("logit"))
```
makepredictcall  Utility Function for Safe Prediction

Description
A utility to help model.frame.default create the right matrices when predicting from models with terms like (univariate) poly or ns.

Usage
makepredictcall(var, call)

Arguments
var      A variable.
call     The term in the formula, as a call.

Details
This is a generic function with methods for poly, bs and ns: the default method handles scale. If model.frame.default encounters such a term when creating a model frame, it modifies the predvars attribute of the terms supplied by replacing the term with one which will work for predicting new data. For example makepredictcall.ns adds arguments for the knots and intercept.

To make use of this, have your model-fitting function return the terms attribute of the model frame, or copy the predvars attribute of the terms attribute of the model frame to your terms object.

To extend this, make sure the term creates variables with a class, and write a suitable method for that class.

Value
A replacement for call for the predvars attribute of the terms.

See Also
model.frame, poly, scale; bs and ns in package splines.
cars for an example of prediction from a polynomial fit.

Examples
require(graphics)

## using poly: this did not work in R < 1.5.0
fm <- lm(weight ~ poly(height, 2), data = women)
plot(women, xlab = "Height (in)", ylab = "Weight (lb)"
ht <- seq(57, 73, length.out = 200)
D <- data.frame(height = ht)
pfm <- predict(fm, D)
lines(ht, pfm)
pf2 <- predict(update(fm, ~ stats::poly(height, 2)), D)
stopifnot(all.equal(pfm, pf2)) ## was off (rel.diff. 0.0766) in R <= 3.5.0

## see also example(cars)
manova

Multivariate Analysis of Variance

Description

A class for the multivariate analysis of variance.

Usage

manova(...)

Arguments

... Arguments to be passed to aov.

Details

Class "manova" differs from class "aov" in selecting a different summary method. Function manova calls aov and then add class "manova" to the result object for each stratum.

Value

See aov and the comments in 'Details' here.

References


See Also

aov, summary.manova, the latter containing more examples.

Examples

## Set orthogonal contrasts.
op <- options(contrasts = c("contr.helmert", "contr.poly"))

## Fake a 2nd response variable
npk2 <- within(npk, foo <- rnorm(24))
( npk2.aov <- manova(cbind(yield, foo) ~ block + N*P*K, npk2) )
summary(npk2.aov)

( npk2.aovE <- manova(cbind(yield, foo) ~ N*P*K + Error(block), npk2) )
summary(npk2.aovE)
mantelhaen.test
Cochran-Mantel-Haenszel Chi-Squared Test for Count Data

Description
Performs a Cochran-Mantel-Haenszel chi-squared test of the null that two nominal variables are conditionally independent in each stratum, assuming that there is no three-way interaction.

Usage
mantelhaen.test(x, y = NULL, z = NULL,
alternative = c("two.sided", "less", "greater"),
correct = TRUE, exact = FALSE, conf.level = 0.95)

Arguments
x either a 3-dimensional contingency table in array form where each dimension is at least 2 and the last dimension corresponds to the strata, or a factor object with at least 2 levels.
y a factor object with at least 2 levels; ignored if x is an array.
z a factor object with at least 2 levels identifying to which stratum the corresponding elements in x and y belong; ignored if x is an array.
alternative indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. Only used in the 2 by 2 by K case.
correct a logical indicating whether to apply continuity correction when computing the test statistic. Only used in the 2 by 2 by K case.
exact a logical indicating whether the Mantel-Haenszel test or the exact conditional test (given the strata margins) should be computed. Only used in the 2 by 2 by K case.
conf.level confidence level for the returned confidence interval. Only used in the 2 by 2 by K case.

Details
If x is an array, each dimension must be at least 2, and the entries should be nonnegative integers. NA’s are not allowed. Otherwise, x, y and z must have the same length. Triples containing NA’s are removed. All variables must take at least two different values.

Value
A list with class "htest" containing the following components:

statistic Only present if no exact test is performed. In the classical case of a 2 by 2 by K table (i.e., of dichotomous underlying variables), the Mantel-Haenszel chi-squared statistic; otherwise, the generalized Cochran-Mantel-Haenszel statistic.
parameter the degrees of freedom of the approximate chi-squared distribution of the test statistic (1 in the classical case). Only present if no exact test is performed.
p.value the p-value of the test.
conf.int  a confidence interval for the common odds ratio. Only present in the 2 by 2 by $K$ case.
estimate an estimate of the common odds ratio. If an exact test is performed, the conditional Maximum Likelihood Estimate is given; otherwise, the Mantel-Haenszel estimate. Only present in the 2 by 2 by $K$ case.
null.value the common odds ratio under the null of independence, 1. Only present in the 2 by 2 by $K$ case.
alternative a character string describing the alternative hypothesis. Only present in the 2 by 2 by $K$ case.
method a character string indicating the method employed, and whether or not continuity correction was used.
data.name a character string giving the names of the data.

Note

The asymptotic distribution is only valid if there is no three-way interaction. In the classical 2 by 2 by $K$ case, this is equivalent to the conditional odds ratios in each stratum being identical. Currently, no inference on homogeneity of the odds ratios is performed.

See also the example below.

References


Examples

```r
## Agresti (1990), pages 231--237, Penicillin and Rabbits
## Investigation of the effectiveness of immediately injected or 1.5
## hours delayed penicillin in protecting rabbits against a lethal
## injection with beta-hemolytic streptococci.
Rabbits <-
array(c(0, 0, 6, 5,
      3, 0, 3, 6,
      6, 2, 0, 4,
      5, 6, 1, 0,
      2, 5, 0, 0),
dim = c(2, 2, 5),
dimnames = list(
    Delay = c("None", "1.5h"),
    Response = c("Cured", "Died"),
    Penicillin.Level = c("1/8", "1/4", "1/2", "1", "4")))
Rabbits
## Classical Mantel-Haenszel test
mantelhaen.test(Rabbits)
## => p = 0.047, some evidence for higher cure rate of immediate
## injection
## Exact conditional test
mantelhaen.test(Rabbits, exact = TRUE)
## => p = 0.040
## Exact conditional test for one-sided alternative of a higher
## cure rate for immediate injection
mantelhaen.test(Rabbits, exact = TRUE, alternative = "greater")
```
## => p = 0.020

## UC Berkeley Student Admissions
mantelhaen.test(UCBAdmissions)
## No evidence for association between admission and gender
## when adjusted for department. However,
apply(UCBAdmissions, 3, function(x) (x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
## This suggests that the assumption of homogeneous (conditional)
## odds ratios may be violated. The traditional approach would be
## using the Woolf test for interaction:
woolf <- function(x) {
x <- x + 1 / 2
k <- dim(x)[3]
or <- apply(x, 3, function(x) (x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
w <- apply(x, 3, function(x) 1 / sum(1 / x))
1 - pchisq(sum(w * (log(or) - weighted.mean(log(or), w)) ^ 2), k - 1)
}
woolf(UCBAdmissions)
## => p = 0.003, indicating that there is significant heterogeneity.
## (And hence the Mantel-Haenszel test cannot be used.)

## Job Satisfaction example.
Satisfaction <-
as.table(array(c(1, 2, 0, 0, 3, 3, 1, 2,
     11, 17, 8, 4, 2, 3, 5, 2,
     1, 0, 0, 0, 1, 3, 0, 1,
     2, 5, 7, 9, 1, 1, 3, 6),
dim = c(4, 4, 2),
dimnames =
list(Income =
c("<5000", "5000-15000", "15000-25000", ">25000"),
"Job Satisfaction" =
c("V_D", "L_S", "M_S", "V_S"),
Gender = c("Female", "Male")))
## (Satisfaction categories abbreviated for convenience.)
ftable(. ~ Gender + Income, Satisfaction)

---

### mauchly.test

**Mauchly’s Test of Sphericity**

**Description**
Tests whether a Wishart-distributed covariance matrix (or transformation thereof) is proportional to a given matrix.

**Usage**

mauchly.test(object, ...)
## S3 method for class 'mlm'
mauchly.test(object, ...)  
## S3 method for class 'SSD'
mauchly.test(object, Sigma = diag(nrow = p),  
             T = Thin.row(Proj(M) - Proj(X)), M = diag(nrow = p), X = ~0,  
             idata = data.frame(index = seq_len(p)), ...)

Arguments

- **object**: object of class SSD or mlm.
- **Sigma**: matrix to be proportional to.
- **T**: transformation matrix. By default computed from M and X.
- **M**: formula or matrix describing the outer projection (see below).
- **X**: formula or matrix describing the inner projection (see below).
- **idata**: data frame describing intra-block design.
- **...**: arguments to be passed to or from other methods.

Details

This is a generic function with methods for classes "mlm" and "SSD".

The basic method is for objects of class SSD the method for mlm objects just extracts the SSD matrix and invokes the corresponding method with the same options and arguments.

The T argument is used to transform the observations prior to testing. This typically involves transformation to intra-block differences, but more complicated within-block designs can be encountered, making more elaborate transformations necessary. A matrix T can be given directly or specified as the difference between two projections onto the spaces spanned by M and X, which in turn can be given as matrices or as model formulas with respect to idata (the tests will be invariant to parametrization of the quotient space M/X).

The common use of this test is in repeated measurements designs, with X = ~1. This is almost, but not quite the same as testing for compound symmetry in the untransformed covariance matrix.

Notice that the defaults involve p, which is calculated internally as the dimension of the SSD matrix, and a couple of hidden functions in the stats namespace, namely proj which calculates projection matrices from design matrices or model formulas and Thin.row which removes linearly dependent rows from a matrix until it has full row rank.

Value

An object of class "htest"

Note

The p-value differs slightly from that of SAS because a second order term is included in the asymptotic approximation in R.

References


See Also

SSD, anova.mlm, rWishart
Examples

```r
utils::example(SSD) # Brings in the mlmfit and reacttime objects

### traditional test of intrasubj. contrasts
mauchly.test(mlmfit, X = ~1)

### tests using intra-subject 3x2 design
idata <- data.frame(deg = gl(3, 1, 6, labels = c(0,4,8)),
                      noise = gl(2, 3, 6, labels = c("A","P")))
mauchly.test(mlmfit, X = ~ deg + noise, idata = idata)
mauchly.test(mlmfit, M = ~ deg + noise, X = ~ noise, idata = idata)
```

mcnemar.test  
 McNemar's Chi-squared Test for Count Data

Description

Performs McNemar's chi-squared test for symmetry of rows and columns in a two-dimensional contingency table.

Usage

```r
mcnemar.test(x, y = NULL, correct = TRUE)
```

Arguments

- **x**: either a two-dimensional contingency table in matrix form, or a factor object.
- **y**: a factor object; ignored if `x` is a matrix.
- **correct**: a logical indicating whether to apply continuity correction when computing the test statistic.

Details

The null is that the probabilities of being classified into cells \([i,j]\) and \([j,i]\) are the same.

If `x` is a matrix, it is taken as a two-dimensional contingency table, and hence its entries should be nonnegative integers. Otherwise, both `x` and `y` must be vectors or factors of the same length. Incomplete cases are removed, vectors are coerced into factors, and the contingency table is computed from these.

Continuity correction is only used in the 2-by-2 case if `correct` is `TRUE`.

Value

A list with class "htest" containing the following components:

- **statistic**: the value of McNemar’s statistic.
- **parameter**: the degrees of freedom of the approximate chi-squared distribution of the test statistic.
- **p.value**: the p-value of the test.
- **method**: a character string indicating the type of test performed, and whether continuity correction was used.
- **data.name**: a character string giving the name(s) of the data.
Examples

## Presidential Approval Ratings.
## Approval of the President’s performance in office in two surveys, one month apart, for a random sample of 1600 voting-age Americans.
Performance <-
matrix(c(794, 86, 150, 570),
nrow = 2,
dimnames = list("1st Survey" = c("Approve", "Disapprove"),
                "2nd Survey" = c("Approve", "Disapprove")))
Performance
mcnemar.test(Performance)
## => significant change (in fact, drop) in approval ratings

median

Median Value

Description

Compute the sample median.

Usage

median(x, na.rm = FALSE, ...)
## Default S3 method:
median(x, na.rm = FALSE, ...)

Arguments

x
an object for which a method has been defined, or a numeric vector containing the values whose median is to be computed.

na.rm
a logical value indicating whether NA values should be stripped before the computation proceeds.

... potentially further arguments for methods; not used in the default method.

Details

This is a generic function for which methods can be written. However, the default method makes use of is.na, sort and mean from package base all of which are generic, and so the default method will work for most classes (e.g., "Date") for which a median is a reasonable concept.

Value

The default method returns a length-one object of the same type as x, except when x is logical or integer of even length, when the result will be double.

If there are no values or if na.rm = FALSE and there are NA values the result is NA of the same type as x (or more generally the result of x[NA_integer_]).
References


See Also

*quantile* for general quantiles.

Examples

```r
median(1:4) # = 2.5 [even number]
median(c(1:3, 100, 1000)) # = 3 [odd, robust]
```

---

**medpolish**

**Median Polish (Robust Twoway Decomposition) of a Matrix**

Description

Fits an additive model (twoway decomposition) using Tukey’s *median polish* procedure.

Usage

```r
medpolish(x, eps = 0.01, maxiter = 10, trace.iter = TRUE,
          na.rm = FALSE)
```

Arguments

- `x` - a numeric matrix.
- `eps` - real number greater than 0. A tolerance for convergence: see ‘Details’.
- `maxiter` - the maximum number of iterations
- `trace.iter` - logical. Should progress in convergence be reported?
- `na.rm` - logical. Should missing values be removed?

Details

The model fitted is additive (constant + rows + columns). The algorithm works by alternately removing the row and column medians, and continues until the proportional reduction in the sum of absolute residuals is less than `eps` or until there have been `maxiter` iterations. The sum of absolute residuals is printed at each iteration of the fitting process, if `trace.iter` is TRUE. If `na.rm` is FALSE the presence of any NA value in `x` will cause an error, otherwise NA values are ignored.

`medpolish` returns an object of class *medpolish* (see below). There are printing and plotting methods for this class, which are invoked via the generics `print` and `plot`.

Value

An object of class *medpolish* with the following named components:

- `overall` - the fitted constant term.
- `row` - the fitted row effects.
- `col` - the fitted column effects.
- `residuals` - the residuals.
- `name` - the name of the dataset.
References


See Also

`median`; `aov` for a *mean* instead of *median* decomposition.

Examples

```r
require(graphics)

## Deaths from sport parachuting; from ABC of EDA, p.224:
deaths <-
  rbind(c(14,15,14),
        c( 7, 4, 7),
        c( 8, 2,10),
        c(15, 9,10),
        c( 0, 2, 0))
dimnames(deaths) <- list(c("1-24", "25-74", "75-199", "200++", "NA"),
                         paste(1973:1975))
deads <-
  medpolish(deaths)
plot(dead)

## Check decomposition:
all(deaths ==
    med.d$overall + outer(med.d$row,med.d$col, +) + med.d$residuals)
```

**model.extract**

*Extract Components from a Model Frame*

**Description**

Returns the response, offset, subset, weights or other special components of a model frame passed as optional arguments to `model.frame`.

**Usage**

```r
model.extract(frame, component)
model.offset(x)
model.response(data, type = "any")
model.weights(x)
```

**Arguments**

- **frame, x, data** a model frame, see `model.frame`.
- **component** literal character string or name. The name of a component to extract, such as "weights" or "subset".
- **type** One of "any", "numeric" or "double". Using either of latter two coerces the result to have storage mode "double".
Details

model.extract is provided for compatibility with S, which does not have the more specific functions. It is also useful to extract e.g. the etastart and mustart components of a glm fit.

model.extract(m, "offset") and model.extract(m, "response") are equivalent to model.offset(m) and model.response(m) respectively. model.offset sums any terms specified by offset terms in the formula or by offset arguments in the call producing the model frame: it does check that the offset is numeric.

model.weights is slightly different from model.extract(, "weights") in not naming the vector it returns.

Value

The specified component of the model frame, usually a vector. model.response() now drops a possible "Asis" class (stemming from I(.)).

model.offset returns NULL if no offset was specified.

See Also

model.frame, offset

Examples

a <- model.frame(cbind(ncases,ncontrols) ~ agegp + tobgp + alcgp, data = esoph)
model.extract(a, "response")
stopifnot(model.extract(a, "response") == model.response(a))

a <- model.frame(ncases/(ncases+ncontrols) ~ agegp + tobgp + alcgp,
data = esoph, weights = ncases+ncontrols)
model.response(a)
(mw <- model.extract(a, "weights"))
stopifnot(identical(unname(mw), model.weights(a)))

a <- model.frame(cbind(ncases,ncontrols) ~ agegp,
something = tobgp, data = esoph)
names(a)
stopifnot(model.extract(a, "something") == esoph$tobgp)
model.frame

subset = NULL, na.action = na.fail,
drop.unused.levels = FALSE, xlev = NULL, ...)

## S3 method for class 'aovlist'
model.frame(formula, data = NULL, ...)

## S3 method for class 'glm'
model.frame(formula, ...)

## S3 method for class 'lm'
model.frame(formula, ...)

get_all_vars(formula, data, ...)

Arguments

formula     a model formula or terms object or an R object.
data        a data.frame, list or environment (or object coercible by as.data.frame to a
data.frame), containing the variables in formula. Neither a matrix nor an array
will be accepted.
subset      a specification of the rows to be used: defaults to all rows. This can be any
valid indexing vector (see [.data.frame) for the rows of data or if that is
not supplied, a data frame made up of the variables used in formula. (See
additional details about how this argument interacts with data-dependent bases
under ‘Details’ below.)
na.action   how NAs are treated. The default is first, any na.action attribute of data, second
a na.action setting of options, and third na.fail if that is unset. The ‘factory-
fresh’ default is na.omit. Another possible value is NULL.
drop.unused.levels
should factors have unused levels dropped? Defaults to FALSE.
xlev        a named list of character vectors giving the full set of levels to be assumed for
each factor.
...         for model.frame methods, a mix of further arguments such as data, na.action,
subset to pass to the default method. Any additional arguments (such as offset
and weights or other named arguments) which reach the default method are
used to create further columns in the model frame, with parenthesised names
such as "(offset)".
For get_all_vars, further named columns to include in the model frame.

Details

Exactly what happens depends on the class and attributes of the object formula. If this is an object
of fitted-model class such as "lm", the method will either return the saved model frame used when
fitting the model (if any, often selected by argument model = TRUE) or pass the call used when fitting
on to the default method. The default method itself can cope with rather standard model objects
such as those of class "lqs" from package MASS if no other arguments are supplied.
The rest of this section applies only to the default method.

If either formula or data is already a model frame (a data frame with a "terms" attribute) and the
other is missing, the model frame is returned. Unless formula is a terms object, as.formula and
then terms is called on it. (If you wish to use the keep.order argument of terms.formula, pass a
terms object rather than a formula.)
Row names for the model frame are taken from the data argument if present, then from the names of the response in the formula (or rownames if it is a matrix), if there is one.

All the variables in formula, subset and in ... are looked for first in data and then in the environment of formula (see the help for formula() for further details) and collected into a data frame. Then the subset expression is evaluated, and it is used as a row index to the data frame. Then the na.action function is applied to the data frame (and may well add attributes). The levels of any factors in the data frame are adjusted according to the drop.unused.levels and xlev arguments: if xlev specifies a factor and a character variable is found, it is converted to a factor (as from R 2.10.0).

Because variables in the formula are evaluated before rows are dropped based on subset, the characteristics of data-dependent bases such as orthogonal polynomials (i.e. from terms using poly) or splines will be computed based on the full data set rather than the subsetted one.

Unless na.action = NULL, time-series attributes will be removed from the variables found (since they will be wrong if NAs are removed).

Note that all the variables in the formula are included in the data frame, even those preceded by -. Only variables whose type is raw, logical, integer, real, complex or character can be included in a model frame: this includes classed variables such as factors (whose underlying type is integer), but excludes lists.

get_all_vars returns a data.frame containing the variables used in formula plus those specified in ... which are recycled to the number of data frame rows. Unlike model.frame.default, it returns the input variables and not those resulting from function calls in formula.

Value

A data.frame containing the variables used in formula plus those specified in .... It will have additional attributes, including "terms" for an object of class "terms" derived from formula, and possibly "na.action" giving information on the handling of NAs (which will not be present if no special handling was done, e.g. by na.pass).

References


See Also

model.matrix for the 'design matrix', formula for formulas and expand.model.frame for model.frame manipulation.

Examples

data.class(model.frame(dist ~ speed, data = cars))

## get_all_vars(): new var.s are recycled (iff length matches: 50 = 2*25)
ncars <- get_all_vars(sqrt(dist) ~ I(speed/2), data = cars, newVar = 2:3)
stopifnot(is.data.frame(ncars),
          identical(cars, ncars[, names(cars)]),
          ncol(ncars) == ncol(cars) + 1)
model.matrix  

Construct Design Matrices

Description

model.matrix creates a design (or model) matrix, e.g., by expanding factors to a set of dummy variables (depending on the contrasts) and expanding interactions similarly.

Usage

model.matrix(object, ...)

## Default S3 method:
model.matrix(object, data = environment(object),
contrasts.arg = NULL, xlev = NULL, ...)

## S3 method for class 'lm'
model.matrix(object, ...)

Arguments

object an object of an appropriate class. For the default method, a model formula or a terms object.
data a data frame created with model.frame. If another sort of object, model.frame is called first.
contrasts.arg a list, whose entries are values (numeric matrices, functions or character strings naming functions) to be used as replacement values for the contrasts replacement function and whose names are the names of columns of data containing factors.
xlev to be used as argument of model.frame if data is such that model.frame is called.
...
further arguments passed to or from other methods.

Details

model.matrix creates a design matrix from the description given in terms(object), using the data in data which must supply variables with the same names as would be created by a call to model.frame(object) or, more precisely, by evaluating attr(terms(object), "variables"). If data is a data frame, there may be other columns and the order of columns is not important. Any character variables are coerced to factors. After coercion, all the variables used on the right-hand side of the formula must be logical, integer, numeric or factor.

If contrasts.arg is specified for a factor it overrides the default factor coding for that variable and any "contrasts" attribute set by C or contrasts. Whereas invalid contrasts.args have been ignored always, they are warned about since R version 3.6.0.

In an interaction term, the variable whose levels vary fastest is the first one to appear in the formula (and not in the term), so in ~ a + b + b:a the interaction will have a varying fastest.

By convention, if the response variable also appears on the right-hand side of the formula it is dropped (with a warning), although interactions involving the term are retained.
Value

The design matrix for a regression-like model with the specified formula and data.

There is an attribute "assign", an integer vector with an entry for each column in the matrix giving the term in the formula which gave rise to the column. Value 0 corresponds to the intercept (if any), and positive values to terms in the order given by the term.labels attribute of the terms structure corresponding to object.

If there are any factors in terms in the model, there is an attribute "contrasts", a named list with an entry for each factor. This specifies the contrasts that would be used in terms in which the factor is coded by contrasts (in some terms dummy coding may be used), either as a character vector naming a function or as a numeric matrix.

References


See Also

model.frame, model.extract, terms

sparse.model.matrix from package Matrix for creating sparse model matrices, which may be more efficient in large dimensions.

Examples

ff <- log(Volume) ~ log(Height) + log(Girth)
utils::str(m <- model.frame(ff, trees))
mat <- model.matrix(ff, m)

dd <- data.frame(a = gl(3,4), b = gl(4,1,12)) # balanced 2-way
options("contrasts") # typically 'treatment' (for unordered factors)
model.matrix(~ a + b, dd)

model.matrix(~ a + b, dd, contrasts.arg = list(a = "contr.sum"))
model.matrix(~ a + b, dd, contrasts.arg = list(a = "contr.sum", b = contr.poly))

m.orth <- model.matrix(~a+b, dd, contrasts.arg = list(a = "contr.helmert"))
crossprod(m.orth) # m.orth is ALMOST orthogonal

# invalid contrasts. ignored with a warning:
stopifnot(identical(
  model.matrix(~ a + b, dd),
  model.matrix(~ a + b, dd, contrasts.arg = "contr.FOO"))))

---

model.tables

Compute Tables of Results from an Aov Model Fit

Description

Computes summary tables for model fits, especially complex aov fits.
model.tables

Usage

model.tables(x, ...)  

## S3 method for class 'aov'
model.tables(x, type = "effects", se = FALSE, cterms, ...)

## S3 method for class 'aovlist'
model.tables(x, type = "effects", se = FALSE, ...)

Arguments

x
a model object, usually produced by aov

type
type of table: currently only "effects" and "means" are implemented. Can be abbreviated.

se
should standard errors be computed?

cterms
A character vector giving the names of the terms for which tables should be computed. The default is all terms.

...
further arguments passed to or from other methods.

Details

For type = "effects" give tables of the coefficients for each term, optionally with standard errors.

For type = "means" give tables of the mean response for each combinations of levels of the factors in a term.

The "aov" method cannot be applied to components of a "aovlist" fit.

Value

An object of class "tables.aov", as list which may contain components

tables A list of tables for each requested term.
n The replication information for each term.
se Standard error information.

Warning

The implementation is incomplete, and only the simpler cases have been tested thoroughly.

Weighted aov fits are not supported.

See Also

aov, proj, replications, TukeyHSD, se.contrast

Examples

options(contrasts = c("contr.helmert", "contr.treatment"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
model.tables(npk.aov, "means", se = TRUE)

## as a test, not particularly sensible statistically
npk.aovE <- aov(yield ~ N*P*K + Error(block), npk)
model.tables(npk.aovE, se = TRUE)
model.tables(npk.aovE, "means")
**monthplot**  
*Plot a Seasonal or other Subseries from a Time Series*

**Description**
These functions plot seasonal (or other) subseries of a time series. For each season (or other category), a time series is plotted.

**Usage**

```r
monthplot(x, ...)  
## S3 method for class 'stl'
monthplot(x, labels = NULL, ylab = choice, choice = "seasonal", ...)

## S3 method for class 'StructTS'
monthplot(x, labels = NULL, ylab = choice, choice = "sea", ...)

## S3 method for class 'ts'
monthplot(x, labels = NULL, times = time(x), phase = cycle(x),
ylab = deparse1(substitute(x)), ...)

## Default S3 method:
monthplot(x, labels = 1L:12L,
ylab = deparse1(substitute(x)),
times = seq_along(x),
phase = (times - 1L)%/%length(labels) + 1L, base = mean,
axes = TRUE, type = c("l", "h"), box = TRUE,
add = FALSE,
col = par("col"), lty = par("lty"), lwd = par("lwd"),
col.base = col, lty.base = lty, lwd.base = lwd, ...)
```

**Arguments**
- **x**  
  Time series or related object.
- **labels**  
  Labels to use for each ‘season’.
- **ylab**  
  y label.
- **times**  
  Time of each observation.
- **phase**  
  Indicator for each ‘season’.
- **base**  
  Function to use for reference line for subseries.
- **choice**  
  Which series of an stl or StructTS object?
- **...**  
  Arguments to be passed to the default method or graphical parameters.
- **axes**  
  Should axes be drawn (ignored if add = TRUE)?
- **type**  
  Type of plot. The default is to join the points with lines, and "h" is for histogram-like vertical lines.
- **box**  
  Should a box be drawn (ignored if add = TRUE)?
- **add**  
  Should thus just add on an existing plot.
monthplot

col, lty, lwd Graphics parameters for the series.
col.base, lty.base, lwd.base Graphics parameters for the segments used for the reference lines.

Details

These functions extract subseries from a time series and plot them all in one frame. The ts, stl, and StructTS methods use the internally recorded frequency and start and finish times to set the scale and the seasons. The default method assumes observations come in groups of 12 (though this can be changed).

If the labels are not given but the phase is given, then the labels default to the unique values of the phase. If both are given, then the phase values are assumed to be indices into the labels array, i.e., they should be in the range from 1 to length(labels).

Value

These functions are executed for their side effect of drawing a seasonal subseries plot on the current graphical window.

Author(s)

Duncan Murdoch

References


See Also

ts, stl, StructTS

Examples

```
require(graphics)

## The CO2 data
fit <- stl(log(co2), s.window = 20, t.window = 20)
plot(fit)
op <- par(mfrow = c(2,2))
monthplot(co2, ylab = "data", cex.axis = 0.8)
monthplot(fit, choice = "seasonal", cex.axis = 0.8)
monthplot(fit, choice = "trend", cex.axis = 0.8)
monthplot(fit, choice = "remainder", type = "h", cex.axis = 0.8)
par(op)

## The CO2 data, grouped quarterly
quarter <- (cycle(co2) - 1) %% 3
monthplot(co2, phase = quarter)

## see also JohnsonJohnson
```
**mood.test**

*Mood Two-Sample Test of Scale*

**Description**

Performs Mood’s two-sample test for a difference in scale parameters.

**Usage**

mood.test(x, ...)

### Default S3 method:

mood.test(x, y,
  alternative = c("two.sided", "less", "greater"), ...)

### S3 method for class 'formula'

mood.test(formula, data, subset, na.action, ...)

**Arguments**

- **x, y** numeric vectors of data values.
- **alternative** indicates the alternative hypothesis and must be one of "two.sided" (default), "greater" or "less" all of which can be abbreviated.
- **formula** a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs a factor with two levels giving the corresponding groups.
- **data** an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
- **subset** an optional vector specifying a subset of observations to be used.
- **na.action** a function which indicates what should happen when the data contain NAs. Defaults togetOption("na.action").
- **...** further arguments to be passed to or from methods.

**Details**

The underlying model is that the two samples are drawn from \( f(x - l) \) and \( f((x - l)/s)/s \), respectively, where \( l \) is a common location parameter and \( s \) is a scale parameter.

The null hypothesis is \( s = 1 \).

There are more useful tests for this problem.

In the case of ties, the formulation of Mielke (1967) is employed.

**Value**

A list with class "htest" containing the following components:

- **statistic** the value of the test statistic.
- **p.value** the p-value of the test.
- **alternative** a character string describing the alternative hypothesis. You can specify just the initial letter.
Multinom

method the character string "Mood two-sample test of scale".
data.name a character string giving the names of the data.

References


See Also

fligner.test for a rank-based (nonparametric) k-sample test for homogeneity of variances; ansari.test for another rank-based two-sample test for a difference in scale parameters; var.test and bartlett.test for parametric tests for the homogeneity in variance.

Examples

## Same data as for the Ansari-Bradley test:
## Serum iron determination using Hyland control sera
ramsay <- c(111, 107, 100, 99, 102, 106, 109, 108, 104, 99,
             101, 96, 97, 102, 107, 113, 116, 113, 110, 98)
jung.parekh <- c(107, 108, 106, 98, 105, 103, 110, 105, 104,
mood.test(ramsay, jung.parekh)
## Compare this to ansari.test(ramsay, jung.parekh)

Multinom

The Multinomial Distribution

Description

Generate multinomially distributed random number vectors and compute multinomial probabilities.

Usage

rmultinom(n, size, prob)
dmultinom(x, size = NULL, prob, log = FALSE)

Arguments

x vector of length K of integers in 0:size.
n number of random vectors to draw.
size integer, say N, specifying the total number of objects that are put into K boxes in the typical multinomial experiment. For dmultinom, it defaults to sum(x).
prob numeric non-negative vector of length K, specifying the probability for the K classes; is internally normalized to sum 1. Infinite and missing values are not allowed.
log logical; if TRUE, log probabilities are computed.
Details

If x is a K-component vector, \( \text{dmultinom}(x, \text{prob}) \) is the probability

\[
P(X_1 = x_1, \ldots, X_K = x_K) = C \times \prod_{j=1}^{K} \pi_j^{x_j}
\]

where \( C \) is the ‘multinomial coefficient’ \( C = N!/(x_1! \cdots x_K!) \) and \( N = \sum_{j=1}^{K} x_j \).

By definition, each component \( X_j \) is binomially distributed as \( \text{Bin}(\text{size}, \text{prob}[j]) \) for \( j = 1, \ldots, K \).

The \( \text{rmultinom()} \) algorithm draws binomials \( X_j \) from \( \text{Bin}(n_j, P_j) \) sequentially, where \( n_1 = N \) (\( N := \text{size} \)), \( P_1 = \pi_1 \) (\( \pi \) is prob scaled to sum 1), and for \( j \geq 2 \), recursively, \( n_j = N - \sum_{k=1}^{j-1} X_k \) and \( P_j = \pi_j/(1 - \sum_{k=1}^{j-1} \pi_k) \).

Value

For \( \text{rmultinom()} \), an integer \( K \times n \) matrix where each column is a random vector generated according to the desired multinomial law, and hence summing to \( \text{size} \). Whereas the transposed result would seem more natural at first, the returned matrix is more efficient because of columnwise storage.

Note

dmultinom is currently not vectorized at all and has no C interface (API); this may be amended in the future.

See Also

\( \textbf{Distributions} \) for standard distributions, including \( \text{dbinom} \) which is a special case conceptually.

Examples

\[
\text{rmultinom}(10, \text{size} = 12, \text{prob} = c(0.1, 0.2, 0.8))
\]

\[
\text{pr} <- c(1, 3, 6, 10) \quad \# \text{normalization not necessary for generation}
\]

\[
\text{rmultinom}(10, 20, \text{prob} = \text{pr})
\]

\[
\text{## all possible outcomes of Multinom}(N = 3, K = 3)
\]

\[
\text{dimnames(X) <- list(letters[1:3], NULL)}
\]

\[
\text{round(apply(X, 2, function(x) \text{dmultinom}(x, prob = c(1, 2, 5))), 3)}
\]
Arguments

object any object whose NA action is given.

... further arguments special methods could require.

Details

na.action is a generic function, and na.action.default its default method. The latter extracts
the "na.action" component of a list if present, otherwise the "na.action" attribute.
When model.frame is called, it records any information on NA handling in a "na.action" attribute.
Most model-fitting functions return this as a component of their result.

Value

Information from the action which was applied to object if NAs were handled specially, or NULL.

References


See Also

options("na.action"), na.omit, na.fail, also for na.exclude, na.pass.

Examples

na.action(na.omit(c(1, NA)))


na.contiguous Find Longest Contiguous Stretch of non-NAs

Description

Find the longest consecutive stretch of non-missing values in a time series object. (In the event of a
tie, the first such stretch.)

Usage

na.contiguous(object, ...)

Arguments

object a univariate or multivariate time series.

... further arguments passed to or from other methods.

Value

A time series without missing values. The class of object will be preserved.

See Also

na.omit and na.omit.ts; na.fail
na.fail

Examples

na.contiguous(presidents)

---

Handle Missing Values in Objects

Description

These generic functions are useful for dealing with NAs in e.g., data frames. `na.fail` returns the object if it does not contain any missing values, and signals an error otherwise. `na.omit` returns the object with incomplete cases removed. `na.pass` returns the object unchanged.

Usage

na.fail(object, ...)
na.omit(object, ...)
na.exclude(object, ...)
na.pass(object, ...)

Arguments

object an R object, typically a data frame
...

Arguments

Details

At present these will handle vectors, matrices and data frames comprising vectors and matrices (only).

If `na.omit` removes cases, the row numbers of the cases form the "na.action" attribute of the result, of class "omit".

`na.exclude` differs from `na.omit` only in the class of the "na.action" attribute of the result, which is "exclude". This gives different behaviour in functions making use of `naresid` and `napredict`: when `na.exclude` is used the residuals and predictions are padded to the correct length by inserting NAs for cases omitted by `na.exclude`.

References


See Also

`na.action`; `options` with argument `na.action` for setting NA actions; and `lm` and `glm` for functions using these. `na.contiguous` as alternative for time series.
Examples

DF <- data.frame(x = c(1, 2, 3), y = c(0, 10, NA))
na.omit(DF)
m <- as.matrix(DF)
na.omit(m)
stopifnot(all(na.omit(1:3) == 1:3)) # does not affect objects with no NA's
try(na.fail(DF)) #> Error: missing values in ...

options("na.action")

naprint adjusted for missing values

Description

Adjust for Missing Values

Use missing value information to report the effects of an na.action.

Usage

naprint(x, ...)

Arguments

x An object produced by an na.action function.

... further arguments passed to or from other methods.

Details

This is a generic function, and the exact information differs by method. naprint.omit reports the number of rows omitted: naprint.default reports an empty string.

Value

A character string providing information on missing values, for example the number.

naresid adjusted for missing values

Description

Adjust for Missing Values

Use missing value information to adjust residuals and predictions.

Usage

naresid(omit, x, ...)
napredict(omit, x, ...)
Arguments

omit: an object produced by an `na.action` function, typically the "na.action" attribute of the result of `na.omit` or `na.exclude`.

x: a vector, data frame, or matrix to be adjusted based upon the missing value information.

... further arguments passed to or from other methods.

Details

These are utility functions used to allow `predict`, `fitted` and `residuals` methods for modelling functions to compensate for the removal of NAs in the fitting process. They are used by the default, "lm", "glm" and "nls" methods, and by further methods in packages `MASS`, `rpart` and `survival`. Also used for the scores returned by `factanal`, `prcomp` and `princomp`.

The default methods do nothing. The default method for the `na.exclude` action is to pad the object with NAs in the correct positions to have the same number of rows as the original data frame.

Currently `naresid` and `napredict` are identical, but future methods need not be. `naresid` is used for residuals, and `napredict` for fitted values, predictions and weights.

Value

These return a similar object to `x`.

Note

In the early 2000s, packages `rpart` and `survival` contained versions of these functions that had an `na.omit` action equivalent to that now used for `na.exclude`.

NegBinomial

The Negative Binomial Distribution

Description

Density, distribution function, quantile function and random generation for the negative binomial distribution with parameters `size` and `prob`.

Usage

\begin{verbatim}
dnbinom(x, size, prob, mu, log = FALSE)
pnbinom(q, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
qnbinom(p, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
rnbinom(n, size, prob, mu)
\end{verbatim}

Arguments

x: vector of (non-negative integer) quantiles.
q: vector of quantiles.
p: vector of probabilities.
n: number of observations. If `length(n) > 1`, the length is taken to be the number required.
**Details**

The negative binomial distribution with size = n and prob = p has density

\[ p(x) = \frac{\Gamma(x + n)}{\Gamma(n)x!} p^n (1 - p)^x \]

for \( x = 0, 1, 2, \ldots, n > 0 \) and \( 0 < p \leq 1 \).

This represents the number of failures which occur in a sequence of Bernoulli trials before a target number of successes is reached. The mean is \( \mu = n(1 - p)/p \) and variance \( n(1 - p)/p^2 \).

A negative binomial distribution can also arise as a mixture of Poisson distributions with mean distributed as a gamma distribution (see pgamma) with scale parameter \((1 - prob)/prob\) and shape parameter size. (This definition allows non-integer values of size.)

An alternative parametrization (often used in ecology) is by the mean \( \mu \) (see above), and size, the dispersion parameter, where prob = size/(size+mu). The variance is \( \mu + \mu^2/\text{size} \) in this parametrization.

If an element of x is not integer, the result of \( \text{dnbinom} \) is zero, with a warning.

The case size == 0 is the distribution concentrated at zero. This is the limiting distribution for size approaching zero, even if \( \mu \) rather than prob is held constant. Notice though, that the mean of the limit distribution is 0, whatever the value of \( \mu \).

The quantile is defined as the smallest value \( x \) such that \( F(x) \geq p \), where \( F \) is the distribution function.

**Value**

dnbinom gives the density, pbinom gives the distribution function, qbinom gives the quantile function, and rbinom generates random deviates.

Invalid size or prob will result in return value NaN, with a warning.

The length of the result is determined by n for rbinom, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

rbinom returns a vector of type integer unless generated values exceed the maximum representable integer when double values are returned.

**Source**

dnbinom computes via binomial probabilities, using code contributed by Catherine Loader (see dbinom).

pbinom uses pbeta.
qnbinom uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.


**See Also**

Distributions for standard distributions, including `dbinom` for the binomial, `dpois` for the Poisson and `dgeom` for the geometric distribution, which is a special case of the negative binomial.

**Examples**

```r
require(graphics)
x <- 0:11
dnbinom(x, size = 1, prob = 1/2) * 2^(1 + x) # == 1
126 / dnbinom(0:8, size = 2, prob = 1/2) # - theoretically integer

## Cumulative ('p') = Sum of discrete prob.s ('d'); Relative error :
summary(1 - cumsum(dnbinom(x, size = 2, prob = 1/2)) / pnbinom(x, size = 2, prob = 1/2))

x <- 0:15
size <- (1:20)/4
persp(x, size, dnb <- outer(x, size, function(x,s) dnbinom(x, s, prob = 0.4)),
xlab = "x", ylab = "s", zlab = "density", theta = 150)
title(tit <- "negative binomial density(x,s, pr = 0.4) vs. x & s")
image (x, size, log10(dnb), main = paste("log [", tit, "]"))
contour(x, size, log10(dnb), add = TRUE)

## Alternative parametrization
x1 <- rnbinom(500, mu = 4, size = 1)
x2 <- rnbinom(500, mu = 4, size = 10)
x3 <- rnbinom(500, mu = 4, size = 100)
h1 <- hist(x1, breaks = 20, plot = FALSE)
h2 <- hist(x2, breaks = h1$breaks, plot = FALSE)
h3 <- hist(x3, breaks = h1$breaks, plot = FALSE)
barplot(rbind(h1$counts, h2$counts, h3$counts),
beside = TRUE, col = c("red", "blue", "cyan"),
names.arg = round(h1$breaks[-length(h1$breaks)]))
```

**nextn**

Find Highly Composite Numbers

**Description**

`nextn` returns the smallest integer, greater than or equal to n, which can be obtained as a product of powers of the values contained in factors.

`nextn()` is intended to be used to find a suitable length to zero-pad the argument of `fft` so that the transform is computed quickly. The default value for factors ensures this.
Usage

nextn(n, factors = c(2,3,5))

Arguments

n | a vector of integer numbers (of type "integer" or "double").
factors | a vector of positive integer factors (at least 2 and preferably relative prime, see the note).

Value

a vector of the same length as n, of type "integer" when the values are small enough (determined before computing them) and "double" otherwise.

Note

If the factors in factors are not relative prime, i.e., have themselves a common factor larger than one, the result may be wrong in the sense that it may not be the smallest integer. E.g., nextn(91, c(2,6)) returns 128 instead of 96 as nextn(91, c(2,3)) returns.

When the resulting N <- nextn(...) is larger than 2^53, a warning with the true 64-bit integer value is signalled, as integers above that range may not be representable in double precision.

If you really need to deal with such large integers, it may be advisable to use package gmp.

See Also

convolve, fft.

Examples

nextn(1001) # 1024
table(nextn(599:630))
n <- 1:100 ; plot(n, nextn(n) - n, type = "o", lwd=2, cex=1/2)

nlm

Non-Linear Minimization

Description

This function carries out a minimization of the function f using a Newton-type algorithm. See the references for details.

Usage

nlm(f, p, ..., hessian = FALSE, typsize = rep(1, length(p)),
    fscale = 1, print.level = 0, ndigit = 12, gradtol = 1e-6,
    stepmax = max(1000 * sqrt(sum((p/typsize)^2)), 1000),
    steptol = 1e-6, iterlim = 100, check.analyicals = TRUE)
Arguments

- **f**: the function to be minimized, returning a single numeric value. This should be a function with first argument a vector of the length of `p` followed by any other arguments specified by the `...` argument.
  - If the function value has an attribute called `gradient` or both `gradient` and `hessian` attributes, these will be used in the calculation of updated parameter values. Otherwise, numerical derivatives are used. `deriv` returns a function with suitable `gradient` attribute and optionally a `hessian` attribute.

- **p**: starting parameter values for the minimization.

- **...**: additional arguments to be passed to `f`.

- **hessian**: if `TRUE`, the hessian of `f` at the minimum is returned.

- **typsize**: an estimate of the size of each parameter at the minimum.

- **fscale**: an estimate of the size of `f` at the minimum.

- **print.level**: this argument determines the level of printing which is done during the minimization process. The default value of 0 means that no printing occurs, a value of 1 means that initial and final details are printed and a value of 2 means that full tracing information is printed.

- **ndigit**: the number of significant digits in the function `f`.

- **gradtol**: a positive scalar giving the tolerance at which the scaled gradient is considered close enough to zero to terminate the algorithm. The scaled gradient is a measure of the relative change in `f` in each direction `p[i]` divided by the relative change in `p[i]`.

- **stepmax**: a positive scalar which gives the maximum allowable scaled step length. `stepmax` is used to prevent steps which would cause the optimization function to overflow, to prevent the algorithm from leaving the area of interest in parameter space, or to detect divergence in the algorithm. `stepmax` would be chosen small enough to prevent the first two of these occurrences, but should be larger than any anticipated reasonable step.

- **steptol**: A positive scalar providing the minimum allowable relative step length.

- **iterlim**: a positive integer specifying the maximum number of iterations to be performed before the program is terminated.

- **check.analyticals**: a logical scalar specifying whether the analytic gradients and Hessians, if they are supplied, should be checked against numerical derivatives at the initial parameter values. This can help detect incorrectly formulated gradients or Hessians.

Details

Note that arguments after `...` must be matched exactly.

If a gradient or hessian is supplied but evaluates to the wrong mode or length, it will be ignored if `check.analyticals = TRUE` (the default) with a warning. The hessian is not even checked unless the gradient is present and passes the sanity checks.

The C code for the “perturbed” cholesky, `choldc()` has had a bug in all R versions before 3.4.1.

From the three methods available in the original source, we always use method “1” which is line search.

The functions supplied should always return finite (including not NA and not NaN) values: for the function value itself non-finite values are replaced by the maximum positive value with a warning.
Value

A list containing the following components:

- **minimum**: the value of the estimated minimum of \( f \).
- **estimate**: the point at which the minimum value of \( f \) is obtained.
- **gradient**: the gradient at the estimated minimum of \( f \).
- **hessian**: the hessian at the estimated minimum of \( f \) (if requested).
- **code**: an integer indicating why the optimization process terminated.
  - 1: relative gradient is close to zero, current iterate is probably solution.
  - 2: successive iterates within tolerance, current iterate is probably solution.
  - 3: last global step failed to locate a point lower than estimate. Either estimate is an approximate local minimum of the function or steptol is too small.
  - 4: iteration limit exceeded.
  - 5: maximum step size stepmax exceeded five consecutive times. Either the function is unbounded below, becomes asymptotic to a finite value from above in some direction or stepmax is too small.
- **iterations**: the number of iterations performed.

Source

The current code is by Saikat DebRoy and the R Core team, using a C translation of Fortran code by Richard H. Jones.

References


See Also

- `optim` and `nlminb`.
- `constrOptim` for constrained optimization, `optimize` for one-dimensional minimization and `uniroot` for root finding. `deriv` to calculate analytical derivatives.

For nonlinear regression, `nls` may be better.

Examples

```r
f <- function(x) sum((x-1:length(x))^2)
nlm(f, c(10,10))
nlm(f, c(10,10), print.level = 2)
utils::str(nlm(f, c(5), hessian = TRUE))

f <- function(x, a) sum((x-a)^2)
nlm(f, c(10,10), a = c(3,5))
f <- function(x, a)
{
  res <- sum((x-a)^2)
}
```
nlminb

attr(res, "gradient") <- 2*(x-a)
res
}
nlm(f, c(10,10), a = c(3,5))

## more examples, including the use of derivatives.
## Not run: demo(nlm)

nlminb

Optimization using PORT routines

Description

Unconstrained and box-constrained optimization using PORT routines.
For historical compatibility.

Usage

nlminb(start, objective, gradient = NULL, hessian = NULL, ...,
scale = 1, control = list(), lower = -Inf, upper = Inf)

Arguments

start numeric vector, initial values for the parameters to be optimized.
objective Function to be minimized. Must return a scalar value. The first argument to

objective is the vector of parameters to be optimized, whose initial values
are supplied through start. Further arguments (fixed during the course of the
optimization) to objective may be specified as well (see ...).
gradient Optional function that takes the same arguments as objective and evaluates
the gradient of objective at its first argument. Must return a vector as long as
start.
hessian Optional function that takes the same arguments as objective and evaluates
the hessian of objective at its first argument. Must return a square matrix of order
length(start). Only the lower triangle is used.
... Further arguments to be supplied to objective.
scale See PORT documentation (or leave alone).
control A list of control parameters. See below for details.
lower, upper vectors of lower and upper bounds, replicated to be as long as start. If unspec-
ified, all parameters are assumed to be unconstrained.

Details

Any names of start are passed on to objective and where applicable, gradient and hessian.
The parameter vector will be coerced to double.
If any of the functions returns NA or NaN this is an error for the gradient and Hessian, and such values
for function evaluation are replaced by +Inf with a warning.
Value

A list with components:

- **par**: The best set of parameters found.
- **objective**: The value of objective corresponding to par.
- **convergence**: An integer code. 0 indicates successful convergence.
- **message**: A character string giving any additional information returned by the optimizer, or NULL. For details, see PORT documentation.
- **iterations**: Number of iterations performed.
- **evaluations**: Number of objective function and gradient function evaluations.

Control parameters

Possible names in the control list and their default values are:

- **eval.max**: Maximum number of evaluations of the objective function allowed. Defaults to 200.
- **iter.max**: Maximum number of iterations allowed. Defaults to 150.
- **trace**: The value of the objective function and the parameters is printed every trace’th iteration. Defaults to 0 which indicates no trace information is to be printed.
- **abs.tol**: Absolute tolerance. Defaults to 0 so the absolute convergence test is not used. If the objective function is known to be non-negative, the previous default of 1e-20 would be more appropriate.
- **rel.tol**: Relative tolerance. Defaults to 1e-10.
- **x.tol**: X tolerance. Defaults to 1.5e-8.
- **xf.tol**: False convergence tolerance. Defaults to 2.2e-14.
- **step.min**, **step.max**: Minimum and maximum step size. Both default to 1.
- **sing.tol**: Singular convergence tolerance; defaults to rel.tol.
- **scale.init**: ...
- **diff.g**: An estimated bound on the relative error in the objective function value.

Author(s)

R port: Douglas Bates and Deepayan Sarkar.

Underlying Fortran code by David M. Gay

Source

https://netlib.org/port/

References


See Also

- optim (which is preferred) and nlm.
- optimize for one-dimensional minimization and constrOptim for constrained optimization.
Examples

```r
x <- rbinom(100, mu = 10, size = 10)

hdev <- function(par)
  -sum(dnbinom(x, mu = par[1], size = par[2], log = TRUE))

nlminb(c(9, 12), hdev)

nlminb(c(20, 20), hdev, lower = 0, upper = Inf)

nlminb(c(20, 20), hdev, lower = 0.001, upper = Inf)
```

```r
## slightly modified from the S-PLUS help page for nlminb
# this example minimizes a sum of squares with known solution y
sumsq <- function(x, y) {sum((x-y)^2)}
y <- rep(1,5)
x0 <- rnorm(length(y))
nlminb(start = x0, sumsq, y = y)

# now use bounds with a y that has some components outside the bounds
y <- c(0, 2, 0, -2, 0)
nlminb(start = x0, sumsq, lower = -1, upper = 1, y = y)

# try using the gradient
sumsq.g <- function(x, y) 2*(x-y)
nlminb(start = x0, sumsq, sumsq.g,
       lower = -1, upper = 1, y = y)

# now use the hessian, too
sumsq.h <- function(x, y) diag(2, nrow = length(x))
nlminb(start = x0, sumsq, sumsq.g, sumsq.h,
       lower = -1, upper = 1, y = y)
```

```r
## Rest lifted from optim help page

fr <- function(x) { ## Rosenbrock Banana function
  x1 <- x[1]
x2 <- x[2]
  100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
x1 <- x[1]
x2 <- x[2]
c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
  200 * (x2 - x1 * x1))
}
nlminb(c(-1.2,1), fr)
nlminb(c(-1.2,1), fr, grr)
```

```r
flb <- function(x)
  { p <- length(x); sum(c(1, rep(4, p-1)) * (x - c(1, x[-p])^2)^2) }

## 25-dimensional box constrained
## par[24] is *not* at boundary
nlminb(rep(3, 25), flb, lower = rep(2, 25), upper = rep(4, 25))
```

```r
## trying to use a too small tolerance:
r <- nlminb(rep(3, 25), flb, control = list(rel.tol = 1e-16))
stopifnot(grepl("rel.tol", r$message))
```

---

nls

Nonlinear Least Squares
Description

Determine the nonlinear (weighted) least-squares estimates of the parameters of a nonlinear model.

Usage

nls(formula, data, start, control, algorithm, trace, subset, weights, na.action, model, lower, upper, \ldots)

Arguments

formula a nonlinear model formula including variables and parameters. Will be coerced to a formula if necessary.
data an optional data frame in which to evaluate the variables in formula and weights. Can also be a list or an environment, but not a matrix.
start a named list or named numeric vector of starting estimates. When start is missing (and formula is not a self-starting model, see selfStart), a very cheap guess for start is tried (if algorithm != "plinear").
control an optional list of control settings. See nls.control for the names of the settable control values and their effect.
algorithmc character string specifying the algorithm to use. The default algorithm is a Gauss-Newton algorithm. Other possible values are "plinear" for the Golub-Pereyra algorithm for partially linear least-squares models and "port" for the 'nl2sol' algorithm from the Port library – see the references. Can be abbreviated.
trace logical value indicating if a trace of the iteration progress should be printed. Default is FALSE. If TRUE the residual (weighted) sum-of-squares, the convergence criterion and the parameter values are printed at the conclusion of each iteration. Note that format() is used, so these mostly depend on getOption("digits"). When the "plinear" algorithm is used, the conditional estimates of the linear parameters are printed after the nonlinear parameters. When the "port" algorithm is used the objective function value printed is half the residual (weighted) sum-of-squares.
subset an optional vector specifying a subset of observations to be used in the fitting process.
weights an optional numeric vector of (fixed) weights. When present, the objective function is weighted least squares.
na.action a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit. Value na.exclude can be useful.
model logical. If true, the model frame is returned as part of the object. Default is FALSE.
lower, upper vectors of lower and upper bounds, replicated to be as long as start. If unspecified, all parameters are assumed to be unconstrained. Bounds can only be used with the "port" algorithm. They are ignored, with a warning, if given for other algorithms.
\ldots Additional optional arguments. None are used at present.
Details

An `nls` object is a type of fitted model object. It has methods for the generic functions `anova`, `coef`, `confint`, `deviance`, `df.residual`, `fitted`, `formula`, `logLik`, `predict`, `print`, `profile`, `residuals`, `summary`, `vcov` and `weights`.

Variables in `formula` (and `weights` if not missing) are looked for first in `data`, then the environment of `formula` and finally along the search path. Functions in `formula` are searched for first in the environment of `formula` and then along the search path.

Arguments `subset` and `na.action` are supported only when all the variables in the formula taken from `data` are of the same length: other cases give a warning.

Note that the `anova` method does not check that the models are nested: this cannot easily be done automatically, so use with care.

Value

A list of

- `m` an `nlsModel` object incorporating the model.
- `data` the expression that was passed to `nls` as the data argument. The actual data values are present in the `environment` of the `m` components, e.g., `environment(m$conv)`.
- `call` the matched call with several components, notably `algorithm`.
- `na.action` the "na.action" attribute (if any) of the model frame.
- `dataClasses` the "dataClasses" attribute (if any) of the "terms" attribute of the model frame.
- `model` if `model = TRUE`, the model frame.
- `weights` if `weights` is supplied, the weights.
- `convInfo` a list with convergence information.
- `control` the control list used, see the `control` argument.
- `convergence`, `message` for an `algorithm = "port"` fit only, a convergence code (0 for convergence) and message.

To use these is deprecated, as they are available from `convInfo` now.

Warning

The default settings of `nls` generally fail on artificial “zero-residual” data problems.

The `nls` function uses a relative-offset convergence criterion that compares the numerical imprecision at the current parameter estimates to the residual sum-of-squares. This performs well on data of the form

\[ y = f(x, \theta) + \varepsilon \]

(with \( \text{var}(\varepsilon) > 0 \)). It fails to indicate convergence on data of the form

\[ y = f(x, \theta) \]

because the criterion amounts to comparing two components of the round-off error. To avoid a zero-divide in computing the convergence testing value, a positive constant `scaleOffset` should be added to the denominator sum-of-squares; it is set in `control`, as in the example below; this does not yet apply to `algorithm = "port"`.

The `algorithm = "port"` code appears unfinished, and does not even check that the starting value is within the bounds. Use with caution, especially where bounds are supplied.
Note

Setting `warnOnly = TRUE` in the `control` argument (see `nls.control`) returns a non-converged object (since R version 2.5.0) which might be useful for further convergence analysis, but not for inference.

Author(s)

Douglas M. Bates and Saikat DebRoy: David M. Gay for the Fortran code used by `algorithm = "port"`.

References


https://netlib.org/port/ for the Port library documentation.

See Also

`summary.nls`, `predict.nls`, `profile.nls`.

Self starting models (with ‘automatic initial values’): `selfStart`.

Examples

```r
require(graphics)
DNase1 <- subset(DNase, Run == 1)

## using a selfStart model
fm1DNase1 <- nls(density ~ SSlogis(log(conc), Asym, xmid, scal), DNase1)
summary(fm1DNase1)
## the coefficients only:
coef(fm1DNase1)
## including their SE, etc:
coef(summary(fm1DNase1))

## using conditional linearity
fm2DNase1 <- nls(density ~ 1/(1 + exp((xmid - log(conc))/scal)),
data = DNase1,
start = list(xmid = 0, scal = 1),
algorithm = "plinear")
summary(fm2DNase1)

## without conditional linearity
fm3DNase1 <- nls(density ~ Asym/(1 + exp((xmid - log(conc))/scal)),
data = DNase1,
start = list(Asym = 3, xmid = 0, scal = 1))
summary(fm3DNase1)

## using Port's nl2sol algorithm
fm4DNase1 <- nls(density ~ Asym/(1 + exp((xmid - log(conc))/scal)),
data = DNase1,
start = list(Asym = 3, xmid = 0, scal = 1),
algorithm = "port")
```
summary(fm4DNase1)

## weighted nonlinear regression
Treated <- Puromycin[Puromycin$state == "treated",]

weighted.MM <- function(resp, conc, Vm, K)
{
## Purpose: exactly as white book p. 451 -- RHS for nls()
## Weighted version of Michaelis-Menten model
## ----------------------------------------------------------
## Arguments: 'y', 'x' and the two parameters (see book)
## ----------------------------------------------------------
## Author: Martin Maechler, Date: 23 Mar 2001

pred <- (Vm * conc)/(K + conc)
(pred - resp) / sqrt(pred)
}

Pur.wt <- nls(~ weighted.MM(rate, conc, Vm, K),
              data = Treated,
              start = list(Vm = 200, K = 0.1))
summary(Pur.wt)

## Passing arguments using a list that can not be coerced to a data.frame
lisTreat <- with(Treated,
                 list(conc1 = conc[1], conc.1 = conc[-1], rate = rate))

weighted.MM1 <- function(resp, conc1, conc.1, Vm, K)
{
conc <- c(conc1, conc.1)
pred <- (Vm * conc)/(K + conc)
(pred - resp) / sqrt(pred)
}

Pur.wt1 <- nls(~ weighted.MM1(rate, conc1, conc.1, Vm, K),
                data = lisTreat,
                start = list(Vm = 200, K = 0.1))
stopifnot(all.equal(coef(Pur.wt), coef(Pur.wt1)))

## If the value of the right side [of formula] has an attribute called  
## 'gradient' this should be a matrix with the number of rows equal  
## to the length of the response and one column for each parameter.

weighted.MM.grad <- function(resp, conc1, conc.1, Vm, K)
{
conc <- c(conc1, conc.1)
K.conc <- K+conc
dy.dV <- conc/K.conc
dy.dK <- -Vm*dy.dV/K.conc
pred <- Vm*dy.dV
pred.5 <- sqrt(pred)
dev <- (resp - pred) / pred.5
Ddev <- -0.5*(resp+pred)/(pred.5*pred)
attr(dev, "gradient") <- Ddev * cbind(Vm = dy.dV, K = dy.dK)
dev
}

Pur.wt.grad <- nls(~ weighted.MM.grad(rate, conc1, conc.1, Vm, K),
                   data = lisTreat,
                   start = list(Vm = 200, K = 0.1))
rbind(coef(Pur.wt), coef(Pur.wt1), coef(Pur.wt.grad))

## In this example, there seems no advantage to providing the gradient.
## In other cases, there might be.

## The two examples below show that you can fit a model to
## artificial data with noise but not to artificial data
## without noise.
x <- 1:10
y <- 2*x + 3 # perfect fit
## terminates in an error, because convergence cannot be confirmed:
try(nls(y ~ a + b*x, start = list(a = 0.12345, b = 0.54321)))
## adjusting the convergence test by adding 'scaleOffset' to its denominator RSS:
nls(y ~ a + b*x, start = list(a = 0.12345, b = 0.54321),
   control = list(scaleOffset = 1, printEval=TRUE))
## Alternatively jittering the "too exact" values, slightly:
set.seed(27)
yeps <- y + rnorm(length(y), sd = 0.01) # added noise
nls(yeps ~ a + b*x, start = list(a = 0.12345, b = 0.54321))

## the nls() internal cheap guess for starting values can be sufficient:
x <- -(1:100)/10
y <- 100 + 10 * exp(x / 2) + rnorm(x)/10
nlmod <- nls(y ~ Const + A * exp(B * x))
plot(x,y, main = "nls(*), data, true function and fit, n=100")
curve(100 + 10 * exp(x / 2), col = 4, add = TRUE)
lines(x, predict(nlmod), col = 2)

## Here, requiring close convergence, must use more accurate numerical differentiation,
## as this typically gives Error: "step factor .. reduced below 'minFactor' .."
## IGNORE_RDIFF_BEGIN
try(nlm1 <- update(nlmod, control = list(tol = 1e-7)))
o2 <- options(digits = 10) # more accuracy for 'trace'
## central differencing works here typically (PR#18165: not converging on *some*):
ctr2 <- nls.control(nDcentral=TRUE, tol = 8e-8, # <- even smaller than above
   warnOnly = TRUE || # << work around; e.g. needed on some ATLAS-Lapack setups
   (grepl("aarch64.*linux", R.version$platform) && grepl("NixOS", osVersion)
   )
)(nlm2 <- update(nlmod, control = ctr2, trace = TRUE)); options(o2)
## --> convergence tolerance 4.997e-8 (in 11 iter.)
## IGNORE_RDIFF_END

## The muscle dataset in MASS is from an experiment on muscle
## contraction on 21 animals. The observed variables are Strip
## (identifier of muscle), Conc (Cacl concentration) and Length
## (resulting length of muscle section).
## IGNORE_RDIFF_BEGIN
if(requireNamespace("MASS", quietly = TRUE)) withAutoprint({
## The non linear model considered is
## Length = alpha + beta*exp(-Conc/theta) + error
## where theta is constant but alpha and beta may vary with Strip.
with(MASS::muscle, table(Strip)) # 2, 3 or 4 obs per strip

## We first use the plinear algorithm to fit an overall model,
## ignoring that alpha and beta might vary with Strip.
musc.1 <- nls(Length ~ cbind(1, exp(-Conc/th)), MASS::muscle,
               start = list(th = 1), algorithm = "plinear")
summary(musc.1)

## Then we use nls' indexing feature for parameters in non-linear
## models to use the conventional algorithm to fit a model in which
## alpha and beta vary with Strip. The starting values are provided
## by the previously fitted model.
## Note that with indexed parameters, the starting values must be
## given in a list (with names):
b <- coef(musc.1)
musc.2 <- nls(Length ~ a[Strip] + b[Strip]*exp(-Conc/th), MASS::muscle,
               start = list(a = rep(b[2], 21), b = rep(b[3], 21), th = b[1]))
summary(musc.2)

---

### nls.control

Control the Iterations in nls

**Description**

Allow the user to set some characteristics of the `nls` nonlinear least squares algorithm.

**Usage**

```r
nls.control(maxiter = 50, tol = 1e-05, minFactor = 1/1024,
             printEval = FALSE, warnOnly = FALSE, scaleOffset = 0,
             nDcentral = FALSE)
```

**Arguments**

- `maxiter` A positive integer specifying the maximum number of iterations allowed.
- `tol` A positive numeric value specifying the tolerance level for the relative offset convergence criterion.
- `minFactor` A positive numeric value specifying the minimum step-size factor allowed on any step in the iteration. The increment is calculated with a Gauss-Newton algorithm and successively halved until the residual sum of squares has been decreased or until the step-size factor has been reduced below this limit.
- `printEval` a logical specifying whether the number of evaluations (steps in the gradient direction taken each iteration) is printed.
- `warnOnly` a logical specifying whether `nls()` should return instead of signalling an error in the case of termination before convergence. Termination before convergence happens upon completion of `maxiter` iterations, in the case of a singular gradient, and in the case that the step-size factor is reduced below `minFactor`. 
scaleOffset  a constant to be added to the denominator of the relative offset convergence criterion calculation to avoid a zero divide in the case where the fit of a model to data is very close. The default value of 0 keeps the legacy behaviour of nls(). A value such as 1 seems to work for problems of reasonable scale with very small residuals.

nDcentral only when numerical derivatives are used: logical indicating if central differences should be employed, i.e., numericDeriv(*, central=TRUE) be used.

Value
A list with components
maxiter
tol
minFactor
printEval
warnOnly
scaleOffset
nDcentral

with meanings as explained under ‘Arguments’.

Author(s)
Douglas Bates and Saikat DebRoy; John C. Nash for part of the scaleOffset option.

References

See Also
nls

Examples
nls.control(minFactor = 1/2048)

NLSstAsymptotic

Fit the Asymptotic Regression Model

Description
Fits the asymptotic regression model, in the form \( b_0 + b_1 \times (1 - \exp(-\exp(lrc) \times x)) \) to the xy data. This can be used as a building block in determining starting estimates for more complicated models.

Usage
NLSstAsymptotic(xy)
NLSstClosestX

Arguments

xy a sortedXyData object

Value

A numeric value of length 3 with components labelled b0, b1, and lrc. b0 is the estimated intercept on the y-axis, b1 is the estimated difference between the asymptote and the y-intercept, and lrc is the estimated logarithm of the rate constant.

Author(s)

José Pinheiro and Douglas Bates

See Also

SSasymp

Examples

Lob.329 <- Loblolly[ Lobblolly$Seed == "329", ]
print(NLSstAsymptotic(sortedXyData(expression(age),
expression(height),
Lob.329)), digits = 3)

---

NLSstClosestX  Inverse Interpolation

Description

Use inverse linear interpolation to approximate the x value at which the function represented by xy is equal to yval.

Usage

NLSstClosestX(xy, yval)

Arguments

xy a sortedXyData object

yval a numeric value on the y scale

Value

A single numeric value on the x scale.

Author(s)

José Pinheiro and Douglas Bates

See Also

sortedXyData, NLSstLfAsymptote, NLSstRtAsymptote, selfStart
Examples

 DNase.2 <- DNase[ DNase$Run == "2", ]
 DN.srt <- sortedXyData(expression(log(conc)), expression(density), DNase.2)
 NLSstClosestX(DN.srt, 1.0)

NLSstLfAsymptote

**Horizontal Asymptote on the Left Side**

Description

Provide an initial guess at the horizontal asymptote on the left side (i.e., small values of \( x \)) of the graph of \( y \) versus \( x \) from the \( xy \) object. Primarily used within initial functions for self-starting nonlinear regression models.

Usage

NLSstLfAsymptote(xy)

Arguments

xy

a sortedXyData object

Value

A single numeric value estimating the horizontal asymptote for small \( x \).

Author(s)

José Pinheiro and Douglas Bates

See Also

sortedXyData, NLSstClosestX, NLSstRtAsymptote, selfStart

Examples

 DNase.2 <- DNase[ DNase$Run == "2", ]
 DN.srt <- sortedXyData( expression(log(conc)), expression(density), DNase.2 )
 NLSstLfAsymptote( DN.srt )
**NLSstRtAsymptote**

**Horizontal Asymptote on the Right Side**

**Description**

Provide an initial guess at the horizontal asymptote on the right side (i.e., large values of \( x \)) of the graph of \( y \) versus \( x \) from the \( xy \) object. Primarily used within initial functions for self-starting nonlinear regression models.

**Usage**

```r
NLSstRtAsymptote(xy)
```

**Arguments**

- `xy` a `sortedXyData` object

**Value**

A single numeric value estimating the horizontal asymptote for large \( x \).

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

`sortedXyData`, `NLSstClosestX`, `NLSstRtAsymptote`, `selfStart`

**Examples**

```r
DNase.2 <- DNase[ DNase$Run == "2", ]
DN.srt <- sortedXyData( expression(log(conc)), expression(density), DNase.2 )
NLSstRtAsymptote( DN.srt )
```

---

**nobs**

*Extract the Number of Observations from a Fit.*

**Description**

Extract the number of ‘observations’ from a model fit. This is principally intended to be used in computing BIC (see `AIC`).

**Usage**

```r
nobs(object, ...)
```

## Default S3 method:
```r
nobs(object, use.fallback = FALSE, ...)
```
Arguments

object A fitted model object.
use.fallback logical: should fallback methods be used to try to guess the value?

Details

This is a generic function, with an S4 generic in package stats4. There are methods in this package for objects of classes "lm", "glm", "nls" and "logLik", as well as a default method (which throws an error, unless use.fallback = TRUE when it looks for weights and residuals components – use with care!).

The main usage is in determining the appropriate penalty for BIC, but nobs is also used by the stepwise fitting methods step, add1 and drop1 as a quick check that different fits have been fitted to the same set of data (and not, say, that further rows have been dropped because of NAs in the new predictors).

For lm, glm and nls fits, observations with zero weight are not included.

Value

A single number, normally an integer. Could be NA.

See Also

AIC.

Normal

The Normal Distribution

Description

Density, distribution function, quantile function and random generation for the normal distribution with mean equal to mean and standard deviation equal to sd.

Usage

dnorm(x, mean = 0, sd = 1, log = FALSE)
pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
rnorm(n, mean = 0, sd = 1)

Arguments

x, q vector of quantiles.
p vector of probabilities.
n number of observations. If length(n) > 1, the length is taken to be the number required.
mean vector of means.
sd vector of standard deviations.
log, log.p logical; if TRUE, probabilities p are given as log(p).
lower.tail logical; if TRUE (default), probabilities are \( P[X \leq x] \) otherwise, \( P[X > x] \).
Details

If mean or sd are not specified they assume the default values of 0 and 1, respectively.

The normal distribution has density

\[ f(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x-\mu)^2}{2\sigma^2}} \]

where \( \mu \) is the mean of the distribution and \( \sigma \) the standard deviation.

Value

dnorm gives the density, pnorm gives the distribution function, qnorm gives the quantile function, and rnorm generates random deviates.

The length of the result is determined by n for rnorm, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

For sd = 0 this gives the limit as sd decreases to 0, a point mass at mu. sd < 0 is an error and returns NaN.

Source

For pnorm, based on


For qnorm, the code is based on a C translation of


which provides precise results up to about 16 digits for log.p=FALSE. For log scale probabilities in the extreme tails, since R version 4.1.0, extensively since 4.3.0, asymptotic expansions are used which have been derived and explored in


For rnorm, see RNG for how to select the algorithm and for references to the supplied methods.

References


See Also

Distributions for other standard distributions, including dlnorm for the Lognormal distribution.
Examples

```r
callGraphics()

dnorm(0) == 1/sqrt(2*pi)
dnorm(1) == exp(-1/2)/sqrt(2*pi)
dnorm(1) == 1/sqrt(2*pi*exp(1))

## Using "log = TRUE" for an extended range :
par(mfrow = c(2,1))
plot(function(x) dnorm(x, log = TRUE), -60, 50,
     main = "log Normal density")
curve(log(dnorm(x)), add = TRUE, col = "red", lwd = 2)

mtext("dnorm(x, log=TRUE)", adj = 0)
mtext("log(dnorm(x))", col = "red", adj = 1)

plot(function(x) pnorm(x, log.p = TRUE), -50, 10,
     main = "log Normal Cumulative")
curve(log(pnorm(x)), add = TRUE, col = "red", lwd = 2)

mtext("pnorm(x, log=TRUE)", adj = 0)
mtext("log(pnorm(x))", col = "red", adj = 1)

## if you want the so-called 'error function'
erf <- function(x) 2 * pnorm(x * sqrt(2)) - 1
## (see Abramowitz and Stegun 29.2.29)
## and the so-called 'complementary error function'
erfc <- function(x) 2 * pnorm(x * sqrt(2), lower = FALSE)
## and the inverses
erfinv <- function (x) qnorm((1 + x)/2)/sqrt(2)
erfcinv <- function (x) qnorm(x/2, lower = FALSE)/sqrt(2)
```

dnumericDeriv
dnumericDeriv

Evaluate Derivatives Numerically

dnumericDeriv

dnumericDeriv numerically evaluates the gradient of an expression.

Usage

```r
numericDeriv(expr, theta, rho = parent.frame(), dir = 1,
             eps = .Machine$double.eps ^ (1/if(central) 3 else 2),
             central = FALSE)
```

Arguments

- `expr` expression or call to be differentiated. Should evaluate to a numeric vector.
- `theta` character vector of names of numeric variables used in expr.
- `rho` environment containing all the variables needed to evaluate expr.
- `dir` numeric vector of directions, typically with values in -1, 1 to use for the finite differences; will be recycled to the length of theta.
- `eps` a positive number, to be used as unit step size $h$ for the approximate numerical derivative $(f(x + h) - f(x))/h$ or the central version, see central.
central logical indicating if central divided differences should be computed, i.e., \((f(x + h) - f(x - h)) / 2h\). These are typically more accurate but need more evaluations of \(f()\).

Details

This is a front end to the C function numeric_deriv, which is described in Writing R Extensions. The numeric variables must be of type double and not integer.

Value

The value of eval(expr, envir = rho) plus a matrix attribute "gradient". The columns of this matrix are the derivatives of the value with respect to the variables listed in theta.

Author(s)

Saikat DebRoy <saikat@stat.wisc.edu>; tweaks and eps, central options by R Core Team.

Examples

```r
myenv <- new.env()
myenv$mean <- 0.
myenv$sd  <- 1.
myenv$x   <- seq(-3., 3., length.out = 31)
nD <- numericDeriv(quote(pnorm(x, mean, sd)), c("mean", "sd"), myenv)
str(nD)
```

```r
## Visualize :
require(graphics)
matplot(myenv$x, cbind(c(nD), attr(nD, "gradient")), type="l")
abline(h=0, lty=3)
```

```r
## "gradient" is close to the true derivatives, you don't see any diff.:
curve( - dnorm(x), col=2, lty=3, lwd=2, add=TRUE)
curve(-x*dnorm(x), col=3, lty=3, lwd=2, add=TRUE)
```

```r
## IGNORE_RDIFF_BEGIN
# shows 1.609e-8 on most platforms
all.equal(attr(nD,"gradient"),
          with(myenv, cbind(-dnorm(x), -x*dnorm(x))))
## IGNORE_RDIFF_END
```

offset Include an Offset in a Model Formula

Description

An offset is a term to be added to a linear predictor, such as in a generalised linear model, with known coefficient 1 rather than an estimated coefficient.

Usage

```r
offset(object)
```
Arguments

object An offset to be included in a model frame

Details

There can be more than one offset in a model formula, but - is not supported for offset terms (and is equivalent to +).

Value

The input value.

See Also

model.offset, model.frame.

For examples see glm and Insurance in package MASS.

Description

Test whether two or more samples from normal distributions have the same means. The variances are not necessarily assumed to be equal.

Usage

oneway.test(formula, data, subset, na.action, var.equal = FALSE)

Arguments

formula a formula of the form lhs ~ rhs where lhs gives the sample values and rhs the corresponding groups.
data an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset an optional vector specifying a subset of observations to be used.na.action a function which indicates what should happen when the data contain NAs. Defaults togetOption("na.action").var.equal a logical variable indicating whether to treat the variances in the samples as equal. If TRUE, then a simple F test for the equality of means in a one-way analysis of variance is performed. If FALSE, an approximate method of Welch (1951) is used, which generalizes the commonly known 2-sample Welch test to the case of arbitrarily many samples.

Details

If the right-hand side of the formula contains more than one term, their interaction is taken to form the grouping.
Value

A list with class "htest" containing the following components:

- **statistic**: the value of the test statistic.
- **parameter**: the degrees of freedom of the exact or approximate F distribution of the test statistic.
- **p.value**: the p-value of the test.
- **method**: a character string indicating the test performed.
- **data.name**: a character string giving the names of the data.

References


See Also

The standard t test (**t.test**) as the special case for two samples; the Kruskal-Wallis test (**kruskal.test**) for a nonparametric test for equal location parameters in a one-way layout.

Examples

```r
## Not assuming equal variances
oneway.test(extra ~ group, data = sleep)
## Assuming equal variances
oneway.test(extra ~ group, data = sleep, var.equal = TRUE)
## which gives the same result as
anova(lm(extra ~ group, data = sleep))
```

---

**optim**

*General-purpose Optimization*

Description

General-purpose optimization based on Nelder–Mead, quasi-Newton and conjugate-gradient algorithms. It includes an option for box-constrained optimization and simulated annealing.

Usage

```r
optim(par, fn, gr = NULL, ..., 
      method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN", 
                 "Brent"), 
      lower = -Inf, upper = Inf, 
      control = list(), hessian = FALSE)

optimHess(par, fn, gr = NULL, ..., control = list())
```
Arguments

par  Initial values for the parameters to be optimized over.

fn   A function to be minimized (or maximized), with first argument the vector of
     parameters over which minimization is to take place. It should return a scalar
     result.

gr  A function to return the gradient for the "BFGS", "CG" and "L-BFGS-B" methods.
     If it is NULL, a finite-difference approximation will be used.
     For the "SANN" method it specifies a function to generate a new candidate point.
     If it is NULL a default Gaussian Markov kernel is used.

... Further arguments to be passed to fn and gr.

method The method to be used. See ‘Details’. Can be abbreviated.

lower, upper Bounds on the variables for the "L-BFGS-B" method, or bounds in which to
search for method "Brent".

control a list of control parameters. See ‘Details’.

hessian Logical. Should a numerically differentiated Hessian matrix be returned?

Details

Note that arguments after ... must be matched exactly.

By default optim performs minimization, but it will maximize if control$fnscale is negative.
optimHess is an auxiliary function to compute the Hessian at a later stage if hessian = TRUE was
forgotten.

The default method is an implementation of that of Nelder and Mead (1965), that uses only func-
tion values and is robust but relatively slow. It will work reasonably well for non-differentiable
functions.

Method "BFGS" is a quasi-Newton method (also known as a variable metric algorithm), specifi-
cally that published simultaneously in 1970 by Broyden, Fletcher, Goldfarb and Shanno. This uses
function values and gradients to build up a picture of the surface to be optimized.

Method "CG" is a conjugate gradients method based on that by Fletcher and Reeves (1964) (but
with the option of Polak–Ribiére or Beale–Sorenson updates). Conjugate gradient methods will
generally be more fragile than the BFGS method, but as they do not store a matrix they may be
successful in much larger optimization problems.

Method "L-BFGS-B" is that of Byrd et. al. (1995) which allows box constraints, that is each
variable can be given a lower and/or upper bound. The initial value must satisfy the constraints.
This uses a limited-memory modification of the BFGS quasi-Newton method. If non-trivial bounds
are supplied, this method will be selected, with a warning.

Nocedal and Wright (1999) is a comprehensive reference for the previous three methods.

Method "SANN" is by default a variant of simulated annealing given in Belisle (1992). Simulated-
annealing belongs to the class of stochastic global optimization methods. It uses only function
values but is relatively slow. It will also work for non-differentiable functions. This implementation
uses the Metropolis function for the acceptance probability. By default the next candidate point
is generated from a Gaussian Markov kernel with scale proportional to the actual temperature. If
a function to generate a new candidate point is given, method "SANN" can also be used to solve
combinatorial optimization problems. Temperatures are decreased according to the logarithmic
cooling schedule as given in Belisle (1992, p. 890); specifically, the temperature is set to temp / 
log(((t-1) %/% tmax)*tmax + exp(1)), where t is the current iteration step and temp and tmax
are specifiable via control, see below. Note that the "SANN" method depends critically on the
settings of the control parameters. It is not a general-purpose method but can be very useful in
getting to a good value on a very rough surface.
Method "Brent" is for one-dimensional problems only, using optimize(). It can be useful in cases
where optimize() is used inside other functions where only method can be specified, such as in mle
from package stats4.
Function fn can return NA or Inf if the function cannot be evaluated at the supplied value, but the
initial value must have a computable finite value of fn. (Except for method "L-BFGS-B" where the
values should always be finite.)
optim can be used recursively, and for a single parameter as well as many. It also accepts a zero-
length par, and just evaluates the function with that argument.
The control argument is a list that can supply any of the following components:

trace Non-negative integer. If positive, tracing information on the progress of the optimization
is produced. Higher values may produce more tracing information: for method "L-BFGS-B"
there are six levels of tracing. (To understand exactly what these do see the source code:
higher levels give more detail.)
fnscale An overall scaling to be applied to the value of fn and gr during optimization. If
negative, turns the problem into a maximization problem. Optimization is performed on
fn(par)/fnscale.
parscale A vector of scaling values for the parameters. Optimization is performed on
par/parscale and these should be comparable in the sense that a unit change in any ele-
ment produces about a unit change in the scaled value. Not used (nor needed) for
method = "Brent".
ndeps A vector of step sizes for the finite-difference approximation to the gradient, on
par/parscale scale. Defaults to 1e-3.
maxit The maximum number of iterations. Defaults to 100 for the derivative-based methods, and
500 for "Nelder-Mead". For "SANN" maxit gives the total number of function evaluations: there is no other stopping
criterion. Defaults to 10000.
abstol The absolute convergence tolerance. Only useful for non-negative functions, as a tolerance
for reaching zero.
reltol Relative convergence tolerance. The algorithm stops if it is unable to reduce
the value by a factor of reltol * (abs(val) + reltol) at a step. Defaults to
sqrt(.Machine$double.eps), typically about 1e-8.
alpha, beta, gamma Scaling parameters for the "Nelder-Mead" method. alpha is the reflection
factor (default 1.0), beta the contraction factor (0.5) and gamma the expansion factor (2.0).
REPORT The frequency of reports for the "BFGS", "L-BFGS-B" and "SANN" methods if
control$trace is positive. Defaults to every 10 iterations for "BFGS" and "L-BFGS-B", or
every 100 temperatures for "SANN".
warn.1d.NelderMead a logical indicating if the (default) "Nelder-Mead" method should sig-
nal a warning when used for one-dimensional minimization. As the warning is sometimes
inappropriate, you can suppress it by setting this option to false.
type for the conjugate-gradients method. Takes value 1 for the Fletcher–Reeves update, 2 for
Polak–Ribiere and 3 for Beale–Sorenson.
lmm is an integer giving the number of BFGS updates retained in the "L-BFGS-B" method, It de-
defaults to 5.
factr controls the convergence of the "L-BFGS-B" method. Convergence occurs when the reduct-
ion in the objective is within this factor of the machine tolerance. Default is 1e7, that is a
tolerance of about 1e-8.
pgtol helps control the convergence of the "L-BFGS-B" method. It is a tolerance on the projected gradient in the current search direction. This defaults to zero, when the check is suppressed.

temp controls the "SANN" method. It is the starting temperature for the cooling schedule. Defaults to 10.

tmax is the number of function evaluations at each temperature for the "SANN" method. Defaults to 10.

Any names given to par will be copied to the vectors passed to fn and gr. Note that no other attributes of par are copied over.

The parameter vector passed to fn has special semantics and may be shared between calls: the function should not change or copy it.

**Value**

For optim, a list with components:

- **par** The best set of parameters found.
- **value** The value of fn corresponding to par.
- **counts** A two-element integer vector giving the number of calls to fn and gr respectively. This excludes those calls needed to compute the Hessian, if requested, and any calls to fn to compute a finite-difference approximation to the gradient.
- **convergence** An integer code. 0 indicates successful completion (which is always the case for "SANN" and "Brent"). Possible error codes are
  - 1 indicates that the iteration limit maxit had been reached.
  - 10 indicates degeneracy of the Nelder–Mead simplex.
  - 51 indicates a warning from the "L-BFGS-B" method; see component message for further details.
  - 52 indicates an error from the "L-BFGS-B" method; see component message for further details.
- **message** A character string giving any additional information returned by the optimizer, or NULL.
- **hessian** Only if argument hessian is true. A symmetric matrix giving an estimate of the Hessian at the solution found. Note that this is the Hessian of the unconstrained problem even if the box constraints are active.

For optimHess, the description of the hessian component applies.

**Note**

optim will work with one-dimensional pars, but the default method does not work well (and will warn). Method "Brent" uses optimize and needs bounds to be available; "BFGS" often works well enough if not.

**Source**

The code for methods "Nelder–Mead", "BFGS" and "CG" was based originally on Pascal code in Nash (1990) that was translated by p2c and then hand-optimized. Dr Nash has agreed that the code can be made freely available.

The code for method "L-BFGS-B" is based on Fortran code by Zhu, Byrd, Lu-Chen and Nocedal obtained from Netlib (file ‘opt/lbfgs_bcm.shar’: another version is in ‘toms/778’).

The code for method "SANN" was contributed by A. Trapletti.
References


See Also

`nlm`, `nlminb`.

`optimize` for one-dimensional minimization and `constrOptim` for constrained optimization.

Examples

```r
require(graphics)
fr <- function(x) { ## Rosenbrock Banana function
  x1 <- x[1]
  x2 <- x[2]
  100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
  x1 <- x[1]
  x2 <- x[2]
  c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
    200 * (x2 - x1 * x1))
}
optim(c(-1.2,1), fr)
(res <- optim(c(-1.2,1), fr, grr, method = "BFGS"))
optimHess(res$par, fr, grr)
optim(c(-1.2,1), fr, grr, method = "BFGS", hessian = TRUE)
## These do not converge in the default number of steps
optim(c(-1.2,1), fr, grr, method = "CG")
optim(c(-1.2,1), fr, grr, method = "CG", control = list(type = 2))
optim(c(-1.2,1), fr, grr, method = "L-BFGS-B")
flb <- function(x) {
  p <- length(x); sum(c(1, rep(4, p-1)) * (x - c(1, x[-p])^2)^2)
}
## 25-dimensional box constrained
optim(rep(3, 25), flb, NULL, method = "L-BFGS-B",
     lower = rep(2, 25), upper = rep(4, 25)) # par[24] is *not* at boundary

## "wild" function , global minimum at about -15.81515
fw <- function(x)
  10*sin(0.3*x)*sin(1.3*x^2) + 0.00001*x^4 + 0.2*x+80
```
plot(fw, -50, 50, n = 1000, main = "optim() minimising 'wild function'")

res <- optim(50, fw, method = "SANN",
  control = list(maxit = 20000, temp = 20, parscale = 20))

res

## Now improve locally {typically only by a small bit}:
(r2 <- optim(res$par, fw, method = "BFGS"))
points(r2$par, r2$value, pch = 8, col = "red", cex = 2)

## Combinatorial optimization: Traveling salesman problem
library(stats) # normally loaded

eurodistmat <- as.matrix(eurodist)
distance <- function(sq) {
  # Target function
  sq2 <- embed(sq, 2)
  sum(eurodistmat[cbind(sq2[,2], sq2[,1])])
}
genseq <- function(sq) {
  # Generate new candidate sequence
  idx <- seq(2, NROW(eurodistmat)-1)
  changepoints <- sample(idx, size = 2, replace = FALSE)
  tmp <- sq[changepoints[1]]
  sq[changepoints[1]] <- sq[changepoints[2]]
  sq[changepoints[2]] <- tmp
  sq
}

sq <- c(1:nrow(eurodistmat), 1) # Initial sequence: alphabetic
distance(sq)

# rotate for conventional orientation
loc <- -cmdscale(eurodist, add = TRUE)$points
x <- loc[,1]; y <- loc[,2]
s <- seq_len(nrow(eurodistmat))
tspinit <- loc[s,]
plot(x, y, type = "n", asp = 1, xlab = "", ylab = "",
  main = "initial solution of traveling salesman problem", axes = FALSE)
arrows(tspinit[s,1], tspinit[s,2], tspinit[s+1,1], tspinit[s+1,2],
  angle = 10, col = "green")
text(x, y, labels(eurodist), cex = 0.8)

set.seed(123) # chosen to get a good soln relatively quickly
res <- optim(sq, distance, genseq, method = "SANN",
  control = list(maxit = 30000, temp = 2000, trace = TRUE,
                  REPORT = 500))
res # Near optimum distance around 12842
tspres <- loc[res$par,]
plot(x, y, type = "n", asp = 1, xlab = "", ylab = "",
  main = "optim() 'solving' traveling salesman problem", axes = FALSE)
arrows(tspres[s,1], tspres[s,2], tspres[s+1,1], tspres[s+1,2],
  angle = 10, col = "red")
text(x, y, labels(eurodist), cex = 0.8)

## 1-D minimization: "Brent" or optimize() being preferred.. but NM may be ok and "unavoidable",
## ---------------- so we can suppress the check+warning :
system.time(rO <- optimize(function(x) (x-pi)^2, c(0, 10)))
system.time(ro <- optim(1, function(x) (x-pi)^2, control=list(warn.1d.NelderMead = FALSE)))
ro$minimum - pi # 0 (perfect), on one platform
ro$par - pi # ~1.9e-4  on one platform
utils::str(ro)

---

**optimize**  
One Dimensional Optimization

**Description**  
The function `optimize` searches the interval from `lower` to `upper` for a minimum or maximum of the function `f` with respect to its first argument.  
`optimise` is an alias for `optimize`.

**Usage**  
```
optimize(f, interval, ..., lower = min(interval), upper = max(interval),
maximum = FALSE,
tol = .Machine$double.eps^0.25)
```

```
optimise(f, interval, ..., lower = min(interval), upper = max(interval),
maximum = FALSE,
tol = .Machine$double.eps^0.25)
```

**Arguments**  
- **f**: the function to be optimized. The function is either minimized or maximized over its first argument depending on the value of `maximum`.
- **interval**: a vector containing the end-points of the interval to be searched for the minimum.
- **...**: additional named or unnamed arguments to be passed to `f`.
- **lower**: the lower end point of the interval to be searched.
- **upper**: the upper end point of the interval to be searched.
- **maximum**: logical. Should we maximize or minimize (the default)?
- **tol**: the desired accuracy.

**Details**  
Note that arguments after `...` must be matched exactly.

The method used is a combination of golden section search and successive parabolic interpolation, and was designed for use with continuous functions. Convergence is never much slower than that for a Fibonacci search. If `f` has a continuous second derivative which is positive at the minimum (which is not at `lower` or `upper`), then convergence is superlinear, and usually of the order of about 1.324.

The function `f` is never evaluated at two points closer together than $\epsilon |x_0| + (tol/3)$, where $\epsilon$ is approximately $\sqrt{\cdot \text{Machine}\$double.eps}$ and $x_0$ is the final abscissa `optimize()`$minimum$. If `f` is a unimodal function and the computed values of `f` are always unimodal when separated by at least $\epsilon |x| + (tol/3)$, then $x_0$ approximates the abscissa of the global minimum of `f` on the interval `lower`, `upper` with an error less than $\epsilon |x_0| + tol$. 
If f is not unimodal, then optimize() may approximate a local, but perhaps non-global, minimum to the same accuracy.

The first evaluation of f is always at \( x_1 = a + (1 - \phi)(b - a) \) where \((a, b) = (\text{lower, upper})\) and \( \phi = \left(\frac{\sqrt{5} - 1}{2}\right) = 0.61803.. \) is the golden section ratio. Almost always, the second evaluation is at \( x_2 = a + \phi(b - a) \). Note that a local minimum inside \([x_1, x_2]\) will be found as solution, even when f is constant in there, see the last example.

f will be called as \( f(x, \ldots) \) for a numeric value of \( x \).

The argument passed to f has special semantics and used to be shared between calls. The function should not copy it.

Value

A list with components minimum (or maximum) and objective which give the location of the minimum (or maximum) and the value of the function at that point.

Source

A C translation of Fortran code https://netlib.org/fmm/fmin.f (author(s) unstated) based on the Algol 60 procedure localmin given in the reference.

References


See Also

nlm, uniroot.

Examples

```r
require(graphics)
f <- function (x, a) (x - a)^2
xmin <- optimize(f, c(0, 1), tol = 0.0001, a = 1/3)
xmin
## See where the function is evaluated:
optimize(function(x) x^2*(print(x)-1), lower = 0, upper = 10)
## "wrong" solution with unlucky interval and piecewise constant f():
f <- function(x) ifelse(x > -1, ifelse(x < 4, exp(-1/abs(x - 1)), 10), 10)
fp <- function(x) { print(x); f(x) }
plot(f, -2,5, ylim = 0:1, col = 2)
optimize(fp, c(-4, 20))  # doesn't see the minimum
optimize(fp, c(-7, 20))  # ok
```
order.dendrogram  Ordering or Labels of the Leaves in a Dendrogram

Description

These functions return the order (index) or the "label" attribute for the leaves in a dendrogram. These indices can then be used to access the appropriate components of any additional data.

Usage

order.dendrogram(x)

## S3 method for class 'dendrogram'
labels(object, ...) 

Arguments

x, object  a dendrogram (see as.dendrogram).
...  additional arguments 

Details

The indices or labels for the leaves in left to right order are retrieved.

Value

A vector with length equal to the number of leaves in the dendrogram is returned. From r <- order.dendrogram(), each element is the index into the original data (from which the dendrogram was computed).

Author(s)

R. Gentleman (order.dendrogram) and Martin Maechler (labels.dendrogram).

See Also

reorder.dendrogram.

Examples

set.seed(123)
x <- rnorm(10)
hc <- hclust(dist(x))
hc$order
dd <- as.dendrogram(hc)
order.dendrogram(dd) ## the same :
stopifnot(hc$order == order.dendrogram(dd))

d2 <- as.dendrogram(hclust(dist(USArrests)))
labels(d2) ## in this case the same as
stopifnot(identical(labels(d2),
                     rownames(USArrests)[order.dendrogram(d2)]))
p.adjust

Adjust P-values for Multiple Comparisons

Description

Given a set of p-values, returns p-values adjusted using one of several methods.

Usage

p.adjust(p, method = p.adjust.methods, n = length(p))

p.adjust.methods
# c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
# "fdr", "none")

Arguments

p numeric vector of p-values (possibly with NAs). Any other R object is coerced by as.numeric.
method correction method, a character string. Can be abbreviated.
n number of comparisons, must be at least length(p); only set this (to non-default) when you know what you are doing!

Details

The adjustment methods include the Bonferroni correction ("bonferroni") in which the p-values are multiplied by the number of comparisons. Less conservative corrections are also included by Holm (1979) ("holm"), Hochberg (1988) ("hochberg"), Hommel (1988) ("hommel"), Benjamini & Hochberg (1995) ("BH" or its alias "fdr"), and Benjamini & Yekutieli (2001) ("BY"), respectively. A pass-through option ("none") is also included. The set of methods are contained in the p.adjust.methods vector for the benefit of methods that need to have the method as an option and pass it on to p.adjust.

The first four methods are designed to give strong control of the family-wise error rate. There seems no reason to use the unmodified Bonferroni correction because it is dominated by Holm’s method, which is also valid under arbitrary assumptions.

Hochberg’s and Hommel’s methods are valid when the hypothesis tests are independent or when they are non-negatively associated (Sarkar, 1998; Sarkar and Chang, 1997). Hommel’s method is more powerful than Hochberg’s, but the difference is usually small and the Hochberg p-values are faster to compute.

The "BH" (aka "fdr") and "BY" methods of Benjamini, Hochberg, and Yekutieli control the false discovery rate, the expected proportion of false discoveries amongst the rejected hypotheses. The false discovery rate is a less stringent condition than the family-wise error rate, so these methods are more powerful than the others.

Note that you can set n larger than length(p) which means the unobserved p-values are assumed to be greater than all the observed p for "bonferroni" and "holm" methods and equal to 1 for the other methods.

Value

A numeric vector of corrected p-values (of the same length as p, with names copied from p).
References


See Also

pairwise.* functions such as pairwise.t.test.

Examples

```r
require(graphics)
set.seed(123)
x <- rnorm(50, mean = c(rep(0, 25), rep(3, 25)))
p <- 2*pnorm(sort(-abs(x)))
round(p, 3)
round(p.adjust(p), 3)
round(p.adjust(p, "BH"), 3)

## or all of them at once (dropping the "fdr" alias):
p.adj <- sapply(p.adjust.M, function(meth) p.adjust(p, meth))
p.adj.60 <- sapply(p.adjust.M, function(meth) p.adjust(p, meth, n = 60))
stopifnot(identical(p.adj[,"none"], p), p.adj <= p.adj.60)
round(p.adj, 3)
## or a bit nicer:
noquote(apply(p.adj, 2, format.pval, digits = 3))

## and a graphic:
matplot(p, p.adj, ylab="p.adjust(p, meth)", type = "l", asp = 1, lty = 1:6,
main = "P-value adjustments")
legend(0.7, 0.6, p.adjust.M, col = 1:6, lty = 1:6)
```
### Can work with NA's:
pN <- p; iN <- c(46, 47); pN[iN] <- NA
pN.a <- sapply(p.adjust.M, function(meth) p.adjust(pN, meth))
## The smallest 20 P-values all affected by the NA's:
round((pN.a / p.adj)[1:20, , 4])

---

#### Description

Combines two vectors into an object of class "Pair"”

#### Usage

```r
Pair(x, y)
```

#### Arguments

- `x`: Vector. 1st element of pair.
- `y`: Vector. 2nd element of pair. Should be same length as `x`

#### Value

A 2-column matrix of class "Pair"

#### Note

Mostly designed as part of the formula interface to paired tests.

#### See Also

t.test and wilcox.test

---

#### pairwise.prop.test

**Pairwise comparisons for proportions**

#### Description

Calculate pairwise comparisons between pairs of proportions with correction for multiple testing

#### Usage

```r
pairwise.prop.test(x, n, p.adjust.method = p.adjust.methods, ...)
```
pairwise.t.test

Arguments

- **x**: Vector of counts of successes or a matrix with 2 columns giving the counts of successes and failures, respectively.
- **n**: Vector of counts of trials; ignored if `x` is a matrix.
- **...**: Additional arguments to pass to `prop.test`

Value

Object of class "pairwise.htest"

See Also

- `prop.test`, `p.adjust`

Examples

```r
smokers <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
pairwise.prop.test(smokers, patients)
```

pairwise.t.test  Pairwise t tests

Description

Calculate pairwise comparisons between group levels with corrections for multiple testing

Usage

```r
pairwise.t.test(x, g, p.adjust.method = p.adjust.methods, pool.sd = !paired, paired = FALSE, alternative = c("two.sided", "less", "greater"), ...
```

Arguments

- **x**: response vector.
- **g**: grouping vector or factor.
- **p.adjust.method**: Method for adjusting p values (see `p.adjust`).
- **pool.sd**: switch to allow/disallow the use of a pooled SD
- **paired**: a logical indicating whether you want paired t-tests.
- **alternative**: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". Can be abbreviated.
- **...**: additional arguments to pass to `t.test`.
Details

The pool.sd switch calculates a common SD for all groups and uses that for all comparisons (this can be useful if some groups are small). This method does not actually call `t.test`, so extra arguments are ignored. Pooling does not generalize to paired tests so pool.sd and paired cannot both be TRUE.

Only the lower triangle of the matrix of possible comparisons is being calculated, so setting alternative to anything other than "two.sided" requires that the levels of g are ordered sensibly.

Value

Object of class "pairwise.htest"

See Also

`t.test`, `p.adjust`

Examples

```r
attach(airquality)
Month <- factor(Month, labels = month.abb[5:9])
pairwise.t.test(Ozone, Month)
pairwise.t.test(Ozone, Month, p.adjust.method = "bonf")
pairwise.t.test(Ozone, Month, pool.sd = FALSE)
detach()
```

---

**pairwise.table**

Tabulate p values for pairwise comparisons

Description

Creates table of p values for pairwise comparisons with corrections for multiple testing.

Usage

```r
pairwise.table(compare.levels, level.names, p.adjust.method)
```

Arguments

- `compare.levels` a function to compute (raw) p value given indices i and j.
- `level.names` names of the group levels
- `p.adjust.method` a character string specifying the method for multiple testing adjustment; almost always one of `p.adjust.methods`. Can be abbreviated.

Details

Functions that do multiple group comparisons create separate `compare.levels` functions (assumed to be symmetrical in i and j) and passes them to this function.
pairwise.wilcox.test

Value
Table of p values in lower triangular form.

See Also
pairwise.t.test

pairwise.wilcox.test  Pairwise Wilcoxon Rank Sum Tests

Description
Calculate pairwise comparisons between group levels with corrections for multiple testing.

Usage
pairwise.wilcox.test(x, g, p.adjust.method = p.adjust.methods, paired = FALSE, ...)

Arguments
x  response vector.
g  grouping vector or factor.
paired  a logical indicating whether you want a paired test.
...  additional arguments to pass to wilcox.test.

Details
Extra arguments that are passed on to wilcox.test may or may not be sensible in this context. In particular, only the lower triangle of the matrix of possible comparisons is being calculated, so setting alternative to anything other than "two.sided" requires that the levels of g are ordered sensibly.

Value
Object of class "pairwise.htest"

See Also
wilcox.test, p.adjust

Examples
attach(airquality)
Month <- factor(Month, labels = month.abb[5:9])
## These give warnings because of ties :
pairwise.wilcox.test(Ozone, Month)
pairwise.wilcox.test(Ozone, Month, p.adjust.method = "bonf")
detach()
plot.acf

Plot Autocovariance and Autocorrelation Functions

Description

Plot method for objects of class "acf".

Usage

```r
## S3 method for class 'acf'
plot(x, ci = 0.95, type = "h", xlab = "Lag", ylab = NULL,
ylim = NULL, main = NULL,
    ci.col = "blue", ci.type = c("white", "ma"),
    max.mfrow = 6, ask = Npgs > 1 && dev.interactive(),
    mar = if(nser > 2) c(3,2,2,0.8) else par("mar"),
    oma = if(nser > 2) c(1,1.2,1,1) else par("oma"),
    mgp = if(nser > 2) c(1.5,0.6,0) else par("mgp"),
    xpd = par("xpd"),
    cex.main = if(nser > 2) 1 else par("cex.main"),
    verbose = getOption("verbose"),
    ...)```

Arguments

- `x`: an object of class "acf".
- `ci`: coverage probability for confidence interval. Plotting of the confidence interval is suppressed if `ci` is zero or negative.
- `type`: the type of plot to be drawn, default to histogram like vertical lines.
- `xlab`: the x label of the plot.
- `ylab`: the y label of the plot.
- `ylim`: numeric of length 2 giving the y limits for the plot.
- `main`: overall title for the plot.
- `ci.col`: colour to plot the confidence interval lines.
- `ci.type`: should the confidence limits assume a white noise input or for lag `k` an MA(`k-1`) input? Can be abbreviated.
- `max.mfrow`: positive integer; for multivariate `x` indicating how many rows and columns of plots should be put on one page, using `par(mfrow = c(m,m))`.
- `ask`: logical; if TRUE, the user is asked before a new page is started.
- `mar`, `oma`, `mgp`, `xpd`, `cex.main`: graphics parameters as in `par(*)`, by default adjusted to use smaller than default margins for multivariate `x` only.
- `verbose`: logical. Should `R` report extra information on progress?
- `...`: graphics parameters to be passed to the plotting routines.

Note

The confidence interval plotted in `plot.acf` is based on an uncorrelated series and should be treated with appropriate caution. Using `ci.type = "ma"` may be less potentially misleading.
plot.density

See Also

acf which calls plot.acf by default.

Examples

require(graphics)

z4 <- ts(matrix(rnorm(400), 100, 4), start = c(1961, 1), frequency = 12)
z7 <- ts(matrix(rnorm(700), 100, 7), start = c(1961, 1), frequency = 12)
acf(z4)
acf(z7, max.mfrow = 7)  # squeeze onto 1 page
acf(z7)  # multi-page

---

plot.density  

Plot Method for Kernel Density Estimation

Description

The plot method for density objects.

Usage

## S3 method for class 'density'
plot(x, main = NULL, xlab = NULL, ylab = "Density", type = "l",
     zero.line = TRUE, ...)

Arguments

x  a "density" object.
main, xlab, ylab, type  plotting parameters with useful defaults.
...  further plotting parameters.
zero.line  logical; if TRUE, add a base line at y = 0

Value

None.

See Also

density.
plot.HoltWinters  

Plot function for HoltWinters objects

Description

Produces a chart of the original time series along with the fitted values. Optionally, predicted values (and their confidence bounds) can also be plotted.

Usage

### S3 method for class 'HoltWinters'

```r
plot(x, predicted.values = NA, intervals = TRUE, separator = TRUE, col = 1, col.predicted = 2, col.intervals = 4, col.separator = 1, lty = 1, lty.predicted = 1, lty.intervals = 1, lty.separator = 3, ylab = "Observed / Fitted", main = "Holt-Winters filtering", ylim = NULL, ...)```

Arguments

- `x`: Object of class "HoltWinters"
- `predicted.values`: Predicted values as returned by `predict.HoltWinters`
- `intervals`: If TRUE, the prediction intervals are plotted (default).
- `separator`: If TRUE, a separating line between fitted and predicted values is plotted (default).
- `col, lty`: Color/line type of original data (default: black solid).
- `col.predicted, lty.predicted`: Color/line type of fitted and predicted values (default: red solid).
- `col.intervals, lty.intervals`: Color/line type of prediction intervals (default: blue solid).
- `col.separator, lty.separator`: Color/line type of observed/predicted values separator (default: black dashed).
- `ylab`: Label of the y-axis.
- `main`: Main title.
- `ylim`: Limits of the y-axis. If NULL, the range is chosen such that the plot contains the original series, the fitted values, and the predicted values if any.
- `...`: Other graphics parameters.

Author(s)

David Meyer <David.Meyer@wu.ac.at>

References

- C. C. Holt (1957) Forecasting trends and seasonals by exponentially weighted moving averages, *ONR Research Memorandum, Carnegie Institute of Technology* 52.
See Also

HoltWinters, predict.HoltWinters

plot.isoreg

Plot Method for isoreg Objects

Description

The plot and lines method for R objects of class isoreg.

Usage

## S3 method for class 'isoreg'
plot(x, plot.type = c("single", "row.wise", "col.wise"),
     main = paste("Isotonic regression", deparse(x$call)),
     main2 = "Cumulative Data and Convex Minorant",
     xlab = "x0", ylab = "x$y",
     par.fit = list(col = "red", cex = 1.5, pch = 13, lwd = 1.5),
     mar = if (both) 0.1 + c(3.5, 2.5, 1, 1) else par("mar"),
     mgp = if (both) c(1.6, 0.7, 0) else par("mgp"),
     grid = length(x$x) < 12, ...)

## S3 method for class 'isoreg'
lines(x, col = "red", lwd = 1.5,
      do.points = FALSE, cex = 1.5, pch = 13, ...)

Arguments

x

an isoreg object.

plot.type

character indicating which type of plot is desired. The first (default) only draws the data and the fit, where the others add a plot of the cumulative data and fit. Can be abbreviated.

main

main title of plot, see title.

main2

title for second (cumulative) plot.

xlab, ylab

x- and y- axis annotation.

par.fit

a list of arguments (for points and lines) for drawing the fit.

mar, mgp

graphical parameters, see par, mainly for the case of two plots.

grid

logical indicating if grid lines should be drawn. If true, grid() is used for the first plot, while as vertical lines are drawn at ‘touching’ points for the cumulative plot.

do.points

for lines(): logical indicating if the step points should be drawn as well (and as they are drawn in plot()).

col, lwd, cex, pch

graphical arguments for lines(), where cex and pch are only used when do.points is TRUE.

...

further arguments passed to and from methods.
See Also

isoereg for computation of isoreg objects.

Examples

require(graphics)

utils::example(isoreg) # for the examples there

plot(y3, main = "simple plot(.) + lines(<isoreg>)")
lines(ir3)

## 'same' plot as above, "proving" that only ranks of 'x' are important
plot(isoreg(2^(1:9), c(1,0,4,3,3,5,4,2,0)), plot.type = "row", log = "x")

plot(ir3, plot.type = "row", ylab = "y3")
plot(isoreg(y3 - 4), plot.type = "r", ylab = "y3 - 4")
plot(ir4, plot.type = "ro", ylab = "y4", xlab = "x = 1:n")

## experiment a bit with these (C-c C-j):
plot(isoreg(sample(9), y3), plot.type = "row")
plot(isoreg(sample(9), y3), plot.type = "col.wise")

plot(ir <- isoreg(sample(10), sample(10, replace = TRUE)),
     plot.type = "r")

plot.lm

Plot Diagnostics for an lm Object

Description

Six plots (selectable by which) are currently available: a plot of residuals against fitted values, a Scale-Location plot of \( \sqrt{|\text{residuals}|} \) against fitted values, a Q-Q plot of residuals, a plot of Cook’s distances versus row labels, a plot of residuals against leverages, and a plot of Cook’s distances against leverage/(1-leverage). By default, the first three and 5 are provided.

Usage

## S3 method for class 'lm'
plot(x, which = c(1,2,3,5),
caption = c("Residuals vs Fitted", "Q-Q Residuals",
  "Scale-Location", "Cook's distance",
  "Residuals vs Leverage",
  "Cook's dist vs Leverage* h[ii] / (1 - h[ii])"),
expression("Cook's dist vs Leverage* " * h[ii] / (1 - h[ii]))),
panel = if(add.smooth) function(x, y, ...)
  panel.smooth(x, y, iter=iter.smooth, ...) else points,
sub.caption = NULL, main = "",
ask = prod(par("mfcol")) < length(which) & dev.interactive(),
...

id.n = 3, labels.id = names(residuals(x)), cex.id = 0.75,
qline = TRUE, cook.levels = c(0.5, 1.0),
cook.col = 8, cook.lty = 2, cook.legendChanges = list(),

plot.lm
Arguments

x

1m object, typically result of 1m or glm.

which

a subset of the numbers 1:6, by default 1:3, 5, referring to

1. "Residuals vs Fitted", aka 'Tukey-Anscombe' plot
2. "Residual Q-Q" plot
3. "Scale-Location"
4. "Cook's distance"
5. "Residuals vs Leverage"
6. "Cook's dist vs Lev./(1-Lev.)"

See also 'Details' below.

caption
captions to appear above the plots; character vector or list of valid graphics annotations, see as.graphicsAnnot, of length 6, the j-th entry corresponding to which[j], see also the default vector in 'Usage'. Can be set to "" or NA to suppress all captions.

panel
d Panel function. The useful alternative to points, panel.smooth can be chosen by add.smooth = TRUE.

sub.caption
common title—above the figures if there are more than one; used as sub (s.title) otherwise. If NULL, as by default, a possible abbreviated version of deparse(x$call) is used.

main
title to each plot—in addition to caption.

ask
logical; if TRUE, the user is asked before each plot, see par(ask=).

... other parameters to be passed through to plotting functions.

id.n
number of points to be labelled in each plot, starting with the most extreme.

labels.id
vector of labels, from which the labels for extreme points will be chosen. NULL uses observation numbers.

cex.id
magnification of point labels.

qqline
logical indicating if a qline() should be added to the normal Q-Q plot.

cook.levels
g levels of Cook's distance at which to draw contours.

cook.col, cook.lty
color and line type to use for these contour lines.

cook.legendChanges
a list (or NULL to suppress the call) of arguments to legend which should be modified from (or added to) the plot.lm() default list(x = "bottomleft", legend = "Cook's distance", lty = cook.lty, col = cook.col, text.col = cook.col, bty = "n", x.intersp = 1/4, y.intersp = 1/8).

add.smooth
logical indicating if a smoother should be added to most plots; see also panel above.
iter.smooth the number of robustness iterations, the argument iter in panel.smooth(); the default uses no such iterations for glm fits which is particularly desirable for the (predominant) case of binary observations, but also for other models where the response distribution can be highly skewed.

label.pos positioning of labels, for the left half and right half of the graph respectively, for plots 1-3, 5, 6.

cex.caption controls the size of caption.

cex.oma.main controls the size of the sub.caption only if that is above the figures when there is more than one.

extend.ylim.f a numeric vector of length 1 or 2, to be used in ylim <- extendrange(r=ylim, f = *) for plots 1 and 5 when id.n is non-empty.

Details

sub.caption—by default the function call—is shown as a subtitle (under the x-axis title) on each plot when plots are on separate pages, or as a subtitle in the outer margin (if any) when there are multiple plots per page.

The ‘Scale-Location’ plot (which=3), also called ‘Spread-Location’ or ‘S-L’ plot, takes the square root of the absolute residuals in order to diminish skewness ($\sqrt{|E|}$ is much less skewed than $|E|$ for Gaussian zero-mean $E$).

The ‘S-L’, the Q-Q, and the Residual-Leverage (which=5) plot use standardized residuals which have identical variance (under the hypothesis). They are given as $R_i/(s \times \sqrt{1 - h_{ii}})$ where the ‘leverages’ $h_{ii}$ are the diagonal entries of the hat matrix, influence()$hat (see also hat), and where the Residual-Leverage plot uses the standardized Pearson residuals (residuals.glm(type = “pearson”)) for $R_i[i]$. The Residual-Leverage plot (which=5) shows contours of equal Cook’s distance, for values of cook.levels (by default 0.5 and 1) and omits cases with leverage one with a warning. If the leverages are constant (as is typically the case in a balanced aov situation) the plot uses factor level combinations instead of the leverages for the x-axis. (The factor levels are ordered by mean fitted value.)

In the Cook’s distance vs leverage/(1-leverage) (= “leverage*”) plot (which=6), contours of standardized residuals ($rstandard(.)$) that are equal in magnitude are lines through the origin. These lines are labelled with the magnitudes. The x-axis is labeled with the (non equidistant) leverages $h_{ii}$.

For the glm case, the Q-Q plot is based on the absolute value of the standardized deviance residuals. When the saddlepoint approximation applies, these have an approximate half-normal distribution. The saddlepoint approximation is exact for the normal and inverse Gaussian family, and holds approximately for the Gamma family with small dispersion (large shape) and for the Poisson and binomial families with large counts (Dunn and Smyth 2018).

Author(s)

John Maindonald and Martin Maechler.

References


See Also
termplot, lm.influence, cooks.distance, hatvalues.

Examples

```r
require(graphics)

## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)
plot(lm.SR)

## 4 plots on 1 page;
## allow room for printing model formula in outer margin:
par(mfrow = c(2, 2), oma = c(0, 0, 2, 0)) -> opar
plot(lm.SR)
plot(lm.SR, id.n = NULL) # no id's
plot(lm.SR, id.n = 5, labels.id = NULL) # 5 id numbers

## Was default in R <= 2.1.x:
## Cook's distances instead of Residual-Leverage plot
plot(lm.SR, which = 1:4)

## All the above fit a smooth curve where applicable
## by default unless "add.smooth" is changed.
## Give a smoother curve by increasing the lowess span :
plot(lm.SR, panel = function(x, y) panel.smooth(x, y, span = 1))

par(mfrow = c(2,1)) # same oma as above
plot(lm.SR, which = 1:2, sub.caption = "Saving Rates, n=50, p=5")

## Cook's distance tweaking
par(mfrow = c(2,3)) # same oma ...
plot(lm.SR, which = 1:6, cook.col = "royalblue")

## A case where over plotting of the "legend" is to be avoided:
if(dev.interactive(TRUE)) getOption("device") (height = 6, width = 4)
par(mfrow = c(3,1), mar = c(5,5,4,2)/2 +.1, mgp = c(1.4,.5,0))
plot(lm.SR, which = 5, extend.ylim.f = c(0.2, 0.08))
plot(lm.SR, which = 5, cook.lty = "dotdash",
  cook.legendChanges = list(x = "bottomright", legend = "Cook"))
plot(lm.SR, which = 5, cook.legendChanges = NULL) # no "legend"

par(opar) # reset par()s
```
Description

Plot the ridge functions for a projection pursuit regression (ppr) fit.

Usage

## S3 method for class 'ppr'
plot(x, ask, type = "o", cex = 1/2,
     main = quote(bquote("term"[.(i)]*": hat(\(\beta\)[.(i)]) == .(bet.i)))),
     xlab = quote(bquote(bold(alpha)[.(i)]^T * bold(x))),
     ylab = "", ...)  

Arguments

x
ask
type
cex
main, xlab, ylab

...  

Value

None

Side Effects

A series of plots are drawn on the current graphical device, one for each term in the fit.

See Also

ppr, par

Examples

```r
require(graphics)
rock1 <- within(rock, { area1 <- area/10000; peri1 <- peri/10000 })
par(mfrow = c(3,2)) # maybe: , pty = "s"
rock.ppr <- ppr(log(perm) ~ area1 + peri1 + shape,
                 data = rock1, nterms = 2, max.terms = 5)
plot(rock.ppr, main = "ppr(log(perm)~ ., nterms=2, max.terms=5)"
plot(update(rock.ppr, bass = 5), main = "update(..., bass = 5)"
plot(update(rock.ppr, sm.method = "gcv", gcvpen = 2),
     main = "update(..., sm.method="gcv", gcvpen=2)"
```
plot.profile.nls

Plot a profile.nls Object

Description
Displays a series of plots of the profile t function and interpolated confidence intervals for the parameters in a nonlinear regression model that has been fit with nls and profiled with profile.nls.

Usage

## S3 method for class 'profile.nls'
plot(x, levels, conf = c(99, 95, 90, 80, 50)/100,
     absVal = TRUE, ylab = NULL, lty = 2, ...)

Arguments

x an object of class "profile.nls"
levels levels, on the scale of the absolute value of a t statistic, at which to interpolate intervals. Usually conf is used instead of giving levels explicitly.
conf a numeric vector of confidence levels for profile-based confidence intervals on the parameters. Defaults to c(0.99, 0.95, 0.90, 0.80, 0.50).
absVal a logical value indicating whether or not the plots should be on the scale of the absolute value of the profile t. Defaults to TRUE.
lty the line type to be used for axis and dropped lines.
ylab, ... other arguments to the plot.default function can be passed here (but not xlab, xlim, ylim nor type).

Details
The plots are produced in a set of hard-coded colours, but as these are coded by number their effect can be changed by setting the palette. Colour 1 is used for the axes and 4 for the profile itself. Colours 3 and 6 are used for the axis line at zero and the horizontal/vertical lines dropping to the axes.

Author(s)
Douglas M. Bates and Saikat DebRoy

References

See Also
nls, profile, profile.nls
Examples

```r
require(graphics)
# obtain the fitted object
fm1 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
# get the profile for the fitted model
pr1 <- profile(fm1, alphamax = 0.05)
opar <- par(mfrow = c(2,2), oma = c(1.1, 0, 1.1, 0), las = 1)
plot(pr1, conf = c(95, 90, 80, 50)/100)
plot(pr1, conf = c(95, 90, 80, 50)/100, absVal = FALSE)
mtext("Confidence intervals based on the profile sum of squares",
     side = 3, outer = TRUE)
mtext("BOD data - confidence levels of 50%, 80%, 90% and 95%",
     side = 1, outer = TRUE)
par(opar)
```

plot.spec  

Plotting Spectral Densities

Description

Plotting method for objects of class "spec". For multivariate time series it plots the marginal spectra of the series or pairs plots of the coherency and phase of the cross-spectra.

Usage

```r
## S3 method for class 'spec'
plot(x, add = FALSE, ci = 0.95, log = c("yes", "dB", "no"),
     xlab = "frequency", ylab = NULL, type = "l",
     ci.col = "blue", ci.lty = 3,
     main = NULL, sub = NULL,
     plot.type = c("marginal", "coherency", "phase"),
     ...
)
plot.spec.phase(x, ci = 0.95,
                xlab = "frequency", ylab = "phase",
                ylim = c(-pi, pi), type = "l",
                main = NULL, ci.col = "blue", ci.lty = 3, ...)
plot.spec.coherency(x, ci = 0.95,
                    xlab = "frequency",
                    ylab = "squared coherency",
                    ylim = c(0, 1), type = "l",
                    main = NULL, ci.col = "blue", ci.lty = 3, ...)
```

Arguments

- `x` an object of class "spec".
- `add` logical. If TRUE, add to already existing plot. Only valid for `plot.type = "marginal"`.
- `ci` coverage probability for confidence interval. Plotting of the confidence bar/limits is omitted unless `ci` is strictly positive.
log
If "dB", plot on log10 (decibel) scale (as S-PLUS), otherwise use conventional log scale or linear scale. Logical values are also accepted. The default is "yes" unless options(ts.S.compat = TRUE) has been set, when it is "dB". Only valid for plot.type = "marginal".

xlab
the x label of the plot.

ylab
the y label of the plot. If missing a suitable label will be constructed.

type
the type of plot to be drawn, defaults to lines.

ci.col
colour for plotting confidence bar or confidence intervals for coherency and phase.

ci.lty
line type for confidence intervals for coherency and phase.

main
overall title for the plot. If missing, a suitable title is constructed.

sub
a subtitle for the plot. Only used for plot.type = "marginal". If missing, a description of the smoothing is used.

plot.type
For multivariate time series, the type of plot required. Only the first character is needed.

ylim, ...
Graphical parameters.

See Also
spectrum

plot.stepfun

Description
Method of the generic plot for stepfun objects and utility for plotting piecewise constant functions.

Usage

```
## S3 method for class 'stepfun'
plot(x, xval, xlim, ylim = range(c(y, Fn.kn)),
    xlab = "x", ylab = "f(x)", main = NULL,
    add = FALSE, verticals = TRUE, do.points = (n < 1000),
    pch = par("pch"), col = par("col"),
    col.points = col, cex.points = par("cex"),
    col.hor = col, col.vert = col,
    lty = par("lty"), lwd = par("lwd"), ...)

## S3 method for class 'stepfun'
lines(x, ...)
```

plot.stepfun

Plot Step Functions

---

### Description

Method of the generic plot for stepfun objects and utility for plotting piecewise constant functions.

### Usage

```r
## S3 method for class 'stepfun'
plot(x, xval, xlim, ylim = range(c(y, Fn.kn)),
    xlab = "x", ylab = "f(x)", main = NULL,
    add = FALSE, verticals = TRUE, do.points = (n < 1000),
    pch = par("pch"), col = par("col"),
    col.points = col, cex.points = par("cex"),
    col.hor = col, col.vert = col,
    lty = par("lty"), lwd = par("lwd"), ...)

## S3 method for class 'stepfun'
lines(x, ...)
```
Arguments

- **x**: an R object inheriting from "stepfun".
- **xval**: numeric vector of abscissa values at which to evaluate x. Defaults to knots(x) restricted to xlim.
- **xlim, ylim**: limits for the plot region: see plot.window. Both have sensible defaults if omitted.
- **xlab, ylab**: labels for x and y axis.
- **main**: main title.
- **add**: logical; if TRUE only add to an existing plot.
- **verticals**: logical; if TRUE, draw vertical lines at steps.
- **do.points**: logical; if TRUE, also draw points at the (xlim restricted) knot locations. Default is true, for sample size < 1000.
- **pch**: character; point character if do.points.
- **col**: default color of all points and lines.
- **col.points**: character or integer code; color of points if do.points.
- **cex.points**: numeric; character expansion factor if do.points.
- **col.hor**: color of horizontal lines.
- **col.vert**: color of vertical lines.
- **lty, lwd**: line type and thickness for all lines.
- **...**: further arguments of plot(.), or if(add) segments(.).

Value

A list with two components

- **t**: abscissa (x) values, including the two outermost ones.
- **y**: y values ‘in between’ the t[].

Author(s)


See Also

- ecdf for empirical distribution functions as special step functions, approxfun and splinefun.

Examples

```r
require(graphics)

y0 <- c(1,2,4,3)
sfun0 <- stepfun(1:3, y0, f = 0)
sfun.2 <- stepfun(1:3, y0, f = .2)
sfun1 <- stepfun(1:3, y0, right = TRUE)

tt <- seq(0, 3, by = 0.1)
op <- par(mfrow = c(2,2))
plot(sfun0); plot(sfun0, xval = tt, add = TRUE, col.hor = "bisque")
plot(sfun.2);plot(sfun.2, xval = tt, add = TRUE, col = "orange") # all colors
```
plot(sfun1);lines(sfun1, xval = tt, col.hor = "coral")
##-- This is revealing :
for(i in 1:3)
  lines(list(sfun0, sfun.2, stepfun(1:3, y0, f = 1))[i], col = i)
legend(2.5, 1.9, paste("f =", c(0, 0.2, 1)), col = 1:3, lty = 1, y.intersp = 1)

par(op)

# Extend and/or restrict 'viewport':
plot(sfun0, xlim = c(0,5), ylim = c(0, 3.5),
     main = "plot(stepfun(*), xlim= . , ylim = .)"
     legend(2.5, 1.9, paste("f =", c(0, 0.2, 1)), col = 1:3, lty = 1, y.intersp = 1)

plot.ts

Plotting Time-Series Objects

Description

Plotting method for objects inheriting from class "ts".

Usage

## S3 method for class 'ts'
plot(x, y = NULL, plot.type = c("multiple", "single"),
     xy.labels, xy.lines, panel = lines, nc, yax.flip = FALSE,
     mar.multi = c(0, 5.1, 0, if(yax.flip) 5.1 else 2.1),
     oma.multi = c(6, 0, 5, 0), axes = TRUE, ...)

## S3 method for class 'ts'
lines(x, ...)

Arguments

x, y

x y

time series objects, usually inheriting from class "ts".

plot.type

for multivariate time series, should the series by plotted separately (with a common
time axis) or on a single plot? Can be abbreviated.

xy.labels

logical, indicating if text() labels should be used for an x-y plot, or character,
supplying a vector of labels to be used. The default is to label for up to 150
points, and not for more.

xy.lines

logical, indicating if lines should be drawn for an x-y plot. Defaults to the
value of xy.labels if that is logical, otherwise to TRUE.

panel

a function(x, col, bg, pch, type, ...) which gives the action to be carried
out in each panel of the display for plot.type = "multiple". The default is
lines.

nc

the number of columns to use when type = "multiple". Defaults to 1 for up to 4
series, otherwise to 2.

yax.flip

logical indicating if the y-axis (ticks and numbering) should flip from side 2
(left) to 4 (right) from series to series when type = "multiple".
mar.multi, oma.multi
the (default) par settings for plot.type = "multiple". Modify with care!
axes
logical indicating if x- and y- axes should be drawn.
... 
additional graphical arguments, see plot, plot.default and par.

Details

If y is missing, this function creates a time series plot, for multivariate series of one of two kinds depending on plot.type.

If y is present, both x and y must be univariate, and a scatter plot y ~ x will be drawn, enhanced by using text if xy.labels is TRUE or character, and lines if xy.lines is TRUE.

See Also

ts for basic time series construction and access functionality.

Examples

require(graphics)

## Multivariate
z <- ts(matrix(rt(200 * 8, df = 3), 200, 8),
        start = c(1961, 1), frequency = 12)
plot(z, yax.flip = TRUE)
plot(z, axes = FALSE, ann = FALSE, frame.plot = TRUE,
     mar.multi = c(0,0,0,0), oma.multi = c(1,1,5,1))

z <- window(z[,1:3], end = c(1969,12))
plot(z, type = "b")  # multiple

## A phase plot:
plot(nhtemp, lag(nhtemp, 1), cex = .8, col = "blue",
     main = "Lag plot of New Haven temperatures")

## xy.lines and xy.labels are FALSE for large series:
plot(lag(sunspots, 1), sunspots, pch = ".")

SMI <- EuStockMarkets[, "SMI"]
plot(lag(SMI, 1), SMI, pch = ".")
plot(lag(SMI, 20), SMI, pch = ".", log = "xy",
     main = "4 weeks lagged SMI stocks -- log scale", xy.lines = TRUE)

Poisson

The Poisson Distribution

Description

Density, distribution function, quantile function and random generation for the Poisson distribution with parameter lambda.
Poisson

Usage

dpois(x, lambda, log = FALSE)
ppois(q, lambda, lower.tail = TRUE, log.p = FALSE)
qpois(p, lambda, lower.tail = TRUE, log.p = FALSE)
rpois(n, lambda)

Arguments

x       vector of (non-negative integer) quantiles.
q       vector of quantiles.
p       vector of probabilities.
n       number of random values to return.
lambda  vector of (non-negative) means.
log, log.p  logical; if TRUE, probabilities p are given as log(p).
lower.tail logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.

Details

The Poisson distribution has density

$$p(x) = \frac{\lambda^x e^{-\lambda}}{x!}$$

for $x = 0, 1, 2, \ldots$. The mean and variance are $E(X) = Var(X) = \lambda$.

Note that $\lambda = 0$ is really a limit case (setting $0^0 = 1$) resulting in a point mass at 0, see also the example.

If an element of x is not integer, the result of dpois is zero, with a warning. $p(x)$ is computed using Loader's algorithm, see the reference in dbinom.

The quantile is right continuous: qpois(p, lambda) is the smallest integer $x$ such that $P[X \leq x] \geq p$.

Setting lower.tail = FALSE allows to get much more precise results when the default, lower.tail = TRUE would return 1, see the example below.

Value

dpois gives the (log) density, ppois gives the (log) distribution function, qpois gives the quantile function, and rpois generates random deviates.

Invalid lambda will result in return value NaN, with a warning.

The length of the result is determined by n for rpois, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements of the logical arguments are used.

rpois returns a vector of type integer unless generated values exceed the maximum representable integer when double values are returned.
Source

dpois uses C code contributed by Catherine Loader (see dbinom).
pois uses pgamma.
qpois uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

See Also

Distributions for other standard distributions, including dbinom for the binomial and dnbinom for the negative binomial distribution.

poisson.test

Examples

```
require(graphics)

-log(dpois(0:7, lambda = 1) * gamma(1+ 0:7)) # == 1
Ni <- rpois(50, lambda = 4); table(factor(Ni, 0:max(Ni))

1 - ppois(10*(15:25), lambda = 100) # becomes 0 (cancellation)
ppois(10*(15:25), lambda = 100, lower.tail = FALSE) # no cancellation

par(mfrow = c(2, 1))
x <- seq(-0.01, 5, 0.01)
plot(x, ppois(x, 1), type = "s", ylab = "F(x)", main = "Poisson(1) CDF")
plot(x, pbinom(x, 100, 0.01), type = "s", ylab = "F(x)",
    main = "Binomial(100, 0.01) CDF")

## The (limit) case lambda = 0 :
stopifnot(identical(dpois(0,0), 1),
    identical(ppois(0,0), 1),
    identical(qpois(1,0), 0))
```

---

poisson.test *Exact Poisson tests*

Description

Performs an exact test of a simple null hypothesis about the rate parameter in Poisson distribution, or for the ratio between two rate parameters.

Usage

```
poisson.test(x, T = 1, r = 1,
    alternative = c("two.sided", "less", "greater"),
    conf.level = 0.95)
```
Arguments

- **x**: number of events. A vector of length one or two.
- **T**: time base for event count. A vector of length one or two.
- **r**: hypothesized rate or rate ratio
- **alternative**: indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter.
- **conf.level**: confidence level for the returned confidence interval.

Details

Confidence intervals are computed similarly to those of `binom.test` in the one-sample case, and using `binom.test` in the two sample case.

Value

A list with class "htest" containing the following components:

- **statistic**: the number of events (in the first sample if there are two.)
- **parameter**: the corresponding expected count
- **p.value**: the p-value of the test.
- **conf.int**: a confidence interval for the rate or rate ratio.
- **estimate**: the estimated rate or rate ratio.
- **null.value**: the rate or rate ratio under the null, r.
- **alternative**: a character string describing the alternative hypothesis.
- **method**: the character string "Exact Poisson test" or "Comparison of Poisson rates" as appropriate.
- **data.name**: a character string giving the names of the data.

Note

The rate parameter in Poisson data is often given based on a “time on test” or similar quantity (person-years, population size, or expected number of cases from mortality tables). This is the role of the T argument.

The one-sample case is effectively the binomial test with a very large n. The two sample case is converted to a binomial test by conditioning on the total event count, and the rate ratio is directly related to the odds in that binomial distribution.

See Also

- `binom.test`

Examples

- These are paraphrased from data sets in the ISwR package

```
## SMR, Welsh Nickel workers
poisson.test(137, 24.19893)

## eba1977, compare Fredericia to other three cities for ages 55-59
poisson.test(c(11, 6+8+7), c(800, 1083+1050+878))
```
Compute Orthogonal Polynomials

Description

Returns or evaluates orthogonal polynomials of degree 1 to degree over the specified set of points x: these are all orthogonal to the constant polynomial of degree 0. Alternatively, evaluate raw polynomials.

Usage

poly(x, ..., degree = 1, coefs = NULL, raw = FALSE, simple = FALSE)
poly(..., degree = 1, coefs = NULL, raw = FALSE)

## S3 method for class 'poly'
predict(object, newdata, ...)

Arguments

x, newdata: a numeric vector or an object with mode "numeric" (such as a Date) at which to evaluate the polynomial. x can also be a matrix. Missing values are not allowed in x.

degree: the degree of the polynomial. Must be less than the number of unique points when raw is false, as by default.

coefs: for prediction, coefficients from a previous fit.

raw: if true, use raw and not orthogonal polynomials.

simple: logical indicating if a simple matrix (with no further attributes but dimnames) should be returned. For speedup only.

object: an object inheriting from class "poly", normally the result of a call to poly with a single vector argument.

...: poly, polym: further vectors.
predict.poly: arguments to be passed to or from other methods.

Details

Although formally degree should be named (as it follows ...), an unnamed second argument of length 1 will be interpreted as the degree, such that poly(x, 3) can be used in formulas.

The orthogonal polynomial is summarized by the coefficients, which can be used to evaluate it via the three-term recursion given in Kennedy & Gentle (1980, pp. 343–4), and used in the predict part of the code.

poly using ... is just a convenience wrapper for polym: coef is ignored. Conversely, if polym is called with a single argument in ... it is a wrapper for poly.

Value

For poly and polym() (when simple=FALSE and coefs=NULL as per default):
A matrix with rows corresponding to points in x and columns corresponding to the degree, with attributes "degree" specifying the degrees of the columns and (unless raw = TRUE) "coefs" which
contains the centering and normalization constants used in constructing the orthogonal polynomials and class c("poly", "matrix"). For poly(*, simple=TRUE), polym(*, coefs=<non-NULL>), and predict.poly(): a matrix.

**Note**
This routine is intended for statistical purposes such as contr.poly: it does not attempt to orthogonalize to machine accuracy.

**Author(s)**
R Core Team. Keith Jewell (Campden BRI Group, UK) contributed improvements for correct prediction on subsets.

**References**

**See Also**
contr.poly.
cars for an example of polynomial regression.

**Examples**
```r
od <- options(digits = 3) # avoid too much visual clutter
(z <- poly(1:10, 3))
predict(z, seq(2, 4, 0.5))
zapsmall(poly(seq(4, 6, 0.5), 3, coefs = attr(z, "coefs")))

zm <- zapsmall(polym(1:4, c(1, 4:6), degree = 3)) # or just poly():
(z1 <- zapsmall(poly(cbind(1:4, c(1, 4:6)), degree = 3)))
## they are the same:
stopifnot(all.equal(zm, z1, tolerance = 1e-15))

## poly<matrix>, df --- used to fail till July 14 (vive la France!), 2017:
m2 <- cbind(1:4, c(1, 4:6))
zm2 <- zapsmall(poly(m2, 3)) # "unnamed degree = 3"
stopifnot(all.equal(m2, zm2, tolerance = 1e-15))

options(od)
```

---

**power**

Create a Power Link Object

**Description**
Creates a link object based on the link function $\eta = \mu^\lambda$.

**Usage**
```r
power(lambda = 1)
```
power.anova.test

Arguments

lambda a real number.

Details

If lambda is non-positive, it is taken as zero, and the log link is obtained. The default lambda = 1 gives the identity link.

Value

A list with components linkfun, linkinv, mu.eta, and valideta. See make.link for information on their meaning.

References


See Also

make.link, family

To raise a number to a power, see Arithmetic.
To calculate the power of a test, see various functions in the stats package, e.g., power.t.test.

Examples

power()
quasi(link = power(1/3))[c("linkfun", "linkinv")]

---

power.anova.test  Power Calculations for Balanced One-Way Analysis of Variance Tests

Description

Compute power of test or determine parameters to obtain target power.

Usage

power.anova.test(groups = NULL, n = NULL, between.var = NULL, within.var = NULL, sig.level = 0.05, power = NULL)

Arguments

groups Number of groups
n Number of observations (per group)
between.var Between group variance
within.var Within group variance
sig.level Significance level (Type I error probability)
power Power of test (1 minus Type II error probability)
Details

Exactly one of the parameters groups, n, between.var, power, within.var, and sig.level must be passed as NULL, and that parameter is determined from the others. Notice that sig.level has non-NULL default so NULL must be explicitly passed if you want it computed.

Value

Object of class "power.htest", a list of the arguments (including the computed one) augmented with method and note elements.

Note

uniroot is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

Author(s)

Claus Ekstrøm

See Also

anova, lm, uniroot

Examples

```r
power.anova.test(groups = 4, n = 5, between.var = 1, within.var = 3)
# Power = 0.3535594

power.anova.test(groups = 4, between.var = 1, within.var = 3, power = .80)
# n = 11.92613

## Assume we have prior knowledge of the group means:
groupmeans <- c(120, 130, 140, 150)
power.anova.test(groups = length(groupmeans),
                 between.var = var(groupmeans),
                 within.var = 500, power = .90)  # n = 15.18834
```

Description

Compute the power of the two-sample test for proportions, or determine parameters to obtain a target power.

Usage

```r
power.prop.test(n = NULL, p1 = NULL, p2 = NULL, sig.level = 0.05, power = NULL,
                alternative = c("two.sided", "one.sided"),
                strict = FALSE, tol = .Machine$double.eps^0.25)
```
power.prop.test

Arguments

- `n`: number of observations (per group)
- `p1`: probability in one group
- `p2`: probability in other group
- `sig.level`: significance level (Type I error probability)
- `power`: power of test (1 minus Type II error probability)
- `alternative`: one- or two-sided test. Can be abbreviated.
- `strict`: use strict interpretation in two-sided case
- `tol`: numerical tolerance used in root finding, the default providing (at least) four significant digits.

Details

Exactly one of the parameters `n`, `p1`, `p2`, `power`, and `sig.level` must be passed as NULL, and that parameter is determined from the others. Notice that `sig.level` has a non-NULL default so NULL must be explicitly passed if you want it computed.

If `strict = TRUE` is used, the power will include the probability of rejection in the opposite direction of the true effect, in the two-sided case. Without this the power will be half the significance level if the true difference is zero.

Note that not all conditions can be satisfied, e.g., for

```
power.prop.test(n=30, p1=0.90, p2=NULL, power=0.8, strict=TRUE)
```

there is no proportion `p2` between `p1 = 0.9` and 1, as you’d need a sample size of at least `n = 74` to yield the desired power for `(p1, p2) = (0.9, 1)`.

For these impossible conditions, currently a warning (`warning`) is signalled which may become an error (`stop`) in the future.

Value

Object of class "power.htest", a list of the arguments (including the computed one) augmented with `method` and `note` elements.

Note

`uniroot` is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given. If one of `p1` and `p2` is computed, then `p1 < p2` is assumed and will hold, but if you specify both, `p2 <= p1` is allowed.

Author(s)

Peter Dalgaard. Based on previous work by Claus Ekstrom

See Also

`prop.test, uniroot`
Examples

```r
power.prop.test(n = 50, p1 = .50, p2 = .75)  ## => power = 0.740
power.prop.test(p1 = .50, p2 = .75, power = .90) ## => n = 76.7
power.prop.test(n = 50, p1 = .5, power = .90)  ## => p2 = 0.8026
power.prop.test(n = 50, p1 = .5, p2 = 0.9, power = .90, sig.level=NULL)  
## => sig.l = 0.00131
power.prop.test(p1 = .5, p2 = 0.501, sig.level=.001, power=0.90)
## => n = 10451937
```

```r
try(
  power.prop.test(n=30, p1=0.90, p2=NULL, power=0.8)
)
# a warning (which may become an error)
## Reason:
power.prop.test( p1=0.90, p2= 1.0, power=0.8)  ##-> n = 73.37
```

Description

Power calculations for one and two sample t tests

Usage

```r
power.t.test(n = NULL, delta = NULL, sd = 1, sig.level = 0.05, 
power = NULL, 
type = c("two.sample", "one.sample", "paired"),
alternative = c("two.sided", "one.sided"),
strict = FALSE, tol = .Machine$double.eps^0.25)
```

Arguments

- `n` number of observations (per group)
- `delta` true difference in means
- `sd` standard deviation
- `sig.level` significance level (Type I error probability)
- `power` power of test (1 minus Type II error probability)
- `type` string specifying the type of t test. Can be abbreviated.
- `alternative` one- or two-sided test. Can be abbreviated.
- `strict` use strict interpretation in two-sided case
- `tol` numerical tolerance used in root finding, the default providing (at least) four significant digits.

Details

Exactly one of the parameters `n`, `delta`, `power`, `sd`, and `sig.level` must be passed as `NULL`, and that parameter is determined from the others. Notice that the last two have non-`NULL` defaults, so `NULL` must be explicitly passed if you want to compute them.

If `strict = TRUE` is used, the power will include the probability of rejection in the opposite direction of the true effect, in the two-sided case. Without this the power will be half the significance level if the true difference is zero.
**Value**

Object of class "power.htest", a list of the arguments (including the computed one) augmented with method and note elements.

**Note**

uniroot is used to solve the power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

**Author(s)**

Peter Dalgaard. Based on previous work by Claus Ekstrøm

**See Also**

t.test, uniroot

**Examples**

```r
power.t.test(n = 20, delta = 1)
power.t.test(power = .90, delta = 1)
power.t.test(power = .90, delta = 1, alternative = "one.sided")
```

---

### PP.test

**Phillips-Perron Test for Unit Roots**

**Description**

Computes the Phillips-Perron test for the null hypothesis that x has a unit root against a stationary alternative.

**Usage**

```r
PP.test(x, lshort = TRUE)
```

**Arguments**

- `x`: a numeric vector or univariate time series.
- `lshort`: a logical indicating whether the short or long version of the truncation lag parameter is used.

**Details**

The general regression equation which incorporates a constant and a linear trend is used and the corrected t-statistic for a first order autoregressive coefficient equals one is computed. To estimate sigma^2 the Newey-West estimator is used. If lshort is TRUE, then the truncation lag parameter is set to trunc(4*(n/100)^0.25), otherwise trunc(12*(n/100)^0.25) is used. The p-values are interpolated from Table 4.2, page 103 of Banerjee et al (1993).

Missing values are not handled.
Value
A list with class "htest" containing the following components:

- statistic: the value of the test statistic.
- parameter: the truncation lag parameter.
- p.value: the p-value of the test.
- method: a character string indicating what type of test was performed.
- data.name: a character string giving the name of the data.

Author(s)
A. Trapletti

References


Examples
```r
x <- rnorm(1000)
PP.test(x)
y <- cumsum(x) # has unit root
PP.test(y)
```

Description
Generates the sequence of probability points \((1:m - a)/(m + (1-a)*a)\) where \(m\) is either \(n\), if \(\text{length}(n)==1\), or \(\text{length}(n)\).

Usage
```
ppoints(n, a = if(n <= 10) 3/8 else 1/2)
```

Arguments
```r
n

either the number of points generated or a vector of observations.

a
the offset fraction to be used; typically in \((0, 1)\).
```
If \( 0 < a < 1 \), the resulting values are within \((0, 1)\) (excluding boundaries). In any case, the resulting sequence is symmetric in \([0, 1]\), i.e., \( p + \text{rev}(p) = 1 \).

ppoints() is used in qqplot and qqnorm to generate the set of probabilities at which to evaluate the inverse distribution.

The choice of \( a \) follows the documentation of the function of the same name in Becker et al (1988), and appears to have been motivated by results from Blom (1958) on approximations to expect normal order statistics (see also quantile).

The probability points for the continuous sample quantile types 5 to 9 (see quantile) can be obtained by taking \( a \) as, respectively, \(1/2\), \(0\), \(1\), \(1/3\), and \(3/8\).

### References


### See Also

qqplot, qqnorm.

### Examples

```r
ppoints(4) # the same as ppoints(1:4)
ppoints(10)
ppoints(10, a = 1/2)

## Visualize including the fractions :
require(graphics)
p.ppoints <- function(n, ..., add = FALSE, col = par("col")) {
  pn <- ppoints(n, ...)
  if(add)
    points(pn, pn, col = col)
  else {
    tit <- match.call(); tit[[1]] <- quote(ppoints)
    plot(pn,pn, main = deparse(tit), col=col,
         xlim = 0:1, ylim = 0:1, xaxs = "i", yaxs = "i")
    abline(0, 1, col = adjustcolor(1, 1/4), lty = 3)
  }
  if(!add & requireNamespace("MASS", quietly = TRUE))
    text(pn, pn, as.character(MASS::fractions(pn)),
         adj = c(0,0)-1/4, cex = 3/4, xpd = NA, col=col)
    abline(h = pn, v = pn, col = adjustcolor(col, 1/2), lty = 2, lwd = 1/2)
}

p.ppoints(4)
p.ppoints(10)
p.ppoints(10, a = 1/2)
p.ppoints(21)
p.ppoints(8) ; p.ppoints(8, a = 1/2, add=TRUE, col="tomato")
```
**ppr**

**Projection Pursuit Regression**

**Description**

Fit a projection pursuit regression model.

**Usage**

```r/ppr(x, ...)

## S3 method for class 'formula'
ppr(formula, data, weights, subset, na.action,
    contrasts = NULL, ..., model = FALSE)

## Default S3 method:
ppr(x, y, weights = rep(1, n),
    ww = rep(1, q), nterms, max.terms = nterms, optlevel = 2,
    sm.method = c("supsmu", "spline", "gcvspline"),
    bass = 0, span = 0, df = 5, gcvpen = 1, trace = FALSE, ...)
```

**Arguments**

- `formula`: a formula specifying one or more numeric response variables and the explanatory variables.
- `x`: numeric matrix of explanatory variables. Rows represent observations, and columns represent variables. Missing values are not accepted.
- `y`: numeric matrix of response variables. Rows represent observations, and columns represent variables. Missing values are not accepted.
- `nterms`: number of terms to include in the final model.
- `data`: a data frame (or similar: see `model.frame`) from which variables specified in `formula` are preferentially to be taken.
- `weights`: a vector of weights \( w_i \) for each case.
- `ww`: a vector of weights for each response, so the fit criterion is the sum over case \( i \) and responses \( j \) of \( w_i \) \( ww_j \) \((y_{ij} - \text{fit}_{ij})^2\) divided by the sum of \( w_i \).
- `subset`: an index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
- `na.action`: a function to specify the action to be taken if NAs are found. The default action is given by `getOption("na.action")`. (NOTE: If given, this argument must be named.)
- `contrasts`: the contrasts to be used when any factor explanatory variables are coded.
- `max.terms`: maximum number of terms to choose from when building the model.
- `optlevel`: integer from 0 to 3 which determines the thoroughness of an optimization routine in the SMART program. See the 'Details' section.
- `sm.method`: the method used for smoothing the ridge functions. The default is to use Friedman’s super smoother `supsmu`. The alternatives are to use the smoothing spline code underlying `smooth.spline`, either with a specified (equivalent) degrees of
freedom for each ridge functions, or to allow the smoothness to be chosen by GCV.
Can be abbreviated.

bass  super smoother bass tone control used with automatic span selection (see supsmu); the range of values is 0 to 10, with larger values resulting in increased smoothing.

span  super smoother span control (see supsmu). The default, 0, results in automatic span selection by local cross validation. span can also take a value in (0, 1].

df  if sm.method is "spline" specifies the smoothness of each ridge term via the requested equivalent degrees of freedom.
gcvpen  if sm.method is "gcvspline" this is the penalty used in the GCV selection for each degree of freedom used.
trace  logical indicating if each spline fit should produce diagnostic output (about lambda and df), and the supsmu fit about its steps.

...  arguments to be passed to or from other methods.
model logical. If true, the model frame is returned.

Details

The basic method is given by Friedman (1984), and is essentially the same code used by S-PLUS’s pprreg. This code is extremely sensitive to the compiler used.

The algorithm first adds up to max. terms ridge terms one at a time; it will use less if it is unable to find a term to add that makes sufficient difference. It then removes the least important term at each step until nterms terms are left.

The levels of optimization (argument optlevel) differ in how thoroughly the models are refitted during this process. At level 0 the existing ridge terms are not refitted. At level 1 the projection directions are not refitted, but the ridge functions and the regression coefficients are.

Levels 2 and 3 refit all the terms and are equivalent for one response; level 3 is more careful to re-balance the contributions from each regressor at each step and so is a little less likely to converge to a saddle point of the sum of squares criterion.

Value

A list with the following components, many of which are for use by the method functions.

call  the matched call
p  the number of explanatory variables (after any coding)
q  the number of response variables
mu  the argument nterms
ml  the argument max.terms
gof  the overall residual (weighted) sum of squares for the selected model
gofn  the overall residual (weighted) sum of squares against the number of terms, up to max.terms. Will be invalid (and zero) for less than nterms.
df  the argument df
edf  if sm.method is "spline" or "gcvspline" the equivalent number of degrees of freedom for each ridge term used.
xnames  the names of the explanatory variables
ynames the names of the response variables
alpha a matrix of the projection directions, with a column for each ridge term
beta a matrix of the coefficients applied for each response to the ridge terms: the rows are the responses and the columns the ridge terms
yb the weighted means of each response
ys the overall scale factor used: internally the responses are divided by ys to have unit total weighted sum of squares.
fitted.values the fitted values, as a matrix if q > 1.
residuals the residuals, as a matrix if q > 1.
smod internal work array, which includes the ridge functions evaluated at the training set points.
model (only if model = TRUE) the model frame.

Source
Friedman (1984): converted to double precision and added interface to smoothing splines by B. D. Ripley, originally for the MASS package.

References

See Also
plot.ppr, supsmu, smooth.spline

Examples

require(graphics)

# Note: your numerical values may differ
attach(rock)
area1 <- area/10000; peri1 <- peri/10000
rock.ppr <- ppr(log(perm) ~ area1 + peri1 + shape,
                data = rock, nterms = 2, max.terms = 5)
rock.ppr
# Call:
# ppr.formula(formula = log(perm) ~ area1 + peri1 + shape, data = rock,
#             nterms = 2, max.terms = 5)
#
# Goodness of fit:
# 2 terms 3 terms 4 terms 5 terms
# 8.737806 5.289517 4.745799 4.490378

summary(rock.ppr)
# ...... (same as above)
# ......
# Projection direction vectors ('alpha'):
#     term 1   term 2
# area  0.34357179 0.37071027
# peri  -0.93781471 -0.61923542
# shape  0.04961846 0.69218595
#
# Coefficients of ridge terms:
#     term 1   term 2
# 1.6079271 0.5460971

par(mfrow = c(3,2))  # maybe: , pty = "s")
plot(rock.ppr, main = "ppr(log(perm)~ ., nterms=2, max.terms=5)"
plot(update(rock.ppr, bass = 5), main = "update(..., bass = 5)"
plot(update(rock.ppr, sm.method = "gcv", gcvpen = 2),
    main = "update(..., sm.method="gcv", gcvpen=2)"
cbind(perm = rock$perm, prediction = round(exp(predict(rock.ppr)), 1))
detach()

---

**prcomp**  
*Principal Components Analysis*

**Description**

Performs a principal components analysis on the given data matrix and returns the results as an object of class `prcomp`.

**Usage**

```r
prcomp(x, ...)
```

### S3 method for class 'formula'

```r
prcomp(formula, data = NULL, subset, na.action, ...)
```

### Default S3 method:

```r
prcomp(x, retx = TRUE, center = TRUE, scale. = FALSE,
    tol = NULL, rank. = NULL, ...)
```

### S3 method for class 'prcomp'

```r
predict(object, newdata, ...)
```

**Arguments**

- **formula**  
a formula with no response variable, referring only to numeric variables.
- **data**  
an optional data frame (or similar: see `model.frame`) containing the variables in the formula formula. By default the variables are taken from `environment(formula)`.
- **subset**  
an optional vector used to select rows (observations) of the data matrix `x`.
- **na.action**  
a function which indicates what should happen when the data contain NAs. The default is set by the `na.action` setting of `options`, and is `na.fail` if that is unset. The ‘factory-fresh’ default is `na.omit`.
- **...**  
arguments passed to or from other methods. If `x` is a formula one might specify `scale.` or `tol`. 
prcomp

x a numeric or complex matrix (or data frame) which provides the data for the principal components analysis.

retx a logical value indicating whether the rotated variables should be returned.

center a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.

scale. a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with S, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of x can be supplied. The value is passed to scale.

tol a value indicating the magnitude below which components should be omitted. (Components are omitted if their standard deviations are less than or equal to tol times the standard deviation of the first component.) With the default null setting, no components are omitted (unless rank. is specified less than min(dim(x)).) Other settings for tol could be tol = 0 or tol = sqrt(.Machine$double.eps), which would omit essentially constant components.

rank. optionally, a number specifying the maximal rank, i.e., maximal number of principal components to be used. Can be set as alternative or in addition to tol, useful notably when the desired rank is considerably smaller than the dimensions of the matrix.

object object of class inheriting from "prcomp"

newdata An optional data frame or matrix in which to look for variables with which to predict. If omitted, the scores are used. If the original fit used a formula or a data frame or a matrix with column names, newdata must contain columns with the same names. Otherwise it must contain the same number of columns, to be used in the same order.

Details

The calculation is done by a singular value decomposition of the (centered and possibly scaled) data matrix, not by using eigen on the covariance matrix. This is generally the preferred method for numerical accuracy. The print method for these objects prints the results in a nice format and the plot method produces a scree plot.

Unlike princomp, variances are computed with the usual divisor \( N - 1 \).

Note that scale = TRUE cannot be used if there are zero or constant (for center = TRUE) variables.

Value

prcomp returns a list with class "prcomp" containing the following components:

sdev the standard deviations of the principal components (i.e., the square roots of the eigenvalues of the covariance/correlation matrix, though the calculation is actually done with the singular values of the data matrix).

rotation the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors). The function princomp returns this in the element loadings.

x if retx is true the value of the rotated data (the centred (and scaled if requested) data multiplied by the rotation matrix) is returned. Hence, \( \text{cov}(x) \) is the diagonal matrix \( \text{diag}(\text{sdev}^2) \). For the formula method, napredict() is applied to handle the treatment of values omitted by the na.action.

center, scale the centering and scaling used, or FALSE.
Note

The signs of the columns of the rotation matrix are arbitrary, and so may differ between different programs for PCA, and even between different builds of R.

References


See Also

biplot.prcomp, screeplot, princomp, cor, cov, svd, eigen.

Examples

C <- chol(S <- toeplitz(.9 ^ (0:31))) # Cov.matrix and its root
all.equal(S, crossprod(C))
set.seed(17)
X <- matrix(rnorm(32000), 1000, 32)
Z <- X %*% C # cov(Z) == C'C == S
all.equal(cov(Z), S, tolerance = 0.00)
pZ <- prcomp(Z, tol = 0.1)
summary(pZ) # only ~14 PCs (out of 32)
## or choose only 3 PCs more directly:
pz3 <- prcomp(Z, rank. = 3)
summary(pz3) # same numbers as the first 3 above
stopifnot(ncol(pZ$rotation) == 14, ncol(pz3$rotation) == 3,
  all.equal(pz3$sdev, pZ$sdev, tolerance = 1e-15)) # exactly equal typically

## signs are random
require(graphics)
## the variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
prcomp(USArrests) # inappropriate
prcomp(USArrests, scale. = TRUE)
prcomp(~ Murder + Assault + Rape, data = USArrests, scale. = TRUE)
plot(prcomp(USArrests))
summary(prcomp(USArrests, scale. = TRUE))
biplot(prcomp(USArrests, scale. = TRUE))

Model Predictions

predict is a generic function for predictions from the results of various model fitting functions. The function invokes particular methods which depend on the class of the first argument.
predict

Usage

predict (object, ...)

Arguments

object a model object for which prediction is desired.
...
additional arguments affecting the predictions produced.

Details

Most prediction methods which are similar to those for linear models have an argument newdata specifying the first place to look for explanatory variables to be used for prediction. Some considerable attempts are made to match up the columns in newdata to those used for fitting, for example that they are of comparable types and that any factors have the same level set in the same order (or can be transformed to be so).

Time series prediction methods in package stats have an argument n.ahead specifying how many time steps ahead to predict.

Many methods have a logical argument se.fit saying if standard errors are to returned.

Value

The form of the value returned by predict depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

References


See Also

SafePrediction for prediction from (univariable) polynomial and spline fits.

Examples

require(utils)
## All the "predict" methods found
## NB most of the methods in the standard packages are hidden.
## Output will depend on what namespaces are (or have been) loaded.
## IGNORE_RDIFF_BEGIN
for(fn in methods("predict"))
  try(
    f <- eval(substitute(getAnywhere(fn)$objs[[1]], list(fn = fn)))
    cat(fn, "\n\t", deparse(args(f)), "\n")
  ), silent = TRUE)
## IGNORE_RDIFF_END
**predict.Arima**

*Forecast from ARIMA fits*

### Description

Forecast from models fitted by `arima`.

### Usage

```r
## S3 method for class 'Arima'
predict(object, n.ahead = 1, newxreg = NULL,
         se.fit = TRUE, ...)
```

### Arguments

- `object`: The result of an `arima` fit.
- `n.ahead`: The number of steps ahead for which prediction is required.
- `newxreg`: New values of `xreg` to be used for prediction. Must have at least `n.ahead` rows.
- `se.fit`: Logical: should standard errors of prediction be returned?
- `...`: arguments passed to or from other methods.

### Details

Finite-history prediction is used, via `KalmanForecast`. This is only statistically efficient if the MA part of the fit is invertible, so `predict.Arima` will give a warning for non-invertible MA models.

The standard errors of prediction exclude the uncertainty in the estimation of the ARMA model and the regression coefficients. According to Harvey (1993, pp. 58–9) the effect is small.

### Value

A time series of predictions, or if `se.fit = TRUE`, a list with components `pred`, the predictions, and `se`, the estimated standard errors. Both components are time series.

### References


### See Also

`arima`
Examples

od <- options(digits = 5) # avoid too much spurious accuracy
predict(arima(lh, order = c(3,0,0)), n.ahead = 12)

(fit <- arima(USAccDeaths, order = c(0,1,1),
seasonal = list(order = c(0,1,1))))
predict(fit, n.ahead = 6)
options(od)

predict.glm

Predict Method for GLM Fits

Description

Obtains predictions and optionally estimates standard errors of those predictions from a fitted generalized linear model object.

Usage

## S3 method for class 'glm'
predict(object, newdata = NULL,
type = c("link", "response", "terms"),
se.fit = FALSE, dispersion = NULL, terms = NULL,
na.action = na.pass, ...)

Arguments

object

a fitted object of class inheriting from "glm".

newdata

optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.

type

the type of prediction required. The default is on the scale of the linear predictors; the alternative "response" is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and type = "response" gives the predicted probabilities. The "terms" option returns a matrix giving the fitted values of each term in the model formula on the linear predictor scale.

The value of this argument can be abbreviated.

se.fit

logical switch indicating if standard errors are required.

dispersion

the dispersion of the GLM fit to be assumed in computing the standard errors. If omitted, that returned by summary applied to the object is used.

terms

with type = "terms" by default all terms are returned. A character vector specifies which terms are to be returned.

na.action

function determining what should be done with missing values in newdata. The default is to predict NA.

...

further arguments passed to or from other methods.
predict.glm

Details

If `newdata` is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear (in predictions and standard errors), with residual value NA. See also `napredict`.

Value

If `se.fit = FALSE`, a vector or matrix of predictions. For `type = "terms"` this is a matrix with a column per term, and may have an attribute "constant".

If `se.fit = TRUE`, a list with components

- `fit`: Predictions, as for `se.fit = FALSE`.
- `se.fit`: Estimated standard errors.
- `residual.scale`: A scalar giving the square root of the dispersion used in computing the standard errors.

Note

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

See Also

`glm`, `SafePrediction`

Examples

```r
require(graphics)

## example from Venables and Ripley (2002, pp. 190-2.)
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20-numdead)
budworm.lg <- glm(SF ~ sex*ldose, family = binomial)
summary(budworm.lg)

plot(c(1,32), c(0,1), type = "n", xlab = "dose", ylab = "prob", log = "x")
for(sex in levels(sex))
  text(2^ldose, numdead/20, as.character(sex))
ld <- seq(0, 5, 0.1)
lines(2^ld, predict(budworm.lg, data.frame(ldose = ld, sex = factor(rep("M", length(ld)), levels = levels(sex)), type = "response")))
lines(2^ld, predict(budworm.lg, data.frame(ldose = ld, sex = factor(rep("F", length(ld)), levels = levels(sex)), type = "response")))

## example with different environment (e.g., with missing values)

## simulate data
n <- 100
incidence <- 0.002
n1 <- 20
n2 <- 180
inc2 <- incidence/2
x <- rnorm(n)
y <- c(rnorm(n1, 0, inc2), rnorm(n2, incidence, 1))
dx <- c(rep(0, n1), rep(1, n2))

## fit logistic glm
model <- glm(cbind(x, 1-x) ~ dx, family = binomial)

## predict logistic glm
plot(c(0, 1), c(0, 1), type = "n", xlab = "observed", ylab = "predicted")
for(i in 1:n)
  text(model$fitted.values[i], model$linear.predictors[i], i)
```
predict.HoltWinters

Description

Computes predictions and prediction intervals for models fitted by the Holt-Winters method.

Usage

## S3 method for class 'HoltWinters'
predict(object, n.ahead = 1, prediction.interval = FALSE, level = 0.95, ...)

Arguments

object
An object of class HoltWinters.
n.ahead
Number of future periods to predict.
prediction.interval
logical. If TRUE, the lower and upper bounds of the corresponding prediction intervals are computed.
level
Confidence level for the prediction interval.
...
arguments passed to or from other methods.

Value

A time series of the predicted values. If prediction intervals are requested, a multiple time series is returned with columns fit, lwr and upr for the predicted values and the lower and upper bounds respectively.

Author(s)

David Meyer <David.Meyer@wu.ac.at>

References


See Also

HoltWinters

Examples

require(graphics)
m <- HoltWinters(co2)
p <- predict(m, 50, prediction.interval = TRUE)
plot(m, p)
predict.lm

**Predict method for Linear Model Fits**

**Description**

Predicted values based on linear model object.

**Usage**

```r
## S3 method for class 'lm'
predict(object, newdata, se.fit = FALSE, scale = NULL, df = Inf,
    interval = c("none", "confidence", "prediction"),
    level = 0.95, type = c("response", "terms"),
    terms = NULL, na.action = na.pass,
    pred.var = res.var/weights, weights = 1,
    rankdeficient = c("warnif", "simple", "non-estim", "NA", "NAwarn"),
    tol = 1e-6, verbose = FALSE,
    ...)
```

**Arguments**

- **object**  
  Object of class inheriting from "lm"
- **newdata**  
  An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
- **se.fit**  
  A switch indicating if standard errors are required.
- **scale**  
  Scale parameter for std.err. calculation.
- **df**  
  Degrees of freedom for scale.
- **interval**  
  Type of interval calculation. Can be abbreviated.
- **level**  
  Tolerance/confidence level.
- **type**  
  Type of prediction (response or model term). Can be abbreviated.
- **terms**  
  If type = "terms", which terms (default is all terms), a character vector.
- **na.action**  
  Function determining what should be done with missing values in newdata. The default is to predict NA.
- **pred.var**  
  The variance(s) for future observations to be assumed for prediction intervals. See 'Details'.
- **weights**  
  Variance weights for prediction. This can be a numeric vector or a one-sided model formula. In the latter case, it is interpreted as an expression evaluated in newdata.
- **rankdeficient**  
  A character string specifying what should happen in the case of a rank deficient model, i.e., when object$rank < ncol(model.matrix(object)).
  "warnif": gives a warning only in case of predicting 'non-estimable' cases, i.e., vectors not in the same predictor subspace as the original data (with tolerance tol). In that case, the non-estimable indices are also returned as attribute "non-estim" (see rankdeficient="non-estim").
  "simple": is back compatible to R < 4.3.0, possibly giving dubious predictions in non-estimable cases, and always signalling a warning.
"non-estim": gives the same predictions without warning, and with an attribute `attr(*, "non-estim")` with indices in `1:nrow(newdata)` of new data observations which are deemed non-estimable.

"NA": predicts NA for non-estimable new data, silently. Often recommended in new code.

"NAwarn": predicts NA for non-estimable new data with a warning.

tol
non-negative number determining how non-estimability is determined in rank deficient cases.

verbose logical indicating if messages should be produced about rank deficiency handling.

... further arguments passed to or from other methods.

Details

`predict.lm` produces predicted values, obtained by evaluating the regression function in the frame `newdata` (which defaults to `model.frame(object)`). If the logical `se.fit` is `TRUE`, standard errors of the predictions are calculated. If the numeric argument `scale` is set (with optional `df`), it is used as the residual standard deviation in the computation of the standard errors, otherwise this is extracted from the model fit. Setting `intervals` specifies computation of confidence or prediction (tolerance) intervals at the specified `level`, sometimes referred to as narrow vs. wide intervals.

If the fit is rank-deficient, some of the columns of the design matrix will have been dropped during the `lm` computations, and corresponding `coef()` components set to `NA`. Prediction from such a fit only makes sense if `newdata` is contained in the same subspace as the original data. Other `newdata` entries (rows) are non-estimable. This is now checked (up to numerical tolerance `tol`) unless `rankdeficient == "simple"`, which corresponds to previous behaviour, warns always and predicts using the non-NA coefficients with the corresponding columns of the design matrix. The new default option, `rankdeficient == "warnif"` checks if there are “non-estimable” cases (up to tolerance `tol`) and only warns in that case. All further `rankdeficient` options also check and either predict NA or mark the non-estimable cases differently.

If `newdata` is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit are handled is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the predictions, whereas if `na.action = na.exclude` they will appear (in predictions, standard errors or interval limits), with value `NA`.

See also `napredict`.

The prediction intervals are for a single observation at each case in `newdata` (or by default, the data used for the fit) with error variance(s) `pred.var`. This can be a multiple of `res.var`, the estimated value of $\sigma^2$: the default is to assume that future observations have the same error variance as those used for fitting. If `weights` is supplied, the inverse of this is used as a scale factor. For a weighted fit, if the prediction is for the original data frame, `weights` defaults to the weights used for the model fit, with a warning since it might not be the intended result. If the fit was weighted and `newdata` is given, the default is to assume constant prediction variance, with a warning.

Value

`predict.lm` produces a vector of predictions or a matrix of predictions and bounds with column names `fit`, `lwr`, and `upr` if `interval` is set. For `type = "terms"` this is a matrix with a column per term and may have an attribute "constant".

If `se.fit` is `TRUE`, a list with the following components is returned:

- `fit`: vector or matrix as above
- `se.fit`: standard error of predicted means
Note

Variables are first looked for in *newdata* and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in *newdata* if it was supplied.

Notice that prediction variances and prediction intervals always refer to future observations, possibly corresponding to the same predictors as used for the fit. The variance of the residuals will be smaller.

Strictly speaking, the formula used for prediction limits assumes that the degrees of freedom for the fit are the same as those for the residual variance. This may not be the case if *res.var* is not obtained from the fit.

See Also

The model fitting function `lm`, `predict`

SafePrediction for prediction from (univariable) polynomial and spline fits.

Examples

```r
require(graphics)

## Predictions
x <- rnorm(15)
y <- x + rnorm(15)
predict(lm(y ~ x))
new <- data.frame(x = seq(-3, 3, 0.5))
predict(lm(y ~ x), new, se.fit = TRUE)
pred.w.plim <- predict(lm(y ~ x), new, interval = "prediction")
pred.w.clim <- predict(lm(y ~ x), new, interval = "confidence")
matplot(new$x, cbind(pred.w.clim, pred.w.plim[, -1]),
       lty = c(1, 2, 2, 3, 3), type = "l", ylab = "predicted y")

## Prediction intervals, special cases
## The first three of these throw warnings
w <- 1 + x^2
fit <- lm(y ~ x)
wfit <- lm(y ~ x, weights = w)
predict(fit, interval = "prediction")
predict(wfit, interval = "prediction")
predict(wfit, new, interval = "prediction", weights = (new$x)^2)
predict(wfit, new, interval = "prediction", weights = -x^2)

##-- From aov(.) example ---- predict(.. terms)
npk.aov <- aov(yield ~ block + N*P*K, npk)
(termL <- attr(terms(npk.aov), "term.labels"))
(pt <- predict(npk.aov, type = "terms"))
pt. <- predict(npk.aov, type = "terms", terms = termL[1:4])
stopifnot(all.equal(pt[, 1:4], pt,
               tolerance = 1e-12, check.attributes = FALSE))
```
**predict.loess**  

Predict Loess Curve or Surface

## Description

Predictions from a `loess` fit, optionally with standard errors.

## Usage

```r
## S3 method for class 'loess'
predict(object, newdata = NULL, se = FALSE,
        na.action = na.pass, ...)
```

## Arguments

- **object**: an object fitted by `loess`.
- **newdata**: an optional data frame in which to look for variables with which to predict, or a matrix or vector containing exactly the variables needs for prediction. If missing, the original data points are used.
- **se**: should standard errors be computed?
- **na.action**: function determining what should be done with missing values in data frame `newdata`. The default is to predict `NA`.
- **...**: arguments passed to or from other methods.

## Details

The standard errors calculation `se = TRUE` is slower than prediction, notably as it needs a relatively large workspace (memory), notably matrices of dimension $N \times f$ where $f = \text{span}$, i.e., `se = TRUE` is $O(N^2)$ and hence stops when the sample size $N$ is larger than about 40,600 (for default `span = 0.75`).

When the fit was made using `surface = "interpolate"` (the default), `predict.loess` will not extrapolate – so points outside an axis-aligned hypercube enclosing the original data will have missing (NA) predictions and standard errors.

## Value

If `se = FALSE`, a vector giving the prediction for each row of `newdata` (or the original data). If `se = TRUE`, a list containing components:

- **fit**: the predicted values.
- **se**: an estimated standard error for each predicted value.
- **residual.scale**: the estimated scale of the residuals used in computing the standard errors.
- **df**: an estimate of the effective degrees of freedom used in estimating the residual scale, intended for use with t-based confidence intervals.

If `newdata` was the result of a call to `expand.grid`, the predictions (and s.e.'s if requested) will be an array of the appropriate dimensions.

Predictions from infinite inputs will be `NA` since `loess` does not support extrapolation.
Note

Variables are first looked for in newdata and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in newdata if it was supplied.

Author(s)

B. D. Ripley, based on the cloess package of Cleveland, Grosse and Shyu.

See Also

loess

Examples

cars.lo <- loess(dist ~ speed, cars)
predict(cars.lo, data.frame(speed = seq(5, 30, 1)), se = TRUE)
# to get extrapolation
cars.lo2 <- loess(dist ~ speed, cars,
       control = loess.control(surface = "direct"))
predict(cars.lo2, data.frame(speed = seq(5, 30, 1)), se = TRUE)

predict.nls

Predicting from Nonlinear Least Squares Fits

Description

predict.nls produces predicted values, obtained by evaluating the regression function in the frame newdata. If the logical se.fit is TRUE, standard errors of the predictions are calculated. If the numeric argument scale is set (with optional df), it is used as the residual standard deviation in the computation of the standard errors, otherwise this is extracted from the model fit. Setting intervals specifies computation of confidence or prediction (tolerance) intervals at the specified level.

At present se.fit and interval are ignored.

Usage

## S3 method for class 'nls'
predict(object, newdata, se.fit = FALSE, scale = NULL, df = Inf,
       interval = c("none", "confidence", "prediction"),
       level = 0.95, ...)

Arguments

object An object that inherits from class nls.
newdata A named list or data frame in which to look for variables with which to predict. If newdata is missing the fitted values at the original data points are returned.
se.fit A logical value indicating if the standard errors of the predictions should be calculated. Defaults to FALSE. At present this argument is ignored.
predict.nls

scale A numeric scalar. If it is set (with optional df), it is used as the residual standard deviation in the computation of the standard errors, otherwise this information is extracted from the model fit. At present this argument is ignored.

df A positive numeric scalar giving the number of degrees of freedom for the scale estimate. At present this argument is ignored.

interval A character string indicating if prediction intervals or a confidence interval on the mean responses are to be calculated. At present this argument is ignored.

level A numeric scalar between 0 and 1 giving the confidence level for the intervals (if any) to be calculated. At present this argument is ignored.

... Additional optional arguments. At present no optional arguments are used.

Value

predict.nls produces a vector of predictions. When implemented, interval will produce a matrix of predictions and bounds with column names fit, lwr, and upr. When implemented, if se.fit is TRUE, a list with the following components will be returned:

- fit vector or matrix as above
- se.fit standard error of predictions
- residual.scale residual standard deviations
- df degrees of freedom for residual

Note

Variables are first looked for in newdata and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in newdata if it was supplied.

See Also

The model fitting function nls, predict.

Examples

require(graphics)

fm <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
predict(fm) # fitted values at observed times

## Form data plot and smooth line for the predictions
opar <- par(las = 1)
plot(demand ~ Time, data = BOD, col = 4,
     main = "BOD data and fitted first-order curve",
     xlim = c(0,7), ylim = c(0, 20) )
tt <- seq(0, 8, length.out = 101)
lines(tt, predict(fm, list(Time = tt)))
par(opar)
predict.smooth.spline  Predict from Smoothing Spline Fit

Description

Predict a smoothing spline fit at new points, return the derivative if desired. The predicted fit is linear beyond the original data.

Usage

## S3 method for class 'smooth.spline'
predict(object, x, deriv = 0, ...)

Arguments

object  a fit from smooth.spline.

x  the new values of x.

deriv  integer; the order of the derivative required.

...  further arguments passed to or from other methods.

Value

A list with components

x  The input x.

y  The fitted values or derivatives at x.

See Also

smooth.spline

Examples

require(graphics)
attach(cars)
cars.spl <- smooth.spline(speed, dist, df = 6.4)

## "Proof" that the derivatives are okay, by comparing with approximation
diff.quot <- function(x, y) {
  # Difference quotient (central differences where available)
  n <- length(x); i1 <- 1:2; i2 <- (n-1):n
  c(diff(y[i1]) / diff(x[i1]), (y[-i1] - y[-i2]) / (x[-i1] - x[-i2]),
    diff(y[i2]) / diff(x[i2]))
}

xx <- unique(sort(c(seq(0, 30, by = .2), kn <- unique(speed))))
i.kn <- match(kn, xx) # indices of knots within xx
op <- par(mfrow = c(2,2))
plot(speed, dist, xlim = range(xx), main = "Smooth.spline & derivatives")
lines(pp <- predict(cars.spl, xx), col = "red")
preplot  

Pre-computations for a Plotting Object

Description

Compute an object to be used for plots relating to the given model object.

Usage

preplot(object, ...)

Arguments

object  
a fitted model object.

...  
additional arguments for specific methods.

Details

Only the generic function is currently provided in base R, but some add-on packages have methods. Principally here for S compatibility.

Value

An object set up to make a plot that describes object.

princomp  

Principal Components Analysis

Description

princomp performs a principal components analysis on the given numeric data matrix and returns the results as an object of class princomp.
Usage

princomp(x, ...)

## S3 method for class 'formula'
princomp(formula, data = NULL, subset, na.action, ...)

## Default S3 method:
princomp(x, cor = FALSE, scores = TRUE, covmat = NULL,
        subset = rep_len(TRUE, nrow(as.matrix(x))), fix_sign = TRUE, ...)

## S3 method for class 'princomp'
predict(object, newdata, ...)

Arguments

formula a formula with no response variable, referring only to numeric variables.
data an optional data frame (or similar: see model.frame) containing the variables in the formula.
        By default the variables are taken from environment(formula).
subset an optional vector used to select rows (observations) of the data matrix x.
na.action a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit.
x a numeric matrix or data frame which provides the data for the principal components analysis.
cor a logical value indicating whether the calculation should use the correlation matrix or the covariance matrix. (The correlation matrix can only be used if there are no constant variables.)
scores a logical value indicating whether the score on each principal component should be calculated.
covmat a covariance matrix, or a covariance list as returned by cov.wt (and cov.mve or cov.mcd from package MASS). If supplied, this is used rather than the covariance matrix of x.
fix_sign Should the signs of the loadings and scores be chosen so that the first element of each loading is non-negative?
... arguments passed to or from other methods. If x is a formula one might specify cor or scores.
object Object of class inheriting from "princomp".
newdata An optional data frame or matrix in which to look for variables with which to predict. If omitted, the scores are used. If the original fit used a formula or a data frame or a matrix with column names, newdata must contain columns with the same names. Otherwise it must contain the same number of columns, to be used in the same order.

Details

princomp is a generic function with "formula" and "default" methods.
The calculation is done using eigen on the correlation or covariance matrix, as determined by cor. This is done for compatibility with the S-PLUS result. A preferred method of calculation is to use svd on x, as is done in prcomp.
Note that the default calculation uses divisor $n$ for the covariance matrix.

The `print` method for these objects prints the results in a nice format and the `plot` method produces a scree plot (`screeplot`). There is also a `biplot` method.

If $x$ is a formula then the standard NA-handling is applied to the scores (if requested): see `napredict`.

`princomp` only handles so-called R-mode PCA, that is feature extraction of variables. If a data matrix is supplied (possibly via a formula) it is required that there are at least as many units as variables. For Q-mode PCA use `prcomp`.

**Value**

`princomp` returns a list with class "princomp" containing the following components:

- `sdev` the standard deviations of the principal components.
- `loadings` the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors). This is of class "loadings": see `loadings` for its `print` method.
- `center` the means that were subtracted.
- `scale` the scalings applied to each variable.
- `n.obs` the number of observations.
- `scores` if `scores = TRUE`, the scores of the supplied data on the principal components. These are non-null only if $x$ was supplied, and if `covmat` was also supplied if it was a covariance list. For the formula method, `napredict()` is applied to handle the treatment of values omitted by the `na.action`.
- `call` the matched call.
- `na.action` If relevant.

**Note**

The signs of the columns of the loadings and scores are arbitrary, and so may differ between different programs for PCA, and even between different builds of R: `fix_sign = TRUE` alleviates that.

**References**


**See Also**

`summary.princomp`, `screeplot`, `biplot.princomp`, `prcomp`, `cor`, `cov`, `eigen`.

**Examples**

```r
require(graphics)

## The variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
(pc.cr <- princomp(USArrests)) # inappropriate
princomp(USArrests, cor = TRUE) # = prcomp(USArrests, scale=TRUE)
## Similar, but different:
## The standard deviations differ by a factor of sqrt(49/50)
```
summary(pc.cr <- princomp(USArrests, cor = TRUE))
loadings(pc.cr)  # note that blank entries are small but not zero
## The signs of the columns of the loadings are arbitrary
plot(pc.cr)  # shows a screeplot.
biplot(pc.cr)

## Formula interface
princomp(~ ., data = USArrests, cor = TRUE)

## NA-handling
USArrests[1, 2] <- NA
pc.cr <- princomp(~ Murder + Assault + UrbanPop,
                  data = USArrests, na.action = na.exclude, cor = TRUE)

## (Simple) Robust PCA:
## Classical:
(pc.cl <- princomp(stackloss))
## Robust:
(pc.rob <- princomp(stackloss, covmat = MASS::cov.rob(stackloss)))

print.power.htest  Print Methods for Hypothesis Tests and Power Calculation Objects

Description

Printing objects of class "htest" or "power.htest", respectively, by simple print methods.

Usage

## S3 method for class 'htest'
print(x, digits = getOption("digits"), prefix = "\t", ...)

## S3 method for class 'power.htest'
print(x, digits = getOption("digits"), ...)

Arguments

x object of class "htest" or "power.htest".
digits number of significant digits to be used.
prefix string, passed to strwrap for displaying the method component of the htest object.
... further arguments to be passed to or from methods.

Details

Both print methods traditionally have not obeyed the digits argument properly. They now do, the htest method mostly in expressions like max(1, digits - 2).

A power.htest object is just a named list of numbers and character strings, supplemented with method and note elements. The method is displayed as a title, the note as a footnote, and the remaining elements are given in an aligned ‘name = value’ format.
Value

the argument \( x \), invisibly, as for all \texttt{print} methods.

Author(s)

Peter Dalgaard

See Also

\texttt{power.t.test}, \texttt{power.prop.test}

Examples

\begin{verbatim}
(ptt <- power.t.test(n = 20, delta = 1))
print(ptt, digits = 4) # using less digits than default
print(ptt, digits = 12) # using more
\end{verbatim}

Description

Notably for calendar related time series objects, \texttt{format} and \texttt{print} methods showing years, months and or quarters respectively.

Usage

\begin{verbatim}
## S3 method for class 'ts'
print(x, calendar, ...) .preformat.ts(x, calendar, ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{x} a time series object.
  \item \texttt{calendar} enable/disable the display of information about month names, quarter names or year when printing. The default is \texttt{TRUE} for a frequency of 4 or 12, \texttt{FALSE} otherwise.
  \item \texttt{...} additional arguments to \texttt{print} (or \texttt{format} methods).
\end{itemize}

Details

The \texttt{print} method for "ts" objects prints a header (basically of \texttt{tsp(x)}), if calendar is false, and then prints the result of \texttt{.preformat.ts(x, *)}, which is typically a \texttt{matrix} with \texttt{rownames} built from the calendar times where applicable.

See Also

\texttt{print, ts}. 

Examples

```r
print(ts(1:10, frequency = 7, start = c(12, 2)), calendar = TRUE)

print(sunsp.1 <- window(sunspot.month, end=c(1756, 12)))
m <- .preformat.ts(sunsp.1) # a character matrix
```

Description

Utility function to be used in higher-level `print` methods, such as those for `summary.lm`, `summary.glm` and `anova`. The goal is to provide a flexible interface with smart defaults such that often, only `x` needs to be specified.

Usage

```r
printCoefmat(x, digits = max(3, getOption("digits") - 2),
             signif.stars = getOption("show.signif.stars"),
             signif.legend = signif.stars,
             dig.tst = max(1, min(5, digits - 1)),
             cs.ind = 1L:k, tst.ind = k + 1L,
             zap.ind = integer(), P.values = NULL,
             has.Pvalue = nc >= 4L && length(cn <- colnames(x)) &&
               substr(cn[nc], 1L, 3L) %in% c("Pr(" ,"p-v" ),
               eps.Pvalue = .Machine$double.eps,
             na.print = "NA", quote = FALSE, right = TRUE, ...)```

Arguments

- **x**: a numeric matrix like object, to be printed.
- **digits**: minimum number of significant digits to be used for most numbers.
- **signif.stars**: logical; if `TRUE`, P-values are additionally encoded visually as 'significance stars' in order to help scanning of long coefficient tables. It defaults to the show.signif.stars slot of `options`.
- **signif.legend**: logical; if `TRUE`, a legend for the 'significance stars' is printed provided signif.stars = `TRUE`.
- **dig.tst**: minimum number of significant digits for the test statistics, see `tst.ind`.
- **cs.ind**: indices (integer) of column numbers which are (like) coefficients and standard errors to be formatted together.
- **tst.ind**: indices (integer) of column numbers for test statistics.
- **zap.ind**: indices (integer) of column numbers which should be formatted by `zapsmall`, i.e., by 'zapping' values close to 0.
- **P.values**: logical or `NULL`; if `TRUE`, the last column of `x` is formatted by `format.pval` as P values. If `P.values = NULL`, the default, it is set to `TRUE` only if `options("show.coef.Pvalue")` is `TRUE` and `x` has at least 4 columns and the last column name of `x` starts with "Pr(["."].
has.Pvalue logical; if TRUE, the last column of x contains P values; in that case, it is printed if and only if P.values (above) is true.

eps.Pvalue number, passed to format.pval() as eps.
a.print a character string to code NA values in printed output.
quote, right, ... further arguments passed to print.default.

Value
Invisibly returns its argument, x.

Author(s)
Martin Maechler

See Also
print.summary.lm, format.pval, format.

Examples
    cmat <- cbind(rnorm(3, 10), sqrt(rchisq(3, 12)))
    cmat <- cbind(cmat, cmat[, 1]/cmat[, 2])
    cmat <- cbind(cmat, 2*pnorm(-cmat[, 3]))
    colnames(cmat) <- c("Estimate", "Std.Err", "Z value", "Pr(>z)")
    printCoefmat(cmat[, 1:3])
    printCoefmat(cmat)
    op <- options(show.coef.Pvalues = FALSE)
    printCoefmat(cmat, digits = 2)
    printCoefmat(cmat, digits = 2, P.values = TRUE)
    options(op) # restore

profile

Generic Function for Profiling Models

Description
Investigates behavior of objective function near the solution represented by fitted.
See documentation on method functions for further details.

Usage
profile(fitted, ...)
profile.nls

Method for Profiling nls Objects

Description

Investigates the profile log-likelihood function for a fitted model of class "nls".

Usage

## S3 method for class 'nls'
profile(fitted, which = 1:npar, maxpts = 100, alphamax = 0.01,
delta.t = cutoff/5, ...)

Arguments

- `fitted`: the original fitted model object.
- `which`: the original model parameters which should be profiled. This can be a numeric or character vector. By default, all non-linear parameters are profiled.
- `maxpts`: maximum number of points to be used for profiling each parameter.
- `alphamax`: highest significance level allowed for the profile t-statistics.
- `delta.t`: suggested change on the scale of the profile t-statistics. Default value chosen to allow profiling at about 10 parameter values.
- `...`: further arguments passed to or from other methods.

Details

The profile t-statistics is defined as the square root of change in sum-of-squares divided by residual standard error with an appropriate sign.

Value

A list with an element for each parameter being profiled. The elements are data-frames with two variables

- `par.vals`: a matrix of parameter values for each fitted model.
- `tau`: the profile t-statistics.

Author(s)

Of the original version, Douglas M. Bates and Saikat DebRoy

References

proj

See Also
nls, profile, plot.profile.nls

Examples

# obtain the fitted object
fm1 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
# get the profile for the fitted model: default level is too extreme
pr1 <- profile(fm1, alphamax = 0.05)
# profiled values for the two parameters
## IGNORE_RDIFF_BEGIN
pr1$A
pr1$lrc
## IGNORE_RDIFF_END
# see also example(plot.profile.nls)

proj

Projections of Models

Description

proj returns a matrix or list of matrices giving the projections of the data onto the terms of a linear model. It is most frequently used for aov models.

Usage

proj(object, ...)

## S3 method for class 'aov'
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)

## S3 method for class 'aovlist'
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)

## Default S3 method:
proj(object, onedf = TRUE, ...)

## S3 method for class 'lm'
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)

Arguments

object An object of class "lm" or a class inheriting from it, or an object with a similar structure including in particular components qr and effects.
onedf A logical flag. If TRUE, a projection is returned for all the columns of the model matrix. If FALSE, the single-column projections are collapsed by terms of the model (as represented in the analysis of variance table).
unweighted.scale If the fit producing object used weights, this determines if the projections correspond to weighted or unweighted observations.
...
Swallow and ignore any other arguments.
Details

A projection is given for each stratum of the object, so for aov models with an Error term the result is a list of projections.

Value

A projection matrix or (for multi-stratum objects) a list of projection matrices.

Each projection is a matrix with a row for each observations and either a column for each term (onedf = FALSE) or for each coefficient (onedf = TRUE). Projection matrices from the default method have orthogonal columns representing the projection of the response onto the column space of the Q matrix from the QR decomposition. The fitted values are the sum of the projections, and the sum of squares for each column is the reduction in sum of squares from fitting that column (after those to the left of it).

The methods for lm and aov models add a column to the projection matrix giving the residuals (the projection of the data onto the orthogonal complement of the model space).

Strictly, when onedf = FALSE the result is not a projection, but the columns represent sums of projections onto the columns of the model matrix corresponding to that term. In this case the matrix does not depend on the coding used.

Author(s)

The design was inspired by the S function of the same name described in Chambers et al (1992).

References


See Also

aov, lm, model.tables

Examples

N <- c(0,1,0,1,1,0,0,0,1,1,0,1,0,0,1,0,1,0,1,0,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,0,0,0,1,0,1,0,1,0,0,1,1,0)
K <- c(1,0,0,1,0,1,0,1,0,1,0,1,0,0,0,1,1,0,1,0,0,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,55.0,62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)
npk <- data.frame(block = gl(6,4), N = factor(N), P = factor(P), K = factor(K), yield = yield)
npk.aov <- aov(yield ~ block + N*P*K, npk)
proj(npk.aov)

## as a test, not particularly sensible
options(contrasts = c("contr.helmert", "contr.treatment"))
npk.aovE <- aov(yield ~ N*P*K + Error(block), npk)
proj(npk.aovE)
prop.test

Test of Equal or Given Proportions

Description

prop.test can be used for testing the null that the proportions (probabilities of success) in several groups are the same, or that they equal certain given values.

Usage

prop.test(x, n, p = NULL,
    alternative = c("two.sided", "less", "greater"),
    conf.level = 0.95, correct = TRUE)

Arguments

x a vector of counts of successes, a one-dimensional table with two entries, or a two-dimensional table (or matrix) with 2 columns, giving the counts of successes and failures, respectively.

n a vector of counts of trials; ignored if x is a matrix or a table.

p a vector of probabilities of success. The length of p must be the same as the number of groups specified by x, and its elements must be greater than 0 and less than 1.

alternative a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter. Only used for testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.

conf.level confidence level of the returned confidence interval. Must be a single number between 0 and 1. Only used when testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.

correct a logical indicating whether Yates’ continuity correction should be applied where possible.

Details

Only groups with finite numbers of successes and failures are used. Counts of successes and failures must be nonnegative and hence not greater than the corresponding numbers of trials which must be positive. All finite counts should be integers.

If p is NULL and there is more than one group, the null tested is that the proportions in each group are the same. If there are two groups, the alternatives are that the probability of success in the first group is less than, not equal to, or greater than the probability of success in the second group, as specified by alternative. A confidence interval for the difference of proportions with confidence level as specified by conf.level and clipped to [−1, 1] is returned. Continuity correction is used only if it does not exceed the difference of the sample proportions in absolute value. Otherwise, if there are more than 2 groups, the alternative is always "two.sided", the returned confidence interval is NULL, and continuity correction is never used.

If there is only one group, then the null tested is that the underlying probability of success is p, or .5 if p is not given. The alternative is that the probability of success is less than, not equal to, or greater than p or 0.5, respectively, as specified by alternative. A confidence interval for the
underlying proportion with confidence level as specified by \texttt{conf.level} and clipped to \([0, 1]\) is returned. Continuity correction is used only if it does not exceed the difference between sample and null proportions in absolute value. The confidence interval is computed by inverting the score test. Finally, if \(p\) is given and there are more than 2 groups, the null tested is that the underlying probabilities of success are those given by \(p\). The alternative is always "two.sided", the returned confidence interval is NULL, and continuity correction is never used.

\textbf{Value}

A list with class \"htest\" containing the following components:

- \texttt{statistic} the value of Pearson's chi-squared test statistic.
- \texttt{parameter} the degrees of freedom of the approximate chi-squared distribution of the test statistic.
- \texttt{p.value} the p-value of the test.
- \texttt{estimate} a vector with the sample proportions \(x/n\).
- \texttt{conf.int} a confidence interval for the true proportion if there is one group, or for the difference in proportions if there are 2 groups and \(p\) is not given, or NULL otherwise. In the cases where it is not NULL, the returned confidence interval has an asymptotic confidence level as specified by \texttt{conf.level}, and is appropriate to the specified alternative hypothesis.
- \texttt{null.value} the value of \(p\) if specified by the null, or NULL otherwise.
- \texttt{alternative} a character string describing the alternative.
- \texttt{method} a character string indicating the method used, and whether Yates' continuity correction was applied.
- \texttt{data.name} a character string giving the names of the data.

\textbf{References}


\textbf{See Also}

\texttt{binom.test} for an exact test of a binomial hypothesis.

\textbf{Examples}

```r
heads <- rbinom(1, size = 100, prob = .5)
prop.test(heads, 100) # continuity correction TRUE by default
prop.test(heads, 100, correct = FALSE)
```

## Data from Fleiss (1981), p. 139.
## H0: The null hypothesis is that the four populations from which
## the patients were drawn have the same true proportion of smokers.
## A: The alternative is that this proportion is different in at least one of the populations.

```r
smokers <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
prop.test(smokers, patients)
```

---

### Description

Performs chi-squared test for trend in proportions, i.e., a test asymptotically optimal for local alternatives where the log odds vary in proportion with score. By default, score is chosen as the group numbers.

### Usage

```r
prop.trend.test(x, n, score = seq_along(x))
```

### Arguments

- `x`: Number of events
- `n`: Number of trials
- `score`: Group score

### Value

An object of class "htest" with title, test statistic, p-value, etc.

### Note

This really should get integrated with `prop.test`

### Author(s)

Peter Dalgaard

### See Also

`prop.test`

### Examples

```r
smokers <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
prop.test(smokers, patients)
prop.trend.test(smokers, patients)
prop.trend.test(smokers, patients, c(0,0,1))
```


Description

qqnorm is a generic function the default method of which produces a normal QQ plot of the values in y. qqline adds a line to a “theoretical”, by default normal, quantile-quantile plot which passes through the probs quantiles, by default the first and third quartiles.

qqplot produces a QQ plot of two datasets. If conf.level is given, a confidence band for a function transforming the distribution of x into the distribution of y is plotted based on Switzer (1976). The QQ plot can be understood as an estimate of such a treatment function. If exact = NULL (the default), an exact confidence band is computed if the product of the sample sizes is less than 10000, with or without ties. Otherwise, asymptotic distributions are used whose approximations may be inaccurate in small samples. Monte-Carlo approximations based on B random permutations are computed when simulate = TRUE. Confidence bands are in agreement with Smirnov’s test, that is, the bisecting line is covered by the band iff the null of both samples coming from the same distribution cannot be rejected at the same level.

Graphical parameters may be given as arguments to qqnorm, qqplot and qqline.

Usage

\begin{verbatim}
qqnorm(y, ...)  
## Default S3 method:  
## qqnorm(y, ylim, main = "Normal Q-Q Plot",  
## xlab = "Theoretical Quantiles", ylab = "Sample Quantiles",  
## plot.it = TRUE, datax = FALSE, ...)  
qqline(y, datax = FALSE, distribution = qnorm,  
## probs = c(0.25, 0.75), qtype = 7, ...)  
qqplot(x, y, plot.it = TRUE,  
## xlab = deparse1(substitute(x)),  
## ylab = deparse1(substitute(y)), ...,  
## conf.level = NULL,  
## conf.args = list(exact = NULL, simulate.p.value = FALSE,  
## B = 2000, col = NA, border = NULL))
\end{verbatim}

Arguments

- **x** The first sample for qqplot.
- **y** The second or only data sample.
- **xlab**, **ylab**, **main** plot labels. The xlab and ylab refer to the y and x axes respectively if datax = TRUE.
- **plot.it** logical. Should the result be plotted?
- **datax** logical. Should data values be on the x-axis?
- **distribution** quantile function for reference theoretical distribution.
- **probs** numeric vector of length two, representing probabilities. Corresponding quantile pairs define the line drawn.
qqnorm

qtype

the type of quantile computation used in quantile.

ylim, ...

graphical parameters.

conf.level

confidence level of the band. The default, NULL, does not lead to the computation of a confidence band.

conf.args

list of arguments defining confidence band computation and visualisation: exact is NULL (see details) or a logical indicating whether an exact p-value should be computed. simulate.p.value is a logical indicating whether to compute p-values by Monte Carlo simulation. B defines the number of replicates used in the Monte Carlo test, col and border define the color for filling and border of the confidence band (the default, NA and NULL, is to leave the band unfilled with black borders.

Value

For qnorm and qqplot, a list with components

x

The x coordinates of the points that were/would be plotted

y

The original y vector, i.e., the corresponding y coordinates including NAs. If conf.level was specified to qqplot, the list contains additional components lwr and upr defining the confidence band.

References


See Also

ppoints, used by qnorm to generate approximations to expected order statistics for a normal distribution.

Examples

require(graphics)

y <- rt(200, df = 5)
qnorm(y); qqline(y, col = 2)
qqplot(y, rt(300, df = 5))

qnorm(precip, ylab = "Precipitation [in/yr] for 70 US cities")

### "QQ-Chisquare" : -----------------------------
y <- rchisq(500, df = 3)
### Q-Q plot for Chi^2 data against true theoretical distribution:
qqplot(qchisq(ppoints(500), df = 3), y, 
    main = expression("Q-Q plot for" ~~ {chi^2}[nu == 3]))
qqline(y, distribution = function(p) qchisq(p, df = 3),
    probs = c(0.1, 0.6), col = 2)
mtext("qqline(*, dist = qchisq(., df=3), prob = c(0.1, 0.6))")
### (Note that the above uses ppoints() with a = 1/2, giving the
### probability points for quantile type 5: so theoretically, using
### qqline(qtype = 5) might be preferable.)
## Figure 1 in Switzer (1976), knee angle data

```r
switzer <- data.frame(
  angle = c(-31, -30, -25, -25, -23, -23, -22, -20, -20, -18,
            -18, -18, -16, -15, -15, -14, -13, -11, -10, -9,
            -8, -7, -7, -6, -6, -4, -4, -3, -2,
            -2, -1, 1, 1, 4, 5, 11, 12, 16, 34,
            -31, -20, -18, -16, -16, -15, -14, -14, -14,
            -14, -13, -13, -11, -11, -10, -9, -9, -8, -7,
            -7, -6, -6, -5, -5, -4, -2, -2, -2,
            0, 0, 1, 1, 2, 4, 5, 5, 6, 17),
  sex = gl(2, 40, labels = c("Female", "Male")))
ks.test(angle ~ sex, data = switzer)
d <- with(switzer, split(angle, sex))
with(d, qqplot(Female, Male, pch = 19, xlim = c(-31, 31), ylim = c(-31, 31),
        conf.level = 0.945,
        conf.args = list(col = "lightgrey", exact = TRUE)))
abline(a = 0, b = 1)
## agreement with ks.test
set.seed(1)
x <- rnorm(50)
y <- rnorm(50, mean = .5, sd = .95)
ex <- TRUE
### p = 0.112
(pval <- ks.test(x, y, exact = ex)$p.value)
## 88.8% confidence band with bisecting line
## touching the lower bound
qqplot(x, y, pch = 19, conf.level = 1 - pval,
       conf.args = list(exact = ex, col = "lightgrey"))
abline(a = 0, b = 1)
```

---

**quade.test**  

---

### Description

Performs a Quade test with unreplicated blocked data.

### Usage

```r
quade.test(y, ...)
```

## Default S3 method:
`quade.test(y, groups, blocks, ...)

## S3 method for class 'formula'
`quade.test(formula, data, subset, na.action, ...)
```
quade.test

Arguments

- **y**: either a numeric vector of data values, or a data matrix.
- **groups**: a vector giving the group for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.
- **blocks**: a vector giving the block for the corresponding elements of y if this is a vector; ignored if y is a matrix. If not a factor object, it is coerced to one.
- **formula**: a formula of the form a ~ b | c, where a, b and c give the data values and corresponding groups and blocks, respectively.
- **data**: an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
- **subset**: an optional vector specifying a subset of observations to be used.
- **na.action**: a function which indicates what should happen when the data contain NAs. Defaults to `getOption("na.action")`.
- **...**: further arguments to be passed to or from methods.

Details

quade.test can be used for analyzing unreplicated complete block designs (i.e., there is exactly one observation in y for each combination of levels of groups and blocks) where the normality assumption may be violated.

The null hypothesis is that apart from an effect of blocks, the location parameter of y is the same in each of the groups.

If y is a matrix, groups and blocks are obtained from the column and row indices, respectively. NAs are not allowed in groups or blocks; if y contains NA’s, corresponding blocks are removed.

Value

A list with class "htest" containing the following components:

- **statistic**: the value of Quade’s F statistic.
- **parameter**: a vector with the numerator and denominator degrees of freedom of the approximate F distribution of the test statistic.
- **p.value**: the p-value of the test.
- **method**: the character string "Quade test".
- **data.name**: a character string giving the names of the data.

References


See Also

`friedman.test`. 
Examples

### Conover (1999, p. 375f):
### Numbers of five brands of a new hand lotion sold in seven stores
### during one week.

\[
y <- \text{matrix}(c(5, 4, 7, 10, 12, \\
1, 3, 1, 0, 2, \\
16, 12, 22, 22, 35, \\
5, 4, 3, 5, 4, \\
10, 9, 7, 13, 10, \\
19, 18, 28, 37, 58, \\
10, 7, 6, 8, 7), \\
nrow = 7, \text{byrow} = \text{TRUE}, \\
dimnames = \\
\text{list}(\text{Store} = \text{as.character}(1:7), \\
\text{Brand} = \text{LETTERS}[1:5]))
\]

\[
y
\]

(qTst <- quade.test(y))

### Show equivalence of different versions of test:

\[
\text{utils::str(dy <- as.data.frame(as.table(y)))}
\]

\[
qT. <- \text{quade.test}(\text{Freq} \sim \text{Brand}|\text{Store}, \text{data} = \text{dy})
\]

\[
qT.$\text{data.name} <- \text{qTst$\text{data.name}}
\]

\[
\text{stopifnot}(\text{all.equal(qTst, qT., tolerance = 1e-15))}
\]

\[
dys <- \text{dy}[\text{order(dy[, "\text{Freq}"])},]
\]

\[
qTs <- \text{quade.test}(\text{Freq} \sim \text{Brand}|\text{Store}, \text{data} = \text{dys})
\]

\[
qTs$\text{data.name} <- qTst$\text{data.name}
\]

\[
\text{stopifnot}(\text{all.equal(qTst, qTs, tolerance = 1e-15))}
\]

---

quantile

### Sample Quantiles

**Description**

The generic function `quantile` produces sample quantiles corresponding to the given probabilities. The smallest observation corresponds to a probability of 0 and the largest to a probability of 1.

**Usage**

\[
\text{quantile}(x, \ldots)
\]

### Default S3 method:

\[
\text{quantile}(x, \text{probs} = \text{seq}(0, 1, 0.25), \text{na.rm} = \text{FALSE}, \\
\text{names} = \text{TRUE}, \text{type} = 7, \text{digits} = 7, \ldots)
\]

**Arguments**

- **x** numeric vector whose sample quantiles are wanted, or an object of a class for which a method has been defined (see also ‘details’). `NA` and `NaN` values are not allowed in numeric vectors unless `na.rm` is `TRUE`.

- **probs** numeric vector of probabilities with values in \([0,1]\). (Values up to ‘2e−14’ outside that range are accepted and moved to the nearby endpoint.)

- **na.rm** logical; if true, any `NA` and `NaN`’s are removed from `x` before the quantiles are computed.
quantile

names logical; if true, the result has a names attribute. Set to FALSE for speedup with many probs.
type an integer between 1 and 9 selecting one of the nine quantile algorithms detailed below to be used.
digits used only when names is true: the precision to use when formatting the percentages. In R versions up to 4.0.x, this had been set to max(2, getOption("digits")), internally.

... further arguments passed to or from other methods.

Details

A vector of length length(probs) is returned; if names = TRUE, it has a names attribute. NA and NaN values in probs are propagated to the result.

The default method works with classed objects sufficiently like numeric vectors that sort and (not needed by types 1 and 3) addition of elements and multiplication by a number work correctly. Note that as this is in a namespace, the copy of sort in base will be used, not some S4 generic of that name. Also note that that is no check on the ‘correctly’, and so e.g. quantile can be applied to complex vectors which (apart from ties) will be ordered on their real parts.

There is a method for the date-time classes (see "POSIXt"). Types 1 and 3 can be used for class "Date" and for ordered factors.

Types

quantile returns estimates of underlying distribution quantiles based on one or two order statistics from the supplied elements in x at probabilities in probs. One of the nine quantile algorithms discussed in Hyndman and Fan (1996), selected by type, is employed.

All sample quantiles are defined as weighted averages of consecutive order statistics. Sample quantiles of type i are defined by:

\[ Q_i(p) = (1 - \gamma)x_j + \gamma x_{j+1} \]

where \(1 \leq i \leq 9\), \(\frac{i-m}{n} \leq p < \frac{i-m+1}{n}\), \(x_j\) is the jth order statistic, \(n\) is the sample size, the value of \(\gamma\) is a function of \(j = \lfloor np + m \rfloor\) and \(g = np + m - j\), and \(m\) is a constant determined by the sample quantile type.

Discontinuous sample quantile types 1, 2, and 3

For types 1, 2 and 3, \(Q_i(p)\) is a discontinuous function of \(p\), with \(m = 0\) when \(i = 1\) and \(i = 2\), and \(m = -1/2\) when \(i = 3\).

**Type 1** Inverse of empirical distribution function. \(\gamma = 0\) if \(g = 0\), and 1 otherwise.

**Type 2** Similar to type 1 but with averaging at discontinuities. \(\gamma = 0.5\) if \(g = 0\), and 1 otherwise (SAS default, see Wicklin(2017)).

**Type 3** Nearest even order statistic (SAS default till ca. 2010). \(\gamma = 0\) if \(g = 0\) and \(j\) is even, and 1 otherwise.

Continuous sample quantile types 4 through 9

For types 4 through 9, \(Q_i(p)\) is a continuous function of \(p\), with \(\gamma = g\) and \(m\) given below. The sample quantiles can be obtained equivalently by linear interpolation between the points \((p_k, x_k)\) where \(x_k\) is the \(k\)th order statistic. Specific expressions for \(p_k\) are given below.

**Type 4** \(m = 0\). \(p_k = \frac{k}{n}\). That is, linear interpolation of the empirical cdf.
Type 5 \( m = 1/2 \). \( p_k = \frac{k-0.5}{n} \). That is a piecewise linear function where the knots are the values midway through the steps of the empirical cdf. This is popular amongst hydrologists.

Type 6 \( m = p \). \( p_k = \frac{k}{n} \). Thus \( p_k = \text{E}[F(x_k)] \). This is used by Minitab and by SPSS.

Type 7 \( m = 1 - p \). \( p_k = \frac{k-1}{n+1} \). In this case, \( p_k \approx \text{mode}[F(x_k)] \). This is used by S.

Type 8 \( m = (p+1)/3 \). \( p_k = \frac{k-1/3}{n+1/3} \). Then \( p_k \approx \text{median}[F(x_k)] \). The resulting quantile estimates are approximately median-unbiased regardless of the distribution of \( x \).

Type 9 \( m = p/4 + 3/8 \). \( p_k = \frac{k-3/8}{n+1/4} \). The resulting quantile estimates are approximately unbiased for the expected order statistics if \( x \) is normally distributed.

Further details are provided in Hyndman and Fan (1996) who recommended type 8. The default method is type 7, as used by S and by \( R < 2.0.0 \). Makkonen argues for type 6, also as already proposed by Weibull in 1939. The Wikipedia page contains further information about availability of these 9 types in software.

Author(s)
of the version used in \( R \geq 2.0.0 \), Ivan Frohne and Rob J Hyndman.

References


See Also
ecdf for empirical distributions of which quantile is an inverse; boxplot.stats and fivenum for computing other versions of quartiles, etc.

Examples

```r
quantile(x <- rnorm(1001)) # Extremes & Quartiles by default
table(quantile(x, probs = c(0.1, 0.5, 1, 2, 5, 10, 50, NA)/100)

### Compare different types
quantAll <- function(x, prob, ...) t(vapply(1:9, function(typ) quantile(x, probs = prob, type = typ, ...), quantile(x, prob, type=1, ...)))
p <- c(0.1, 0.5, 1, 2, 5, 10, 50)/100
signif(quantAll(x, p), 4)

# 0% and 100% are equal to min(), max() for all types:
stopifnot(t(quantAll(x, prob=0:1)) == range(x))

# for complex numbers:
z <- complex(real = x, imaginary = -10*x)
signif(quantAll(z, p), 4)
```
Random 2-way Tables with Given Marginals

Description

Generate random 2-way tables with given marginals using Patefield’s algorithm.

Usage

r2dtable(n, r, c)

Arguments

n
a non-negative numeric giving the number of tables to be drawn.

r
a non-negative vector of length at least 2 giving the row totals, to be coerced to integer. Must sum to the same as c.

c
a non-negative vector of length at least 2 giving the column totals, to be coerced to integer.

Value

A list of length n containing the generated tables as its components.

References


Examples

```r
## Fisher's Tea Drinker data.
TeaTasting <- matrix(c(3, 1, 1, 3),
nrow = 2, 
dimnames = list(Guess = c("Milk", "Tea"),
Truth = c("Milk", "Tea")))
## Simulate permutation test for independence based on the maximum Pearson residuals (rather than their sum).
rowTotals <- rowSums(TeaTasting)
colTotals <- colSums(TeaTasting)
nOfCases <- sum(rowTotals)
expected <- outer(rowTotals, colTotals) / nOfCases
maxSqResid <- function(x) max((x - expected) ^ 2 / expected)
simMaxSqResid <- sapply(r2dtable(1000, rowTotals, colTotals), maxSqResid)
sum(simMaxSqResid >= maxSqResid(TeaTasting)) / 1000
## Fisher's exact test gives p = 0.4857 ...
```
Manipulate Flat Contingency Tables

Description

Read, write and coerce ‘flat’ (contingency) tables, aka ftables.

Usage

read.ftable(file, sep = "", quote = "\"", row.var.names, col.vars, skip = 0)

write.ftable(x, file = "", quote = TRUE, append = FALSE, digits = getOption("digits"), sep = " ", ...)

## S3 method for class 'ftable'
format(x, quote = TRUE, digits = getOption("digits"), method = c("non.compact", "row.compact", "col.compact", "compact"), lsep = " | ", justify = c("left", "right"), ...)

## S3 method for class 'ftable'
print(x, digits = getOption("digits"), ...

Arguments

file

either a character string naming a file or a connection which the data are to be read from or written to. "" indicates input from the console for reading and output to the console for writing.

sep

the field separator string. Values on each line of the file are separated by this string.

quote

a character string giving the set of quoting characters for read.ftable; to disable quoting altogether, use quote="". For write.table, a logical indicating whether strings in the data will be surrounded by double quotes.

row.var.names

a character vector with the names of the row variables, in case these cannot be determined automatically.

col.vars

a list giving the names and levels of the column variables, in case these cannot be determined automatically.

skip

the number of lines of the data file to skip before beginning to read data.

x

an object of class "ftable".

append

logical. If TRUE and file is the name of a file (and not a connection or "|cmd"), the output from write.ftable is appended to the file. If FALSE, the contents of file will be overwritten.

digits

an integer giving the number of significant digits to use for (the cell entries of) x.

method

string specifying how the “ftable” object is formatted (and printed if used as in write.ftable() or the print method). Can be abbreviated. Available methods are (see the examples):
"non.compact" the default representation of an ftable object.
"row.compact" a row-compact version without empty cells below the column labels.
"col.compact" a column-compact version without empty cells to the right of the row labels.
"compact" a row- and column-compact version. This may imply a row and a column label sharing the same cell. They are then separated by the string lsep.

lsep only for method = "compact", the separation string for row and column labels.
justify character vector of length (one or) two, specifying how string justification should happen in format(.), first for the labels, then the table entries.

... further arguments to be passed to or from methods; for write() and print(), notably arguments such as method, passed to format().

Details

read.ftable reads in a flat-like contingency table from a file. If the file contains the written representation of a flat table (more precisely, a header with all information on names and levels of column variables, followed by a line with the names of the row variables), no further arguments are needed. Similarly, flat tables with only one column variable the name of which is the only entry in the first line are handled automatically. Other variants can be dealt with by skipping all header information using skip, and providing the names of the row variables and the names and levels of the column variable using row.var.names and col.vars, respectively. See the examples below.

Note that flat tables are characterized by their ‘ragged’ display of row (and maybe also column) labels. If the full grid of levels of the row variables is given, one should instead use read.table to read in the data, and create the contingency table from this using xtabs.

write.ftable writes a flat table to a file, which is useful for generating ‘pretty’ ASCII representations of contingency tables. Different versions are available via the method argument, which may be useful, for example, for constructing LaTeX tables.

References


See Also

ftable for more information on flat contingency tables.

Examples

## Agresti (1990), page 157, Table 5.8.
## Not in ftable standard format, but o.k.
file <- tempfile()
cat(" Intercourse\n", "Race Gender Yes No\n", "White Male  43 134\n", " Female  26 149\n", "Black Male  29  23\n", " Female  22  36\n", file = file)
file.show(file)
ft1 <- read.ftable(file)
ft1
unlink(file)

## Agresti (1990), page 297, Table 8.16.
## Almost o.k., but misses the name of the row variable.
file <- tempfile()
cat("\n"Tonsil Size"\n", "Not Enl." "Enl." "Greatly Enl."\n", "Noncarriers 497 560 269\n", "Carriers 19 29 24\n", file = file)
file.show(file)
ft <- read.ftable(file, skip = 2,
row.var.names = "Status",
col.vars = list("Tonsil Size" =
c("Not Enl.", "Enl.", "Greatly Enl.")
))
ft
unlink(file)

ft22 <- ftable(Titanic, row.vars = 2:1, col.vars = 4:3)
write.ftable(ft22, quote = FALSE) # is the same as
print(ft22) # method=“non.compact” is default
print(ft22, method=“row.compact”)
print(ft22, method=“col.compact”)
print(ft22, method=“compact”)

## using ‘justify’ and ‘quote’:
format(ftable(wool + tension ~ breaks, warpbreaks),
       justify = “none”, quote = FALSE)

---

**rect.hclust**

*Draw Rectangles Around Hierarchical Clusters*

**Description**

Draws rectangles around the branches of a dendrogram highlighting the corresponding clusters. First the dendrogram is cut at a certain level, then a rectangle is drawn around selected branches.

**Usage**

rect.hclust(tree, k = NULL, which = NULL, x = NULL, h = NULL,
            border = 2, cluster = NULL)

**Arguments**

- **tree**: an object of the type produced by hclust.
- **k, h**: Scalar. Cut the dendrogram such that either exactly k clusters are produced or by cutting at height h.
- **which, x**: A vector selecting the clusters around which a rectangle should be drawn. which selects clusters by number (from left to right in the tree), x selects clusters containing the respective horizontal coordinates. Default is which = 1:k.
- **border**: Vector with border colors for the rectangles.
 Optional vector with cluster memberships as returned by `cutree(hclust.obj, k = k)`, can be specified for efficiency if already computed.

**Value**

(Invisibly) returns a list where each element contains a vector of data points contained in the respective cluster.

**See Also**

`hclust`, `identify.hclust`.

**Examples**

```r
require(graphics)

hca <- hclust(dist(USArrests))
plot(hca)
rect.hclust(hca, k = 3, border = "red")
x <- rect.hclust(hca, h = 50, which = c(2,7), border = 3:4)
x
```

---

---

**Description**

The levels of a factor are re-ordered so that the level specified by `ref` is first and the others are moved down. This is useful for `contr.treatment` contrasts which take the first level as the reference.

**Usage**

```
relevel(x, ref, ...) 
```

**Arguments**

`x` an unordered factor.

`ref` the reference level, typically a string.

`...` additional arguments for future methods.

**Details**

This, as `reorder()`, is a special case of simply calling `factor(x, levels = levels(x)[...])`.

**Value**

A factor of the same length as `x`.

**See Also**

`factor`, `contr.treatment`, `levels`, `reorder`. 
Examples

warpbreaks$tension <- relevel(warpbreaks$tension, ref = "M")
summary(lm(breaks ~ wool + tension, data = warpbreaks))

reorder.default

Reorder Levels of a Factor

Description

reorder is a generic function. The "default" method treats its first argument as a categorical variable, and reorders its levels based on the values of a second variable, usually numeric.

Usage

reorder(x, ...)

## Default S3 method:
reorder(x, X, FUN = mean, ..., 
order = is.ordered(x), decreasing = FALSE)

Arguments

x an atomic vector, usually a factor (possibly ordered). The vector is treated as a categorical variable whose levels will be reordered. If x is not a factor, its unique values will be used as the implicit levels.

X a vector of the same length as x, whose subset of values for each unique level of x determines the eventual order of that level.

FUN a function whose first argument is a vector and returns a scalar, to be applied to each subset of X determined by the levels of x.

... optional: extra arguments supplied to FUN

order logical, whether return value will be an ordered factor rather than a factor.

decreasing logical, whether the levels will be ordered in increasing or decreasing order.

Details

This, as relevel(), is a special case of simply calling factor(x, levels = levels(x)[...]).

Value

A factor or an ordered factor (depending on the value of order), with the order of the levels determined by FUN applied to X grouped by x. By default, the levels are ordered such that the values returned by FUN are in increasing order. Empty levels will be dropped.

Additionally, the values of FUN applied to the subsets of X (in the original order of the levels of x) is returned as the "scores" attribute.

Author(s)

Deepayan Sarkar <deepayan.sarkar@r-project.org>
**reorder.dendrogram**

Reorder a Dendrogram

**Description**

A method for the generic function `reorder`.

There are many different orderings of a dendrogram that are consistent with the structure imposed. This function takes a dendrogram and a vector of values and reorders the dendrogram in the order of the supplied vector, maintaining the constraints on the dendrogram.

**Usage**

```r
## S3 method for class 'dendrogram' reorder(x, wts, agglo.FUN = sum, ...)```

**Arguments**

- `x` the (dendrogram) object to be reordered
- `wts` numeric weights (arbitrary values) for reordering.
- `agglo.FUN` a function for weights agglomeration, see below.
- `...` additional arguments

**Details**

Using the weights `wts`, the leaves of the dendrogram are reordered so as to be in an order as consistent as possible with the weights. At each node, the branches are ordered in increasing weights where the weight of a branch is defined as \( f(w_j) \) where \( f \) is `agglo.FUN` and \( w_j \) is the weight of the \( j \)-th sub branch.
Value

A dendrogram where each node has a further attribute value with its corresponding weight.

Author(s)

R. Gentleman and M. Maechler

See Also

reorder.

rev.dendrogram which simply reverses the nodes’ order; heatmap, cophenetic.

Examples

```r
require(graphics)
set.seed(123)
x <- rnorm(10)
hc <- hclust(dist(x))
dd <- as.dendrogram(hc)
dd.reorder <- reorder(dd, 10:1)
plot(dd, main = "random dendrogram 'dd'")

op <- par(mfcol = 1:2)
plot(dd.reorder, main = "reorder(dd, 10:1)")
plot(reorder(dd, 10:1, agglo.FUN = mean), main = "reorder(dd, 10:1, mean)")
par(op)
```

replications

<table>
<thead>
<tr>
<th>replications</th>
<th>Number of Replications of Terms</th>
</tr>
</thead>
</table>

Description

Returns a vector or a list of the number of replicates for each term in the formula.

Usage

`replications(formula, data = NULL, na.action)`

Arguments

- `formula`: a formula or a terms object or a data frame.
- `data`: a data frame used to find the objects in formula.
- `na.action`: function for handling missing values. Defaults to a na.action attribute of data, then a setting of the option na.action, or na.fail if that is not set.

Details

If `formula` is a data frame and `data` is missing, `formula` is used for data with the formula ~ .. Any character vectors in the formula are coerced to factors.
Value

A vector or list with one entry for each term in the formula giving the number(s) of replications for each level. If all levels are balanced (have the same number of replications) the result is a vector, otherwise it is a list with a component for each term, as a vector, matrix or array as required.

A test for balance is `!is.list(replications(formula, data))`.

Author(s)

The design was inspired by the S function of the same name described in Chambers et al (1992).

References


See Also

`model.tables`

Examples

```r
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,0,1,0,1,1,1,0,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,0,0,1,1,0,0,1,0,1,1,0,0,1,1,0,0)
K <- c(1,0,1,0,1,1,0,0,1,1,0,1,0,1,0,0,0,1,1,0,1,0,1,0,1)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,52.0,51.5,49.8,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)
npk <- data.frame(block = gl(6,4), N = factor(N), P = factor(P),
                   K = factor(K), yield = yield)
replications(~ . - yield, npk)
```

Description

This function reshapes a data frame between ‘wide’ format (with repeated measurements in separate columns of the same row) and ‘long’ format (with the repeated measurements in separate rows).

Usage

```r
reshape(data, varying = NULL, v.names = NULL, timevar = "time",
        idvar = "id", ids = 1:NROW(data),
        times = seq_along(varying[[1]]),
        drop = NULL, direction, new.row.names = NULL,
        sep = ".",
        split = if (sep == "") {
          list(regexp = "[A-Za-z][0-9]", include = TRUE)
        } else {
          list(regexp = sep, include = FALSE, fixed = TRUE)}
```
### Typical usage for converting from long to wide format:

```r
# reshape(data, direction = "wide",
#        idvar = "___", timevar = "___", # mandatory
#        v.names = c(___), # time-varying variables
#        varying = list(___)) # auto-generated if missing
```

### Typical usage for converting from wide to long format:

### If names of wide-format variables are in a 'nice' format

```r
# reshape(data, direction = "long",
#        varying = c(___), # vector
#        sep) # to help guess 'v.names' and 'times'
```

### To specify long-format variable names explicitly

```r
# reshape(data, direction = "long",
#        varying = ___, # list / matrix / vector (use with care)
#        v.names = ___, # vector of variable names in long format
#        timevar, times, # name / values of constructed time variable
#        idvar, ids) # name / values of constructed id variable
```

#### Arguments

- **data**
  - a data frame

- **varying**
  - names of sets of variables in the wide format that correspond to single variables in long format ("time-varying"). This is canonically a list of vectors of variable names, but it can optionally be a matrix of names, or a single vector of names. In each case, when direction = "long", the names can be replaced by indices which are interpreted as referring to names(data). See ‘Details’ for more details and options.

- **v.names**
  - names of variables in the long format that correspond to multiple variables in the wide format. See ‘Details’.

- **timevar**
  - the variable in long format that differentiates multiple records from the same group or individual. If more than one record matches, the first will be taken (with a warning).

- **idvar**
  - Names of one or more variables in long format that identify multiple records from the same group/individual. These variables may also be present in wide format.

- **ids**
  - the values to use for a newly created idvar variable in long format.

- **times**
  - the values to use for a newly created timevar variable in long format. See ‘Details’.

- **drop**
  - a vector of names of variables to drop before reshaping.

- **direction**
  - character string, partially matched to either "wide" to reshape to wide format, or "long" to reshape to long format.

- **new.row.names**
  - character or NULL: a non-null value will be used for the row names of the result.
A character vector of length 1, indicating a separating character in the variable names in the wide format. This is used for guessing v.names and times arguments based on the names in varying. If sep == "", the split is just before the first numeral that follows an alphabetic character. This is also used to create variable names when reshaping to wide format.

A list with three components, regexp, include, and (optionally) fixed. This allows an extended interface to variable name splitting. See 'Details'.

Although reshape() can be used in a variety of contexts, the motivating application is data from longitudinal studies, and the arguments of this function are named and described in those terms. A longitudinal study is characterized by repeated measurements of the same variable(s), e.g., height and weight, on each unit being studied (e.g., individual persons) at different time points (which are assumed to be the same for all units). These variables are called time-varying variables. The study may include other variables that are measured only once for each unit and do not vary with time (e.g., gender and race); these are called time-constant variables.

A ‘wide’ format representation of a longitudinal dataset will have one record (row) for each unit, typically with some time-constant variables that occupy single columns, and some time-varying variables that occupy multiple columns (one column for each time point). A ‘long’ format representation of the same dataset will have multiple records (rows) for each individual, with the time-constant variables being constant across these records and the time-varying variables varying across the records. The ‘long’ format dataset will have two additional variables: a ’time’ variable identifying which time point each record comes from, and an ‘id’ variable showing which records refer to the same unit.

The type of conversion (long to wide or wide to long) is determined by the direction argument, which is mandatory unless the data argument is the result of a previous call to reshape. In that case, the operation can be reversed simply using reshape(data) (the other arguments are stored as attributes on the data frame).

Conversion from long to wide format with direction = "wide" is the simpler operation, and is mainly useful in the context of multivariate analysis where data is often expected as a wide-format matrix. In this case, the time variable timevar and id variable idvar must be specified. All other variables are assumed to be time-varying, unless the time-varying variables are explicitly specified via the v.names argument. A warning is issued if time-constant variables are not actually constant.

Each time-varying variable is expanded into multiple variables in the wide format. The names of these expanded variables are generated automatically, unless they are specified as the varying argument in the form of a list (or matrix) with one component (or row) for each time-varying variable. If varying is a vector of names, it is implicitly converted into a matrix, with one row for each time-varying variable. Use this option with care if there are multiple time-varying variables, as the ordering (by column, the default in the matrix constructor) may be unintuitive, whereas the explicit list or matrix form is unambiguous.

Conversion from wide to long with direction = "long" is the more common operation as most (univariate) statistical modeling functions expect data in the long format. In the simpler case where there is only one time-varying variable, the corresponding columns in the wide format input can be specified as the varying argument, which can be either a vector of column names or the corresponding column indices. The name of the corresponding variable in the long format output combining these columns can be optionally specified as the v.names argument, and the name of the time variables as the timevar argument. The values to use as the time values corresponding to the different columns in the wide format can be specified as the times argument. If v.names is unspecified, the function will attempt to guess v.names and times from varying (an explicitly specified times argument is unused in that case). The default expects variable names like x.1, x.2,
where \( \text{sep} = "." \) specifies to split at the dot and drop it from the name. To have alphabetic followed by numeric times use \( \text{sep} = "" \).

Multiple time-varying variables can be specified in two ways, either with \texttt{varying} as an atomic vector as above, or as a list (or a matrix). The first form is useful (and mandatory) if the automatic variable name splitting as described above is used; this requires the names of all time-varying variables to be suitably formatted in the same manner, and \texttt{v.names} to be unspecified. If \texttt{varying} is a list (with one component for each time-varying variable) or a matrix (one row for each time-varying variable), variable name splitting is not attempted, and \texttt{v.names} and \texttt{times} will generally need to be specified, although they will default to, respectively, the first variable name in each set, and sequential times.

Also, guessing is not attempted if \texttt{v.names} is given explicitly, even if \texttt{varying} is an atomic vector. In that case, the number of time-varying variables is taken to be the length of \texttt{v.names}, and \texttt{varying} is implicitly converted into a matrix, with one row for each time-varying variable. As in the case of long to wide conversion, the matrix is filled up by column, so careful attention needs to be paid to the order of variable names (or indices) in \texttt{varying}, which is taken to be like \texttt{x.1, y.1, x.2, y.2} (i.e., variables corresponding to the same time point need to be grouped together).

The \texttt{split} argument should not usually be necessary. The \texttt{split$regexp} component is passed to either \texttt{strsplit} or \texttt{regexpr}, where the latter is used if \texttt{split$include} is \texttt{TRUE}, in which case the splitting occurs after the first character of the matched string. In the \texttt{strsplit} case, the separator is not included in the result, and it is possible to specify fixed-string matching using \texttt{split$fixed}.

### Value

The reshaped data frame with added attributes to simplify reshaping back to the original form.

### See Also

\texttt{stack, aperm, relist} for reshaping the result of \texttt{unlist}. \texttt{xtabs} and \texttt{as.data.frame.table} for creating contingency tables and converting them back to data frames.

### Examples

```r
summary(Indometh) # data in long format

## long to wide (direction = "wide") requires idvar and timevar at a minimum
reshape(Indometh, direction = "wide", idvar = "Subject", timevar = "time")

## can also explicitly specify name of combined variable
wide <- reshape(Indometh, direction = "wide", idvar = "Subject",
               timevar = "time", v.names = "conc", sep = "_.")
wide

## reverse transformation
reshape(wide, direction = "long")
reshape(wide, idvar = "Subject", varying = list(2:12),
       v.names = "conc", direction = "long")

## times need not be numeric
df <- data.frame(id = rep(1:4, rep(2,4)),
                 visit = I(rep(c("Before", "After"), 4)),
                 x = rnorm(4), y = runif(4))
df
reshape(df, timevar = "visit", idvar = "id", direction = "wide")
## warns that y is really varying
```

---

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\( \text{reshape} \)
residuals

residuals(df, timevar = "visit", idvar = "id", direction = "wide", v.names = "x")

## unbalanced 'long' data leads to NA fill in 'wide' form
df2 <- df[1:7, ]
df2
reshape(df2, timevar = "visit", idvar = "id", direction = "wide")

## Alternative regular expressions for guessing names
df3 <- data.frame(id = 1:4, age = c(40,50,60,50),
                 dose1 = c(1,2,1,2),
                 dose2 = c(2,1,2,1),
                 dose4 = c(3,3,3,3))
reshape(df3, direction = "long", varying = 3:5, sep = "")

## an example that isn't longitudinal data
state.x77 <- as.data.frame(state.x77)
long <- reshape(state.x77, idvar = "state", ids = row.names(state.x77),
                times = names(state.x77), timevar = "Characteristic",
                varying = list(names(state.x77)), direction = "long")
reshape(long, direction = "wide")
reshape(long, direction = "wide", new.row.names = unique(long$state))

## multiple id variables
df3 <- data.frame(school = rep(1:3, each = 4),
                 class = rep(9:10, 6),
                 time = rep(c(1,1,2,2), 3),
                 score = rnorm(12))
wide <- reshape(df3, idvar = c("school", "class"), direction = "wide")
wide
## transform back
reshape(wide)

---

residuals

Extract Model Residuals

Description

residuals is a generic function which extracts model residuals from objects returned by modeling functions.

The abbreviated form resid is an alias for residuals. It is intended to encourage users to access object components through an accessor function rather than by directly referencing an object slot.

All object classes which are returned by model fitting functions should provide a residuals method. (Note that the method is for 'residuals' and not 'resid'.)

Methods can make use of naresid methods to compensate for the omission of missing values. The default, nls and smooth.spline methods do.

Usage

residuals(object, ...)
resid(object, ...)

Arguments

object  an object for which the extraction of model residuals is meaningful.
...  other arguments.

Value

Residuals extracted from the object object.

References


See Also

coefficients, fitted.values, glm, lm.

influence.measures for standardized (rstandard) and studentized (rstudent) residuals.

Description

Compute running medians of odd span. This is the ‘most robust’ scatter plot smoothing possible. For efficiency (and historical reason), you can use one of two different algorithms giving identical results.

Usage

runmed(x, k, endrule = c("median", "keep", "constant"),
algorithm = NULL,
na.action = c("+Big_alternate", "-Big_alternate", "na.omit", "fail"),
print.level = 0)

Arguments

x  numeric vector, the ‘dependent’ variable to be smoothed.
k  integer width of median window; must be odd. Turlach had a default of 
k <- 1 + 2 * min((n-1)/%/%2, ceiling(0.1*n)). Use k = 3 for ‘minimal’ robust smoothing eliminating isolated outliers.
endrule  character string indicating how the values at the beginning and the end (of the data) should be treated. Can be abbreviated. Possible values are:
"keep" keeps the first and last k2 values at both ends, where k2 is the half-bandwidth k2 = k %/% 2, i.e., y[j] = x[j] for j \in \{1, \ldots, k_2; n - k_2 + 1, \ldots, n\};
"constant" copies median(y[1:k2]) to the first values and analogously for the last ones making the smoothed ends constant;
"median" the default, smooths the ends by using symmetrical medians of subsequently smaller bandwidth, but for the very first and last value where Tukey's robust end-point rule is applied, see smoothEnds.
**runmed**

**algorithm**
character string (partially matching "Turlach" or "Stuetzle") or the default NULL, specifying which algorithm should be applied. The default choice depends on \( n = \text{length}(x) \) and \( k \) where "Turlach" will be used for larger problems.

**na.action**
character string determining the behavior in the case of NA or NaN in \( x \), (partially matching) one of
- "+Big_alternate" Here, all the NAs in \( x \) are first replaced by alternating \( \pm B \) where \( B \) is a "Big" number (with \( 2B < M^* \), where \( M^* = \text{.Machine}$ double.xmax \)). The replacement values are "from left" \((+B, -B, +B, \ldots)\), i.e. start with "+".
- "-Big_alternate" almost the same as "+Big_alternate", just starting with \(-B\) ("-Big...").
- "na.omit" the result is the same as \( \text{runmed}(x[!\text{is.na}(x)], k, \ldots) \).
- "fail" the presence of NAs in \( x \) will raise an error.

**print.level** integer, indicating verboseness of algorithm; should rarely be changed by average users.

**Details**

Apart from the end values, the result \( y = \text{runmed}(x, k) \) simply has \( y[j] = \text{median}(x[(j-k2):(j+k2)]) \) \((k = 2*k2+1)\), computed very efficiently.

The two algorithms are internally entirely different:

- "Turlach" is the Härdle–Steiger algorithm (see Ref.) as implemented by Berwin Turlach. A tree algorithm is used, ensuring performance \( O(n \log k) \) where \( n = \text{length}(x) \) which is asymptotically optimal.
- "Stuetzle" is the (older) Stuetzle–Friedman implementation which makes use of median updating when one observation enters and one leaves the smoothing window. While this performs as \( O(n \times k) \) which is slower asymptotically, it is considerably faster for small \( k \) or \( n \).

Note that, both algorithms (and the `smoothEnds()` utility) now "work" also when \( x \) contains non-finite entries (\( +\text{Inf}, \text{NaN}, \text{and NA} \)):

- "Turlach" .......
- "Stuetzle" currently simply works by applying the underlying math library (‘libm’) arithmetic for the non-finite numbers; this may optionally change in the future.

Currently long vectors are only supported for algorithm = "Stuetzle".

**Value**

vector of smoothed values of the same length as \( x \) with an attribute \( k \) containing (the ‘oddified’) \( k \).

**Author(s)**

Martin Maechler <maechler@stat.math.ethz.ch>, based on Fortran code from Werner Stuetzle and S-PLUS and C code from Berwin Turlach.

**References**


See Also

smoothEnds which implements Tukey’s end point rule and is called by default from runmed(*, endrule = "median"). smooth uses running medians of 3 for its compound smoothers.

Examples

require(graphics)
utils::example(nhtemp)
myNHT <- as.vector(nhtemp)
plot(myNHT, type = "b", ylim = c(48, 60), main = "Running Medians Example")
lines(runmed(myNHT, 7), col = "red")

## special: multiple y values for one x
plot(cars, main = "'cars' data and runmed(dist, 3)"
lines(cars, col = "light gray", type = "c")
with(cars, lines(speed, runmed(dist, k = 3), col = 2))

## nice quadratic with a few outliers
y <- ys <- (-20:20)^2
y[c(1,10,21,41)] <- c(150, 30, 400, 450)
all(y == runmed(y, 1)) # 1-neighbourhood <==> interpolation
plot(y) ## lines(y, lwd = .1, col = "light gray")
lines(lowess(seq(y), y, f = 0.3), col = "brown")
lines(runmed(y, 7), lwd = 2, col = "blue")
lines(runmed(y, 11), lwd = 2, col = "red")

## Lowess is not robust
y <- ys ; y[21] <- 6666 ; x <- seq(y)
col <- c("black", "brown","blue")
plot(y, col = col[1])
lines(lowess(x, y, f = 0.3), col = col[2])
lines(runmed(y, 7), lwd = 2, col = col[3])
legend(length(y),max(y), c("data", "lowess(y, f = 0.3)", "runmed(y, 7)")
, xjust = 1, col = col, lty = c(0, 1, 1), pch = c(1,NA,NA))

## An example with initial NA's - used to fail badly (notably for "Turlach"):
x15 <- c(rep(NA, 4), c(9, 9, 4, 22, 6, 1, 7, 5, 2, 8, 3))
rS15 <- cbind(Sk.3 = runmed(x15, k = 3, algorithm="S")
Sk.7 = runmed(x15, k = 7, algorithm="S")
Sk.11 = runmed(x15, k =11, algorithm="S")

rT15 <- cbind(Tk.3 = runmed(x15, k = 3, algorithm="T", print.level=1)
Tk.7 = runmed(x15, k = 7, algorithm="T", print.level=1)
Tk.9 = runmed(x15, k = 9, algorithm="T", print.level=1)
Tk.11= runmed(x15, k =11, algorithm="T", print.level=1))
cbind(x15, rS15, rT15) # result for k=11 maybe a bit surprising ..
Tv <- rT15[-(1:3),]
stopifnot(3 <= Tv, Tv <= 9, 5 <= Tv[1:10,])
matplot(y = cbind(x15, rT15), type = "b", ylim = c(1,9), pch=1:5, xlab = NA,
main = "runmed(x15, k, algo = \"Turlach\")")
mtext(paste("x15 <-", deparse(x15)))
points(x15, cex=2)
Wishart

legend("bottomleft", legend=c("data", paste("k = ", c(3,7,9,11))

rWishart

Random Wishart Distributed Matrices

Description

Generate n random matrices, distributed according to the Wishart distribution with parameters Sigma and df, \( W_p(\Sigma, m) \), \( m = df \), \( \Sigma = Sigma \).

Usage

rWishart(n, df, Sigma)

Arguments

n
integer sample size.

df
numeric parameter, “degrees of freedom”.

Sigma
positive definite \((p \times p)\) “scale” matrix, the matrix parameter of the distribution.

Details

If \( X_1, \ldots, X_m, X_i \in \mathbb{R}^p \) is a sample of \( m \) independent multivariate Gaussians with mean (vector) 0, and covariance matrix \( \Sigma \), the distribution of \( M = X'X \) is \( W_p(\Sigma, m) \).

Consequently, the expectation of \( M \) is

\[
E[M] = m \times \Sigma.
\]

Further, if Sigma is scalar \((p = 1)\), the Wishart distribution is a scaled chi-squared \((\chi^2)\) distribution with \( df \) degrees of freedom, \( W_1(\sigma^2, m) = \sigma^2 \chi^2_m \).

The component wise variance is

\[
\text{Var}(M_{ij}) = m(\Sigma^2_{ij} + \Sigma_{ii} \Sigma_{jj}).
\]

Value

a numeric array, say \( R \), of dimension \( p \times p \times n \), where each \( R[,i] \) is a positive definite matrix, a realization of the Wishart distribution \( W_p(\Sigma, m) \), \( m = df \), \( \Sigma = Sigma \).

Author(s)

Douglas Bates

References


See Also

cov, rnorm, rchisq.
Examples

## Artificial
S <- toeplitz((10:1)/10)
set.seed(11)
R <- rWishart(1000, 20, S)
dim(R) # 10 10 1000
mR <- apply(R, 1:2, mean) # ~= E[ Wish(S, 20) ] = 20 * S
stopifnot(all.equal(mR, 20*S, tolerance = .009))

## See Details, the variance is
Va <- 20*(S^2 + tcrossprod(diag(S)))
vR <- apply(R, 1:2, var)
stopifnot(all.equal(vR, Va, tolerance = 1/16))

scatter.smooth
Scatter Plot with Smooth Curve Fitted by Loess

Description

Plot and add a smooth curve computed by loess to a scatter plot.

Usage

scatter.smooth(x, y = NULL, span = 2/3, degree = 1,
family = c("symmetric", "gaussian"),
xlab = NULL, ylab = NULL,
ylim = range(y, pred$y, na.rm = TRUE),
evaluation = 50, ..., lpars = list())

loess.smooth(x, y, span = 2/3, degree = 1,
family = c("symmetric", "gaussian"), evaluation = 50, ...)

Arguments

x, y
the x and y arguments provide the x and y coordinates for the plot. Any reasonable
way of defining the coordinates is acceptable. See the function xy.coords
for details.

span
smoother parameter for loess.

degree
degree of local polynomial used.

family
if "gaussian" fitting is by least-squares, and if family = "symmetric" a re-
descending M estimator is used. Can be abbreviated.

xlab
label for x axis.

ylab
label for y axis.

ylim
the y limits of the plot.

evaluation
number of points at which to evaluate the smooth curve.

...
For scatter.smooth(), graphical parameters, passed to plot() only. For
loess.smooth, control parameters passed to loess.control.

lpars
a list of arguments to be passed to lines().
Details

loess.smooth is an auxiliary function which evaluates the loess smooth at evaluation equally spaced points covering the range of x.

Value

For scatter.smooth, none.

For loess.smooth, a list with two components, x (the grid of evaluation points) and y (the smoothed values at the grid points).

See Also

loess, smoothScatter for scatter plots with smoothed density color representation.

Examples

require(graphics)

with(cars, scatter.smooth(speed, dist))
## or with dotted thick smoothed line results :
with(cars, scatter.smooth(speed, dist, lpar =
    list(col = "red", lwd = 3, lty = 3)))

Description

screeplot.default plots the variances against the number of the principal component. This is also the plot method for classes "princomp" and "prcomp".

Usage

screeplot(x, ...)
## Default S3 method:
screeplot(x,npcs = min(10, length(x$sdev)),
    type = c("barplot", "lines"),
    main = deparse1(substitute(x)), ...)

Arguments

x an object containing a sdev component, such as that returned by princomp() and prcomp().
npcs the number of components to be plotted.
type the type of plot. Can be abbreviated.
main, ... graphics parameters.

References

See Also

princomp and prcomp.

Examples

```r
require(graphics)

## The variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
(pc.cr <- princomp(USArrests, cor = TRUE)) # inappropriate
screeplot(pc.cr)

fit <- princomp(covmat = Harman74.cor)
screepplot(fit)
screepplot(fit, npcs = 24, type = "lines")
```

---

sd  

Standard Deviation

Description

This function computes the standard deviation of the values in x. If na.rm is TRUE then missing values are removed before computation proceeds.

Usage

```r
sd(x, na.rm = FALSE)
```

Arguments

- **x**  
  a numeric vector or an R object but not a factor coercible to numeric by as.double(x).

- **na.rm**  
  logical. Should missing values be removed?

Details

Like var this uses denominator n − 1.

The standard deviation of a length-one or zero-length vector is NA.

See Also

var for its square, and mad, the most robust alternative.

Examples

```r
sd(1:2) ^ 2
```
se.contrast  

Description

Returns the standard errors for one or more contrasts in an aov object.

Usage

se.contrast(object, ...)
## S3 method for class 'aov'
se.contrast(object, contrast.obj,  
            coef = contr.helmert(ncol(contrast))[, 1],  
            data = NULL, ...)

Arguments

object  
A suitable fit, usually from aov.

contrast.obj  
The contrasts for which standard errors are requested. This can be specified via a list or via a matrix. A single contrast can be specified by a list of logical vectors giving the cells to be contrasted. Multiple contrasts should be specified by a matrix, each column of which is a numerical contrast vector (summing to zero).

coef  
used when contrast.obj is a list; it should be a vector of the same length as the list with zero sum. The default value is the first Helmert contrast, which contrasts the first and second cell means specified by the list.

data  
The data frame used to evaluate contrast.obj.

...  
further arguments passed to or from other methods.

Details

Contrasts are usually used to test if certain means are significantly different; it can be easier to use se.contrast than compute them directly from the coefficients.

In multistratum models, the contrasts can appear in more than one stratum, in which case the standard errors are computed in the lowest stratum and adjusted for efficiencies and comparisons between strata. (See the comments in the note in the help for aov about using orthogonal contrasts.) Such standard errors are often conservative.

Suitable matrices for use with coef can be found by calling contrasts and indexing the columns by a factor.

Value

A vector giving the standard errors for each contrast.

See Also

contrasts, model.tables
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se.contrast

Examples
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)
npk <- data.frame(block = gl(6,4), N =
K = factor(K), yield
## Set suitable contrasts.
options(contrasts = c("contr.helmert",
npk.aov1 <- aov(yield ~ block + N + K,
se.contrast(npk.aov1, list(N == "0", N
# or via a matrix
cont <- matrix(c(-1,1), 2, 1, dimnames
se.contrast(npk.aov1, cont[N, , drop =

factor(N), P = factor(P),
= yield)
"contr.poly"))
data = npk)
== "1"), data = npk)
= list(NULL, "N"))
FALSE]/12, data = npk)

## test a multi-stratum model
npk.aov2 <- aov(yield ~ N + K + Error(block/(N + K)), data = npk)
se.contrast(npk.aov2, list(N == "0", N == "1"))
## an example looking at an interaction contrast
## Dataset from R.E. Kirk (1995)
## 'Experimental Design: procedures for the behavioral sciences'
score <- c(12, 8,10, 6, 8, 4,10,12, 8, 6,10,14, 9, 7, 9, 5,11,12,
7,13, 9, 9, 5,11, 8, 7, 3, 8,12,10,13,14,19, 9,16,14)
A <- gl(2, 18, labels = c("a1", "a2"))
B <- rep(gl(3, 6, labels = c("b1", "b2", "b3")), 2)
fit <- aov(score ~ A*B)
cont <- c(1, -1)[A] * c(1, -1, 0)[B]
sum(cont)
# 0
sum(cont*score) # value of the contrast
se.contrast(fit, as.matrix(cont))
(t.stat <- sum(cont*score)/se.contrast(fit, as.matrix(cont)))
summary(fit, split = list(B = 1:2), expand.split = TRUE)
## t.stat^2 is the F value on the A:B: C1 line (with Helmert contrasts)
## Now look at all three interaction contrasts
cont <- c(1, -1)[A] * cbind(c(1, -1, 0), c(1, 0, -1), c(0, 1, -1))[B,]
se.contrast(fit, cont) # same, due to balance.
rm(A, B, score)
## multi-stratum example where efficiencies play a role
## An example from Yates (1932),
## a 2^3 design in 2 blocks replicated 4 times
Block <- gl(8, 4)
A <- factor(c(0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,
0,1,0,1,0,1,0,1,0,1,0,1))
B <- factor(c(0,0,1,1,0,0,1,1,0,1,0,1,1,0,1,0,0,0,1,1,
0,0,1,1,0,0,1,1,0,0,1,1))
C <- factor(c(0,1,1,0,1,0,0,1,0,0,1,1,0,0,1,1,0,1,0,1,
1,0,1,0,0,0,1,1,1,1,0,0))
Yield <- c(101, 373, 398, 291, 312, 106, 265, 450, 106, 306, 324, 449,


```r
272, 89, 407, 338, 87, 324, 279, 471, 323, 128, 423, 334,  
131, 103, 445, 437, 324, 361, 302, 272)
```

```r
aovdat <- data.frame(Block, A, B, C, Yield)
fit <- aov(Yield ~ A + B * C + Error(Block), data = aovdat)
cont1 <- c(-1, 1)[A]/32  # Helmert contrasts
cont2 <- c(-1, 1)[B] * c(-1, 1)[C]/32
cont <- cbind(A = cont1, BC = cont2)
colSums(cont*Yield) # values of the contrasts
se.contrast(fit, as.matrix(cont))
# comparison with lme
library(nlme)
fit2 <- lme(Yield ~ A + B*C, random = ~1 | Block, data = aovdat)
summary(fit2)$tTable # same estimates, similar (but smaller) se's.
```

---

### `selfStart` Construct Self-starting Nonlinear Models

#### Description

Construct self-starting nonlinear models to be used in `nls`, etc. Via function `initial` to compute approximate parameter values from data, such models are “self-starting”, i.e., do not need a `start` argument in, e.g., `nls()`.

#### Usage

```r
selfStart(model, initial, parameters, template)
```

#### Arguments

- **model**: a function object defining a nonlinear model or a nonlinear `formula` object of the form `~ expression`.
- **initial**: a function object, taking arguments `mCall`, `data`, and `LHS`, and ..., representing, respectively, a matched call to the function `model`, a data frame in which to interpret the variables in `mCall`, and the expression from the left-hand side of the model formula in the call to `nls`. This function should return initial values for the parameters in `model`. The ... is used by `nls()` to pass its control and trace arguments for the cases where `initial()` itself calls `nls()` as it does for the ten self-starting nonlinear models in R's `stats` package.
- **parameters**: a character vector specifying the terms on the right hand side of `model` for which initial estimates should be calculated. Passed as the `namevec` argument to the `deriv` function.
- **template**: an optional prototype for the calling sequence of the returned object, passed as the `function.arg` argument to the `deriv` function. By default, a template is generated with the covariates in `model` coming first and the parameters in `model` coming last in the calling sequence.

#### Details

`nls()` calls `getInitial` and the initial function for these self-starting models.

This function is generic; methods functions can be written to handle specific classes of objects.
Value

A function object of class "selfStart", for the formula method obtained by applying deriv to the right hand side of the model formula. An initial attribute (defined by the initial argument) is added to the function to calculate starting estimates for the parameters in the model automatically.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, getInitial.

Each of the following are "selfStart" models (with examples) SSasymp, SSasympOff, SSasympOrig, SSbiexp, SSfol, SSfpl, SSgompertz, SSlogis, SSmicmen, SSweibull.

Further, package nlme's nlsList.

Examples

## self-starting logistic model

```r
## The "initializer" (finds initial values for parameters from data):
initLogis <- function(mCall, data, LHS, ...) {
  xy <- sortedXyData(mCall[['x']], LHS, data)
  if(nrow(xy) < 4)
    stop("too few distinct input values to fit a logistic model")
  z <- xy[['y']]  
  ## transform to proportion, i.e. in (0,1) : 
  rng <- range(z); dz <- diff(rng)
  z <- (z - rng[1L] + 0.05 * dz)/(1.1 * dz)
  xy[['z']] <- log(z/(1 - z)) # logit transformation
  aux <- coef(lm(x ~ z, xy))
  pars <- coef(nls(y ~ 1/(1 + exp((xmid - x)/scal)),
                   data = xy,
                   start = list(xmid = aux[[1L]], scal = aux[[2L]]),
                   algorithm = "plinear", ...))
  setNames(pars [c(".lin", "xmid", "scal")],
           mCall[c("Asym", "xmid", "scal")])
}
```

mySSlogis <- selfStart(~ Asym/(1 + exp((xmid - x)/scal)),
                       initial = initLogis,
                       parameters = c("Asym", "xmid", "scal"))

getInitial(weight ~ mySSlogis(Time, Asym, xmid, scal),
            data = subset(ChickWeight, Chick == 1))

## Not run:
SSfol <- selfStart(first.order.log.model, first.order.log.initial)
```

# 'first.order.log.model' is a function object defining a first order compartment model
# 'first.order.log.initial' is a function object which calculates initial values for the parameters in 'first.order.log.model'
# self-starting first order compartment model
## Not run:
SSfol <- selfStart(first.order.log.model, first.order.log.initial)
setNames

Set the Names in an Object

Description

This is a convenience function that sets the names on an object and returns the object. It is most useful at the end of a function definition where one is creating the object to be returned and would prefer not to store it under a name just so the names can be assigned.

Usage

setNames(object = nm, nm)

Arguments

object an object for which a names attribute will be meaningful

nm a character vector of names to assign to the object

Value

An object of the same sort as object with the new names assigned.

Author(s)

Douglas M. Bates and Saikat DebRoy

See Also

unwrap for removing names.

Examples

setNames( 1:3, c("foo", "bar", "baz") )
# this is just a short form of
tmp <- 1:3
names(tmp) <- c("foo", "bar", "baz")
tmp

## special case of character vector, using default
setNames(nm = c("First", "2nd"))
shapiro.test  Shapiro-Wilk Normality Test

Description
Performs the Shapiro-Wilk test of normality.

Usage
shapiro.test(x)

Arguments
x  a numeric vector of data values. Missing values are allowed, but the number of non-missing values must be between 3 and 5000.

Value
A list with class "htest" containing the following components:

statistic  the value of the Shapiro-Wilk statistic.
p.value  an approximate p-value for the test. This is said in Royston (1995) to be adequate for p.value < 0.1.
method  the character string "Shapiro-Wilk normality test".
data.name  a character string giving the name(s) of the data.

Source
The algorithm used is a C translation of the Fortran code described in Royston (1995). The calculation of the p value is exact for n = 3, otherwise approximations are used, separately for 4 ≤ n ≤ 11 and n ≥ 12.

References


See Also
qqnorm for producing a normal quantile-quantile plot.

Examples
shapiro.test(rnorm(100, mean = 5, sd = 3))
shapiro.test(runif(100, min = 2, max = 4))
**Extract Residual Standard Deviation 'Sigma'**

**Description**

Extract the estimated standard deviation of the errors, the “residual standard deviation” (misnamed also “residual standard error”, e.g., in `summary.lm()`’s output, from a fitted model).

Many classical statistical models have a *scale parameter*, typically the standard deviation of a zero-mean normal (or Gaussian) random variable which is denoted as $\sigma$. `sigma(.)` extracts the *estimated* parameter from a fitted model, i.e., $\hat{\sigma}$.

**Usage**

`sigma(object, ...)`

```r
## Default S3 method:
sigma(object, use.fallback = TRUE, ...)
```

**Arguments**

- `object`: an R object, typically resulting from a model fitting function such as `lm`.
- `use.fallback`: logical, passed to `nobs`.
- `...`: potentially further arguments passed to and from methods. Passed to `deviance(*)` for the default method.

**Details**

The `stats` package provides the S3 generic, a default method, and a method for objects of class "glm". The default method is correct typically for (asymptotically / approximately) generalized gaussian (“least squares”) problems, since it is defined as

```r
sigma.default <- function (object, use.fallback = TRUE, ...)
  sqrt( deviance(object, ...) / (NN - PP) )
```

where `NN <- nobs(object, use.fallback = use.fallback)` and `PP <- sum(!is.na(coef(object)))` – where in older R versions this was `length(coef(object))` which is too large in case of undetermined coefficients, e.g., for rank deficient model fits.

**Value**

Typically a number, the estimated standard deviation of the errors (“residual standard deviation”) for Gaussian models, and—less interpretably—the square root of the residual deviance per degree of freedom in more general models.

Very strictly speaking, $\hat{\sigma}$ (“$\sigma$ hat”) is actually $\sqrt{\sigma^2}$.

For generalized linear models (class "glm"), the `sigma.glm` method returns the square root of the dispersion parameter (See `summary.glm`). For families with free dispersion parameter, `sigma` is estimated from the root mean square of the Pearson residuals. For families with fixed dispersion, `sigma` is not estimated from the residuals but extracted directly from the family of the fitted model. Consequently, for binomial or Poisson GLMs, `sigma` is exactly 1.
For multivariate linear models (class "mlm"), a vector of sigmas is returned, each corresponding to one column of \( Y \).

**Note**

The misnomer "Residual standard error" has been part of too many R (and S) outputs to be easily changed there.

**See Also**

deviance, nobs, vcov, summary.glm.

**Examples**

```r
## -- lm() ------------------------------
lm1 <- lm(Fertility ~ . , data = swiss)
sigma(lm1) # ~= 7.165 = "Residual standard error" printed from summary(lm1)
stopifnot(all.equal(sigma(lm1), summary(lm1)$sigma, tolerance=1e-15))

## -- nls() -----------------------------
DNase1 <- subset(DNase, Run == 1)
fm.DN1 <- nls(density ~ SSlogis(log(conc), Asym, xmid, scal), DNase1)
sigma(fm.DN1) # ~= 0.01919 as from summary(\.)
stopifnot(all.equal(sigma(fm.DN1), summary(fm.DN1)$sigma, tolerance=1e-15))

## -- glm() -----------------------------
## -- a) Binomial -- Example from MASS
dose <- rep(0:5, 2)
umdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20-numdead)
sigma(budworm.lg <- glm(SF ~ sex*dose, family = binomial))

## -- b) Poisson -- from ?glm :
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
sigma(glm.D93 <- glm(counts ~ outcome + treatment, family = poisson()))
## equal to
sqrt(summary(glm.D93)$dispersion) # == 1
## and the *Quasi*poisson's dispersion
sigma(glm.qD93 <- update(glm.D93, family = quasipoisson(\.))
## $2 \# 1.2933 equal to
summary(glm.qD93)$dispersion # == 1.2933

## -- Multivariate lm() "mlm" ---------
utils::example("SSD", echo=FALSE)
sigma(mlmfit) # is the same as (but more efficient than)
sqrt(diag(estVar(mlmfit)))
```
Description

Density, distribution function, quantile function and random generation for the distribution of the Wilcoxon Signed Rank statistic obtained from a sample with size \( n \).

Usage

dsignrank(x, n, log = FALSE)
psignrank(q, n, lower.tail = TRUE, log.p = FALSE)
qsignrank(p, n, lower.tail = TRUE, log.p = FALSE)
rsignrank(nn, n)

Arguments

- \( x, q \) vector of quantiles.
- \( p \) vector of probabilities.
- \( nn \) number of observations. If \( \text{length}(nn) > 1 \), the length is taken to be the number required.
- \( n \) number(s) of observations in the sample(s). A positive integer, or a vector of such integers.
- \( \log, \log.p \) logical; if TRUE, probabilities \( p \) are given as \( \log(p) \).
- \( \text{lower.tail} \) logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).

Details

This distribution is obtained as follows. Let \( x \) be a sample of size \( n \) from a continuous distribution symmetric about the origin. Then the Wilcoxon signed rank statistic is the sum of the ranks of the absolute values \( x[i] \) for which \( x[i] \) is positive. This statistic takes values between 0 and \( n(n + 1)/2 \), and its mean and variance are \( n(n + 1)/4 \) and \( n(n + 1)(2n + 1)/24 \), respectively.

If either of the first two arguments is a vector, the recycling rule is used to do the calculations for all combinations of the two up to the length of the longer vector.

Value

dsignrank gives the density, psignrank gives the distribution function, qsignrank gives the quantile function, and rsignrank generates random deviates.

The length of the result is determined by \( nn \) for rsignrank, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than \( nn \) are recycled to the length of the result. Only the first elements of the logical arguments are used.

Author(s)

Kurt Hornik; efficiency improvement by Ivo Ugrina.
**simulate**

Simulate one or more responses from the distribution corresponding to a fitted model object.

**Usage**

```r
simulate(object, nsim = 1, seed = NULL, ...)
```

**Arguments**

- `object` an object representing a fitted model.
- `nsim` number of response vectors to simulate. Defaults to 1.
- `seed` an object specifying if and how the random number generator should be initialized ("seeded"). For the "lm" method, either `NULL` or an integer that will be used in a call to `set.seed` before simulating the response vectors. If set, the value is saved as the "seed" attribute of the returned value. The default, `NULL` will not change the random generator state, and return `.Random.seed` as the "seed" attribute, see 'Value'.
- `...` additional optional arguments.

**Details**

This is a generic function. Consult the individual modeling functions for details on how to use this function.

Package **stats** has a method for "lm" objects which is used for `lm` and `glm` fits. There is a method for fits from `glm.nb` in package **MASS**, and hence the case of negative binomial families is not covered by the "lm" method.

The methods for linear models fitted by `lm` or `glm(family = "gaussian")` assume that any weights which have been supplied are inversely proportional to the error variance. For other GLMs the...
simulate component of the family object is used—there is no appropriate simulation method for ‘quasi’ models as they are specified only up to two moments.

For binomial and Poisson GLMs the dispersion is fixed at one. Integer prior weights \( w_i \) can be interpreted as meaning that observation \( i \) is an average of \( w_i \) observations, which is natural for binomials specified as proportions but less so for a Poisson, for which prior weights are ignored with a warning.

For a gamma GLM the shape parameter is estimated by maximum likelihood (using function gamma.shape in package MASS). The interpretation of weights is as multipliers to a basic shape parameter, since dispersion is inversely proportional to shape.

For an inverse gaussian GLM the model assumed is \( IG(\mu_i, \lambda w_i) \) (see https://en.wikipedia.org/wiki/Inverse_Gaussian_distribution) where \( \lambda \) is estimated by the inverse of the dispersion estimate for the fit. The variance is \( \mu_i^3/ (\lambda w_i) \) and hence inversely proportional to the prior weights. The simulation is done by function rinvGauss from the SuppDists package, which must be installed.

Value

Typically, a list of length nsim of simulated responses. Where appropriate the result can be a data frame (which is a special type of list).

For the "lm" method, the result is a data frame with an attribute "seed". If argument seed is NULL, the attribute is the value of .Random.seed before the simulation was started; otherwise it is the value of the argument with a "kind" attribute with value as.list(RNGkind()).

See Also

RNG about random number generation in R, fitted.values and residuals for related methods; glm, lm for model fitting.

There are further examples in the 'simulate.R' tests file in the sources for package stats.

Examples

```r
x <- 1:5
mod1 <- lm(c(1:3, 7, 6) ~ x)
S1 <- simulate(mod1, nsim = 4)
## repeat the simulation:
.Random.seed <- attr(S1, "seed")
identical(S1, simulate(mod1, nsim = 4))

S2 <- simulate(mod1, nsim = 200, seed = 101)
rowMeans(S2) # should be about the same as fitted(mod1)

## repeat identically:
(sseed <- attr(S2, "seed")) # seed; RNGkind as attribute
stopifnot(identical(S2, simulate(mod1, nsim = 200, seed = sseed)))

## To be sure about the proper RNGkind, e.g., after
RNGversion("2.7.0")
## first set the RNG kind, then simulate
do.call(RNGkind, attr(sseed, "kind"))
identical(S2, simulate(mod1, nsim = 200, seed = sseed))

## Binomial GLM examples
```
```r
yb1 <- matrix(c(4, 4, 5, 7, 8, 6, 6, 5, 3, 2), ncol = 2)
modb1 <- glm(yb1 ~ x, family = binomial)
S3 <- simulate(modb1, nsim = 4)
# each column of S3 is a two-column matrix.
x2 <- sort(runif(100))
yb2 <- rbinom(100, prob = plogis(2*(x2-1)), size = 1)
yb2 <- factor(1 + yb2, labels = c("failure", "success"))
modb2 <- glm(yb2 ~ x2, family = binomial)
S4 <- simulate(modb2, nsim = 4)
# each column of S4 is a factor
```

---

**Smirnov Distribution of the Smirnov Statistic**

**Description**

Distribution function, quantile function and random generation for the distribution of the Smirnov statistic.

**Usage**

```r
psmirnov(q, sizes, z = NULL, two.sided = TRUE, exact = TRUE, simulate = FALSE, B = 2000, lower.tail = TRUE, log.p = FALSE)
qsmirnov(p, sizes, z = NULL, two.sided = TRUE, exact = TRUE, simulate = FALSE, B = 2000)
rsmirnov(n, sizes, z = NULL, two.sided = TRUE)
```

**Arguments**

- `q`: a numeric vector of quantiles.
- `p`: a numeric vector of probabilities.
- `sizes`: an integer vector of length two giving the sample sizes.
- `z`: a numeric vector of the pooled data values in both samples when the exact conditional distribution of the Smirnov statistic given the data shall be computed.
- `two.sided`: a logical indicating whether absolute (TRUE) or raw differences of frequencies define the test statistic.
- `exact`: NULL or a logical indicating whether the exact (conditional on the pooled data values in z) distribution or the asymptotic distribution should be used.
- `simulate`: a logical indicating whether to compute the distribution function by Monte Carlo simulation.
- `B`: an integer specifying the number of replicates used in the Monte Carlo test.
- `lower.tail`: a logical, if TRUE (default), probabilities are \( P[D < q] \), otherwise, \( P[D \geq q] \).
- `log.p`: a logical, if TRUE (default), probabilities are given as log-probabilities.
- `n`: an integer giving number of observations.
Details

For samples $x$ and $y$ with respective sizes $n_x$ and $n_y$ and empirical cumulative distribution functions $F_{x,n_x}$ and $F_{y,n_y}$, the Smirnov statistic is

$$D = \sup_c |F_{x,n_x}(c) - F_{y,n_y}(c)|$$

in the two-sided case and

$$D = \sup_c (F_{x,n_x}(c) - F_{y,n_y}(c))$$

otherwise.

These statistics are used in the Smirnov test of the null that $x$ and $y$ were drawn from the same distribution, see `ks.test`.

If the underlying common distribution function $F$ is continuous, the distribution of the test statistics does not depend on $F$, and has a simple asymptotic approximation. For arbitrary $F$, one can compute the conditional distribution given the pooled data values $z$ of $x$ and $y$, either exactly (feasible provided that the product $n_x n_y$ of the sample sizes is “small enough”) or approximately Monte Carlo simulation. If the pooled data values $z$ are not specified, a pooled sample without ties is assumed.

Value

`psmirnov` gives the distribution function, `qsmirnov` gives the quantile function, and `rsmirnov` generates random deviates.

See Also

`ks.test` for references on the algorithms used for computing exact distributions.

smooth

Tukey’s (Running Median) Smoothing

Description

Tukey’s smoothers, 3RS3R, 3RSS, 3R, etc.

Usage

```r
smooth(x, kind = c("3RS3R", "3RSS", "3RSR", "3R", "3", "S"),
       twiceit = FALSE, endrule = c("Tukey", "copy"), do.ends = FALSE)
```

Arguments

- **x**: a vector or time series
- **kind**: a character string indicating the kind of smoother required; defaults to "3RS3R".
- **twiceit**: logical, indicating if the result should be ‘twiced’. Twicing a smoother $S(y)$ means $S(y) + S(y - S(y))$, i.e., adding smoothed residuals to the smoothed values. This decreases bias (increasing variance).
- **endrule**: a character string indicating the rule for smoothing at the boundary. Either "Tukey" (default) or "copy".
- **do.ends**: logical, indicating if the 3-splitting of ties should also happen at the boundaries (ends). This is only used for kind = "S".
Details

3 is Tukey’s short notation for running **medians** of length 3,
3R stands for **R**epeated 3 until convergence, and
S for **S**plitting of horizontal stretches of length 2 or 3.
Hence, 3RS3R is a concatenation of 3R, S and 3R, 3RSS similarly whereas 3RSR means first 3R and then (S and 3) **R**epeated until convergence – which can be bad.

Value

An object of class “tukeysmooth” (which has print and summary methods) and is a vector or time series containing the smoothed values with additional attributes.

Note

S and S-PLUS use a different (somewhat better) Tukey smoother in smooth(*). Note that there are other smoothing methods which provide rather better results. These were designed for hand calculations and may be used mainly for didactical purposes.
Since R version 1.2, smooth does really implement Tukey’s end-point rule correctly (see argument endrule).
kind = "3RSR" has been the default till R-1.1, but it can have very bad properties, see the examples.
Note that repeated application of smooth(*) does smooth more, for the "3RS*" kinds.

References


See Also

`runmed` for running medians; `lowess` and `loess`; `supsmu` and `smooth.spline`.

Examples

```r
require(graphics)

## see also  demo(smooth) !
x1 <- c(4, 1, 3, 6, 6, 4, 1, 6, 2, 4, 2) # very artificial
(x3R <- smooth(x1, "3R")) # 2 iterations of "3"
smooth(x3R, kind = "S")

sm.3RS <- function(x, ...)
  smooth(smooth(x, "3R", ...), "S", ...)

y <- c(1, 1, 19:1)
plot(y, main = "misbehaviour of \"3RSR\"", col.main = 3)
lines(sm.3RS(y))
lines(smooth(y))
lines(smooth(y, "3RSR"), col = 3, lwd = 2) # the horror

x <- c(8:10, 10, 0, 0, 9, 9)
plot(x, main = "breakdown of 3R and S and hence 3RSS")
matlines(cbind(smooth(x, "3R"), smooth(x, "S"), smooth(x, "3RSS"), smooth(x)))
presidents[is.na(presidents)] <- 0 # silly
```
smooth.spline

Fit a Smoothing Spline

Description

Fits a cubic smoothing spline to the supplied data.

Usage

smooth.spline(x, y = NULL, w = NULL, df, spar = NULL, lambda = NULL, cv = FALSE,
all.knots = FALSE, nknots = .nknots.smpl,
keep.data = TRUE, df.offset = 0, penalty = 1,
control.spar = list(), tol = 1e-6 * IQR(x), keep.stuff = FALSE)

.nknots.smpl(n)

Arguments

x
a vector giving the values of the predictor variable, or a list or a two-column
matrix specifying x and y.

y
responses. If y is missing or NULL, the responses are assumed to be specified by
x, with x the index vector.

w
optional vector of weights of the same length as x; defaults to all 1.

df
the desired equivalent number of degrees of freedom (trace of the smoother
matrix). Must be in \( (1, n_x] \), \( n_x \) the number of unique x values, see below.

spar
smoothing parameter, typically (but not necessarily) in \( (0, 1] \). When spar is
specified, the coefficient \( \lambda \) of the integral of the squared second derivative in
the fit (penalized log likelihood) criterion is a monotone function of spar, see the
details below. Alternatively \( \lambda \) may be specified instead of the scale free
\( \text{spar}=s \).

lambda
if desired, the internal (design-dependent) smoothing parameter \( \lambda \) can be spec-
ified instead of spar. This may be desirable for resampling algorithms such as
cross validation or the bootstrap.

cv
ordinary leave-one-out (TRUE) or 'generalized' cross-validation (GCV) when
FALSE; is used for smoothing parameter computation only when both spar and
df are not specified; it is used however to determine cv.crit in the result. Setting
it to NA for speedup skips the evaluation of leverages and any score.
all.knots if TRUE, all distinct points in x are used as knots. If FALSE (default), a subset of x[] is used, specifically x[j] where the nknots indices are evenly spaced in 1:n, see also the next argument nknots. Alternatively, a strictly increasing numeric vector specifying "all the knots" to be used; must be rescaled to [0, 1] already such that it corresponds to the ans $fit$knots sequence returned, not repeating the boundary knots.

nknots integer or function giving the number of knots to use when all.knots = FALSE. If a function (as by default), the number of knots is nknots(nx). By default using .nknots.smspl(), for nx > 49 this is less than nx, the number of unique x values, see the Note.

keep.data logical specifying if the input data should be kept in the result. If TRUE (as per default), fitted values and residuals are available from the result.

df.offset allows the degrees of freedom to be increased by df.offset in the GCV criterion.

penalty the coefficient of the penalty for degrees of freedom in the GCV criterion.

control.spar optional list with named components controlling the root finding when the smoothing parameter spar is computed, i.e., missing or NULL, see below.

Note that this is partly experimental and may change with general spar computation improvements!

low: lower bound for spar; defaults to -1.5 (used to implicitly default to 0 in R versions earlier than 1.4).

high: upper bound for spar; defaults to +1.5.

tol: the absolute precision (tolerance) used; defaults to 1e-4 (formerly 1e-3).

tol: the relative precision used; defaults to 2e-8 (formerly 0.00244).

trace: logical indicating if iterations should be traced.

maxit: integer giving the maximal number of iterations; defaults to 500.

Note that spar is only searched for in the interval [low, high],

tol a tolerance for same-ness or uniqueness of the x values. The values are binned into bins of size tol and values which fall into the same bin are regarded as the same. Must be strictly positive (and finite).

keep.stuff an experimental logical indicating if the result should keep extras from the internal computations. Should allow to reconstruct the X matrix and more.

n for .nknots.smspl; typically the number of unique x values (aka nx).

Details

Neither x nor y are allowed to containing missing or infinite values.

The x vector should contain at least four distinct values. ‘Distinct’ here is controlled by tol: values which are regarded as the same are replaced by the first of their values and the corresponding y and w are pooled accordingly.

Unless lambda has been specified instead of spar, the computational \( \lambda \) used (as a function of \( s = \text{spar} \)) is \( \lambda = r \cdot 256^{3s-1} \) where \( r = tr(X'WX)/tr(\Sigma) \), \( \Sigma \) is the matrix given by \( \Sigma_{ij} = \int B_{ij}(t)B_{ij}(t)dt \), \( X \) is given by \( X_{ij} = B_j(x_i) \), \( W \) is the diagonal matrix of weights (scaled such that its trace is \( n \), the original number of observations) and \( B_k(\cdot) \) is the \( k \)-th B-spline.

Note that with these definitions, \( f_i = f(x_i) \), and the B-spline basis representation \( f = Xc \) (i.e., \( c \) is the vector of spline coefficients), the penalized log likelihood is \( L = (y - f)'W(y - f) + \lambda c'\Sigma c \), and hence \( c \) is the solution of the (ridge regression) \( (X'WX + \lambda \Sigma)c = X'Wy \).
If \( \text{spar} \) and \( \lambda \) are missing or NULL, the value of \( \text{df} \) is used to determine the degree of smoothing. If \( \text{df} \) is missing as well, leave-one-out cross-validation (ordinary or ‘generalized’ as determined by \( \text{cv} \)) is used to determine \( \lambda \).

Note that from the above relation, \( \text{spar} \) is \( s = s_0 + 0.0601 \cdot \log \lambda \), which is intentionally different from the S-PLUS implementation of \text{smooth.spline} \( \) (where \( \text{spar} \) is proportional to \( \lambda \)) in R’s \((\log \lambda)\) scale, it makes more sense to vary \( \text{spar} \) linearly.

Note however that currently the results may become very unreliable for \( \text{spar} \) values smaller than about -1 or -2. The same may happen for values larger than 2 or so. Don’t think of setting \( \text{spar} \) or the controls low and high outside such a safe range, unless you know what you are doing! Similarly, specifying \( \lambda \) instead of \( \text{spar} \) is delicate, notably as the range of “safe” values for \( \lambda \) is not scale-invariant and hence entirely data dependent.

The ‘generalized’ cross-validation method GCV will work correctly when there are duplicated points in \( x \). However, it is ambiguous what leave-one-out cross-validation means with duplicated points, and the internal code uses an approximation that involves leaving out groups of duplicated points. \( \text{cv} = \text{TRUE} \) is best avoided in that case.

**Value**

An object of class “\text{smooth.spline}” with components

- \( x \): the distinct \( x \) values in increasing order, see the ‘Details’ above.
- \( y \): the fitted values corresponding to \( x \).
- \( w \): the weights used at the unique values of \( x \).
- \( \text{yin} \): the \( y \) values used at the unique \( y \) values.
- \( \text{tol} \): the \( \text{tol} \) argument (whose default depends on \( x \)).
- \( \text{data} \): only if \( \text{keep.data = TRUE} \): itself a \textbf{list} with components \( x \), \( y \) and \( w \) of the same length. These are the original \((x_i, y_i, w_i), i = 1, \ldots, n\), values where \( \text{data} \$x \) may have repeated values and hence be longer than the above \( x \) component; see details.
- \( n \): an integer; the (original) sample size.
- \( \text{lev} \): (when \( \text{cv} \) was not \( \text{NA} \)) leverages, the diagonal values of the smoother matrix.
- \( \text{cv} \): the \( \text{cv} \) argument used; i.e., \text{FALSE}, \text{TRUE}, or \text{NA}.
- \( \text{cv.crit} \): cross-validation score, ‘generalized’ or true, depending on \( \text{cv} \). The CV score is often called “PRESS” (and labeled on \textbf{print}()), for ‘\text{PREdiction Sum of Squares}’. Note that this is \textit{not} the same as the (CV or GCV) score which is minimized during fitting (and returned in \( \text{crit} \)), e.g., in the case of \( nx < n \) (where \( nx = n_x \) is the number of unique \( x \) values).
- \( \text{pen.crit} \): the penalized criterion, a non-negative number; simply the (weighted) residual sum of squares (RSS), \( \text{sum}(. \$w \ast \text{residuals(.)}^2) \).
- \( \text{crit} \): the criterion value minimized in the underlying \textit{Fortran} routine ‘\texttt{sslvrg}’. When \( df \) has been specified, the criterion is \( 3 + (\text{tr}(S_\lambda) - df)^2 \), where the \( 3+ \) is there for numerical (and historical) reasons.
- \( \text{df} \): equivalent degrees of freedom used. Note that (currently) this value may become quite imprecise when the true \( df \) is between 1 and 2.
- \( \text{spar} \): the value of \( \text{spar} \) computed or given, unless it has been given as \texttt{c(\text{lambda = *})}, when it set to \text{NA} here.
- \( \text{ratio} \): (when \( \text{spar} \) above is not \text{NA}), the value \( r \), the ratio of two matrix traces.
- \( \text{lambda} \): the value of \( \lambda \) corresponding to \( \text{spar} \), see the details above.
smooth.spline

iparms named integer(3) vector where ..$ipars["iter"] gives number of spar computing iterations used.

auxMat experimental; when keep.stuff was true, a “flat” numeric vector containing parts of the internal computations.

fit list for use by predict.smooth.spline, with components

knot: the knot sequence (including the repeated boundary knots), scaled into [0, 1] (via min and range).

nk: number of coefficients or number of ‘proper’ knots plus 2.

coef: coefficients for the spline basis used.

min, range: numbers giving the corresponding quantities of x.

call the matched call.

method(class = "smooth.spline") shows a hatvalues() method based on the lev vector above.

Note

The number of unique x values, nx = n_x, are determined by the tol argument, equivalently to

nx <- length(x) - sum(duplicated( round((x - mean(x)) / tol) ))

The default all.knots = FALSE and nknots = .nknots.smspl, entails using only O(n_x^{0.2}) knots instead of n_x for n_x > 49. This cuts speed and memory requirements, but not drastically anymore since R version 1.5.1 where it is only O(n_k) + O(n) where n_k is the number of knots.

In this case where not all unique x values are used as knots, the result is a regression spline rather than a smoothing spline in the strict sense, but very close unless a small smoothing parameter (or large df) is used.

Author(s)

R implementation by B. D. Ripley and Martin Maechler (spar/lambda, etc).

Source

This function is based on code in the GAMFIT Fortran program by T. Hastie and R. Tibshirani (originally taken from http://lib.stat.cmu.edu/general/gamfit) which makes use of spline code by Finbarr O’Sullivan. Its design parallels the smooth.spline function of Chambers & Hastie (1992).

References


See Also

predict.smooth.spline for evaluating the spline and its derivatives.
Examples

require(graphics)
plot(dist ~ speed, data = cars, main = "data(cars) & smoothing splines")
cars.spl <- with(cars, smooth.spline(speed, dist))
cars.spl
## This example has duplicate points, so avoid cv = TRUE
lines(cars.spl, col = "blue")
ss10 <- smooth.spline(cars[, "speed"], cars[, "dist"], df = 10)
lines(ss10, lty = 2, col = "red")
legend(5, 120, c(paste("default [C.V.] => df =", round(cars.spl$df, 1)),
"s( * , df = 10")", col = c("blue", "red"), lty = 1:2,
bg = 'bisque')

## Residual (Tukey Anscombe) plot:
plot(residuals(cars.spl) ~ fitted(cars.spl))
abline(h = 0, col = "gray")

## consistency check:
stopifnot(all.equal(cars$dist,
fitted(cars.spl) + residuals(cars.spl)))
## The chosen inner knots in original x-scale :
with(cars.spl$fit, min + range * knot[-c(1:3, nk+1 +1:3)]) # == unique(cars$speed)

## Visualize the behavior of .nknots.smspl()
plot(n, nKnots(n), type="l", main = "Vectorize(.nknots.smspl) (n)"
abline(0,1, lty=2, col=c..); text(180,180,"y = x", col=c..)

n0 <- c(50, 200, 800, 3200); c0 <- adjustcolor("blue3", .5)
lines(n0, nKnots(n0), type="h", col=c0)
axis(1, at=n0, line=-2, col.ticks=c0, col=NA, col.axis=c0)
axis(4, at=.nknots.smspl(10000), line=-.5, col=c..,col.axis=c.., las=1)

##-- artificial example
y18 <- c(1:3, 5, 4, 7:3, 2*(2:5), rep(10, 4))
xx <- seq(1, length(y18), length.out = 201)
(s2 <- smooth.spline(y18)) # GCV
(s02 <- smooth.spline(y18, spar = 0.2))
(s02. <- smooth.spline(y18, spar = 0.2, cv = NA)
plot(y18, main = deparse(s2$call), col.main = 2)
lines(s2, col = "gray"); lines(predict(s2, xx), col = 2)
lines(predict(s02, xx), col = 3); mtext(deparse(s02$call), col = 3)

## Specifying 'lambda' instead of usual spar :
(s2. <- smooth.spline(y18, lambda = s2$lambda, tol = s2$tol))

## The following shows the problematic behavior of 'spar' searching:
(s2 <- smooth.spline(y18, control =
smoothEnds

End Points Smoothing (for Running Medians)

Description
Smooth end points of a vector \( y \) using subsequently smaller medians and Tukey’s end point rule at the very end. (of odd span).

Usage
smoothEnds(\( y \), \( k = 3 \))

Arguments
\( y \)  
dependent variable to be smoothed (vector).
\( k \)  
width of largest median window; must be odd.

Details
smoothEnds is used to only do the ‘end point smoothing’, i.e., change at most the observations closer to the beginning/end than half the window \( k \). The first and last value are computed using Tukey’s end point rule, i.e., \( \text{sm}[1] = \text{median}(y[1], \text{sm}[2], 3*\text{sm}[2] - 2*\text{sm}[3], \text{na.rm=TRUE}) \).

In R versions 3.6.0 and earlier, missing values (\( \text{NA} \)) in \( y \) typically lead to an error, whereas now the equivalent of \( \text{median}(*, \text{na.rm=TRUE}) \) is used.

Value
vector of smoothed values, the same length as \( y \).

Author(s)
Martin Maechler

References


See Also
runmed(*, endrule = "median") which calls smoothEnds().
Examples

require(graphics)

y <- ys <- (-20:20)^2
s7k <- runmed(y, 7, endrule = "keep")
s7. <- runmed(y, 7, endrule = "const")
s7m <- runmed(y, 7)
col3 <- c("midnightblue","blue","steelblue")
plot(y, main = "Running Medians -- runmed(*, k=7, endrule = X)"
lines(ys, col = "light gray")
matlines(cbind(s7k, s7.,s7m), lwd = 1.5, lty = 1, col = col3)
eRules <- c("keep","constant","median")
legend("topleft", paste("endrule", eRules, sep = " = "),
    col = col3, lwd = 1.5, lty = 1, bty = "n")

stopifnot(identical(s7m, smoothEnds(s7k, 7)))
## With missing values (for R >= 3.6.1):
yN <- y; yN[c(2,40)] <- NA
rN <- sapply(eRules, function(R) runmed(yN, 7, endrule=R))
matlines(rN, type = "b", pch = 4, lwd = 3, lty=2,
    col = adjustcolor(c("red", "orange4", "orange1"), 0.5))
yN[c(1, 20:21)] <- NA # additionally
rN. <- sapply(eRules, function(R) runmed(yN, 7, endrule=R))
head(rN., 4); tail(rN.) # more NA's too, still not *so* many.
stopifnot(exprs = {
    !anyNA(rN[,2:3]),
    identical(which(is.na(rN,"keep")), c(2L, 40L))
    identical(which(is.na(rN.), arr.ind=TRUE, useNames=FALSE),
        cbind(c(1:2,40L), 1L))
    identical(rN.[38:41, "median"], c(289,289, 397, 470))
})

sortedXyData Create a sortedXyData Object

Description

This is a constructor function for the class of sortedXyData objects. These objects are mostly used in the initial function for a self-starting nonlinear regression model, which will be of the selfStart class.

Usage

sortedXyData(x, y, data)

Arguments

x

a numeric vector or an expression that will evaluate in data to a numeric vector

y

a numeric vector or an expression that will evaluate in data to a numeric vector

data

an optional data frame in which to evaluate expressions for x and y, if they are given as expressions
Value
A sortedXyData object. This is a data frame with exactly two numeric columns, named x and y. The rows are sorted so the x column is in increasing order. Duplicate x values are eliminated by averaging the corresponding y values.

Author(s)
José Pinheiro and Douglas Bates

See Also
selfStart, NLSstClosestX, NLSstLfAsymptote, NLSstRtAsymptote

Examples
DNase.2 <- DNase[DNase$Run == "2",]
sortedXyData(expression(log(conc)), expression(density), DNase.2)

spec.ar

Estimate Spectral Density of a Time Series from AR Fit

Description
Fits an AR model to x (or uses the existing fit) and computes (and by default plots) the spectral density of the fitted model.

Usage
spec.ar(x, n.freq, order = NULL, plot = TRUE, na.action = na.fail,
method = "yule-walker", ...)

Arguments
x A univariate (not yet: or multivariate) time series or the result of a fit by ar.
n.freq The number of points at which to plot.
order The order of the AR model to be fitted. If omitted, the order is chosen by AIC.
plot Plot the periodogram?
na.action NA action function.
method method for ar fit.
... Graphical arguments passed to plot.spec.

Value
An object of class "spec". The result is returned invisibly if plot is true.

Warning
Some authors, for example Thomson (1990), warn strongly that AR spectra can be misleading.
Note
The multivariate case is not yet implemented.

References

See Also
ar, spectrum.

Examples
require(graphics)
spec.ar(1h)
spec.ar(ldeaths)
spec.ar(ldeaths, method = "burg")
spec.ar(log(lynx))
spec.ar(log(lynx), method = "burg", add = TRUE, col = "purple")
spec.ar(log(lynx), method = "mle", add = TRUE, col = "forest green")
spec.ar(log(lynx), method = "ols", add = TRUE, col = "blue")

---

**Description**

spec.pgram calculates the periodogram using a fast Fourier transform, and optionally smooths the result with a series of modified Daniell smoothers (moving averages giving half weight to the end values).

**Usage**

```
spec.pgram(x, spans = NULL, kernel, taper = 0.1, pad = 0, fast = TRUE, demean = FALSE, detrend = TRUE, plot = TRUE, na.action = na.fail, ...)
```

**Arguments**

- `x` univariate or multivariate time series.
- `spans` vector of odd integers giving the widths of modified Daniell smoothers to be used to smooth the periodogram.
- `kernel` alternatively, a kernel smoother of class "tskernel".
taper specifies the proportion of data to taper. A split cosine bell taper is applied to this proportion of the data at the beginning and end of the series.

pad proportion of data to pad. Zeros are added to the end of the series to increase its length by the proportion pad.

fast logical; if TRUE, pad the series to a highly composite length.

demean logical. If TRUE, subtract the mean of the series.

detrend logical. If TRUE, remove a linear trend from the series. This will also remove the mean.

plot plot the periodogram?

na.action NA action function.

... graphical arguments passed to plot.spec.

Details

The raw periodogram is not a consistent estimator of the spectral density, but adjacent values are asymptotically independent. Hence a consistent estimator can be derived by smoothing the raw periodogram, assuming that the spectral density is smooth.

The series will be automatically padded with zeros until the series length is a highly composite number in order to help the Fast Fourier Transform. This is controlled by the fast and not the pad argument.

The periodogram at zero is in theory zero as the mean of the series is removed (but this may be affected by tapering): it is replaced by an interpolation of adjacent values during smoothing, and no value is returned for that frequency.

Value

A list object of class "spec" (see spectrum) with the following additional components:

kernel The kernel argument, or the kernel constructed from spans.

df The distribution of the spectral density estimate can be approximated by a (scaled) chi square distribution with df degrees of freedom.

bandwidth The equivalent bandwidth of the kernel smoother as defined by Bloomfield (1976, page 201).

taper The value of the taper argument.

pad The value of the pad argument.

detrend The value of the detrend argument.

demean The value of the demean argument.

The result is returned invisibly if plot is true.

Author(s)

Originally Martyn Plummer; kernel smoothing by Adrian Trapletti, synthesis by B.D. Ripley

References


spec.taper

Taper a Time Series by a Cosine Bell

Description

Apply a cosine-bell taper to a time series.

Usage

spec.taper(x, p = 0.1)

Arguments

x A univariate or multivariate time series
p The proportion to be tapered at each end of the series, either a scalar (giving the proportion for all series) or a vector of the length of the number of series (giving the proportion for each series).
The cosine-bell taper is applied to the first and last $p[i]$ observations of time series $x[, i]$.

A new time series object.

The spectrum function estimates the spectral density of a time series.

Usage

spectrum(x, ..., method = c("pgram", "ar"))

Arguments

x A univariate or multivariate time series.

method String specifying the method used to estimate the spectral density. Allowed methods are "pgram" (the default) and "ar". Can be abbreviated.

... Further arguments to specific spec methods or plot.spec.

Details

spectrum is a wrapper function which calls the methods spec.pgram and spec.ar.

The spectrum here is defined with scaling $1/\text{frequency}(x)$, following S-PLUS. This makes the spectral density a density over the range $(-\text{frequency}(x)/2, +\text{frequency}(x)/2)$, whereas a more common scaling is $2\pi$ and range $(-0.5, 0.5]$ (e.g., Bloomfield) or 1 and range $(-\pi, \pi]$.

If available, a confidence interval will be plotted by plot.spec: this is asymmetric, and the width of the centre mark indicates the equivalent bandwidth.

Value

An object of class "spec", which is a list containing at least the following components:

freq vector of frequencies at which the spectral density is estimated. (Possibly approximate Fourier frequencies.) The units are the reciprocal of cycles per unit time (and not per observation spacing): see ‘Details’ below.

spec Vector (for univariate series) or matrix (for multivariate series) of estimates of the spectral density at frequencies corresponding to freq.

coh NULL for univariate series. For multivariate time series, a matrix containing the squared coherency between different series. Column $i + (j - 1) \times (j - 2)/2$ of coh contains the squared coherency between columns $i$ and $j$ of $x$, where $i < j$. 

Spectral Density Estimation
The result is returned invisibly if `plot` is true.

**Note**

The default plot for objects of class "spec" is quite complex, including an error bar and default title, subtitle and axis labels. The defaults can all be overridden by supplying the appropriate graphical parameters.

**Author(s)**

Martyn Plummer, B.D. Ripley

**References**


**See Also**

`spec.ar`, `spec.pgram`; `plot.spec`.

**Examples**

```r
require(graphics)

## Examples from Venables & Ripley
## spec.pgram
par(mfrow = c(2,2))
spectrum(lh)
spectrum(lh, spans = 3)
spectrum(lh, spans = c(3,3))
spectrum(lh, spans = c(3,5))
spectrum(ldeaths)
spectrum(ldeaths, spans = c(3,3))
spectrum(ldeaths, spans = c(3,5))
spectrum(ldeaths, spans = c(5,7))
spectrum(ldeaths, spans = c(5,7), log = "dB", ci = 0.8)

# for multivariate examples see the help for spec.pgram

## spec.ar
spectrum(lh, method = "ar")
spectrum(ldeaths, method = "ar")
```
splinefun

Interpolating Splines

Description

Perform cubic (or Hermite) spline interpolation of given data points, returning either a list of points obtained by the interpolation or a function performing the interpolation.

Usage

splinefun(x, y = NULL,
method = c("fmm", "periodic", "natural", "monoH.FC", "hyman"),
ties = mean)

spline(x, y = NULL, n = 3*length(x), method = "fmm",
xmin = min(x), xmax = max(x), xout, ties = mean)

splinefunH(x, y, m)

Arguments

x, y vectors giving the coordinates of the points to be interpolated. Alternatively a single plotting structure can be specified: see xy.coords.
y must be increasing or decreasing for method = "hyman".
m (for splinefunH()): vector of slopes \( m_i \) at the points \((x_i, y_i)\); these together determine the Hermite "spline" which is piecewise cubic, (only) once differentiable continuously.
method specifies the type of spline to be used. Possible values are "fmm", "natural", "periodic", "monoH.FC" and "hyman". Can be abbreviated.
n if xout is left unspecified, interpolation takes place at n equally spaced points spanning the interval \([xmin, xmax]\).
xmin, xmax left-hand and right-hand endpoint of the interpolation interval (when xout is unspecified).
xout an optional set of values specifying where interpolation is to take place.
ties handling of tied x values. The string "ordered" or a function (or the name of a function) taking a single vector argument and returning a single number or a length-2 list of both, see approx and its 'Details' section, and the example below.

Details

The inputs can contain missing values which are deleted, so at least one complete \((x, y)\) pair is required. If method = "fmm", the spline used is that of Forsythe, Malcolm and Moler (an exact cubic is fitted through the four points at each end of the data, and this is used to determine the end conditions). Natural splines are used when method = "natural", and periodic splines when method = "periodic".

The method "monoH.FC" computes a monotone Hermite spline according to the method of Fritsch and Carlson. It does so by determining slopes such that the Hermite spline, determined by \((x_i, y_i, m_i)\), is monotone (increasing or decreasing) iff the data are.
Method "hyman" computes a monotone cubic spline using Hyman filtering of an method = "fmm" fit for strictly monotonic inputs.

These interpolation splines can also be used for extrapolation, that is prediction at points outside the range of x. Extrapolation makes little sense for method = "fmm"; for natural splines it is linear using the slope of the interpolating curve at the nearest data point.

Value

spline returns a list containing components x and y which give the ordinates where interpolation took place and the interpolated values.

splinefun returns a function with formal arguments x and deriv, the latter defaulting to zero. This function can be used to evaluate the interpolating cubic spline (deriv = 0), or its derivatives (deriv = 1, 2, 3) at the points x, where the spline function interpolates the data points originally specified. It uses data stored in its environment when it was created, the details of which are subject to change.

Warning

The value returned by splinefun contains references to the code in the current version of R: it is not intended to be saved and loaded into a different R session. This is safer in R >= 3.0.0.

Author(s)

R Core Team.

Simon Wood for the original code for Hyman filtering.

References


See Also

approx and approxfun for constant and linear interpolation.

Package splines, especially interpSpline and periodicSpline for interpolation splines. That package also generates spline bases that can be used for regression splines.

smooth.spline for smoothing splines.
Examples

```
require(graphics)

op <- par(mfrow = c(2,1), mgp = c(2,.8,0), mar = 0.1+c(3,3,3,1))
n <- 9
x <- 1:n
y <- rnorm(n)
plot(x, y, main = paste("spline[fun](.) through", n, "points"))
lines(spline(x, y))
lines(spline(x, y, n = 201), col = 2)

y <- (x-6)^2
plot(x, y, main = "spline(.) -- 3 methods")
lines(spline(x, y, n = 201), col = 2)
lines(spline(x, y, n = 201, method = "natural"), col = 3)
lines(spline(x, y, n = 201, method = "periodic"), col = 4)
legend(6, 25, c("fmm","natural","periodic"), col = 2:4, lty = 1)

y <- sin((x-0.5)*pi)
f <- splinefun(x, y)
ls(envir = environment(f))
splinecoef <- get("z", envir = environment(f))
curve(f(x), 1, 10, col = "green", lwd = 1.5)
points(splinecoef, col = "purple", cex = 2)
curve(f(x, deriv = 1), 1, 10, col = 2, lwd = 1.5)
curve(f(x, deriv = 2), 1, 10, col = 2, lwd = 1.5, n = 401)
curve(f(x, deriv = 3), 1, 10, col = 2, lwd = 1.5, n = 401)
par(op)

## Manual spline evaluation --- demo the coefficients :
.x <- splinecoef$x
.u <- seq(3, 6, by = 0.25)
(ii <- findInterval(u, .x))
dx <- u - .x[ii]
f.u <- with(splinecoef,
  y[ii] + dx*(b[ii] + dx*(c[ii] + dx* d[ii])))
stopifnot(all.equal(f(u), f.u))

## An example with ties (non-unique x values):
set.seed(1); x <- round(rnorm(30), 1); y <- sin(pi * x) + rnorm(30)/10
plot(x, y, main = "spline(x,y) when x has ties")
lines(spline(x, y, n = 201), col = 2)
## visualizes the non-unique ones:
 tx <- table(x); mx <- as.numeric(names(tx[tx > 1]))
 ry <- matrix(unlist(tapply(y, match(x, mx), range, simplify = FALSE)),
  ncol = 2, byrow = TRUE)
segments(mx, ry[, 1], mx, ry[, 2], col = "blue", lwd = 2)

## Another example with sorted x, but ties:
set.seed(8); x <- sort(round(rnorm(30), 1)); y <- round(sin(pi * x) + rnorm(30)/10, 3)
supply(dif(x) == 0) # => 7 duplicated x-values
str(spline(x, y, n = 201, ties="ordered")) # all 'y' entries are NaN
## The default (ties=mean) is ok, but most efficient to use instead is
sxyo <- spline(x, y, n = 201, ties= list("ordered", mean))
sapply(sxyo, summary)# all fine now
plot(x, y, main = "spline(x,y, ties=list("ordered", mean)) for when x has ties")
```
## An example of monotone interpolation

```r
n <- 20
set.seed(11)
x. <- sort(runif(n)) ; y. <- cumsum(abs(rnorm(n)))
plot(x., y.)
curve(splinefun(x., y.)(x), add = TRUE, col = 2, n = 1001)
curve(splinefun(x., y., method = "monoH.FC")(x), add = TRUE, col = 3, n = 1001)
curve(splinefun(x., y., method = "hyman") (x), add = TRUE, col = 4, n = 1001)
legend("topleft",
paste0("splinefun( "", c("fmm", "monoH.FC", "hyman"), "\" \")"),
col = 2:4, lty = 1, bty = "n")
```

## and one from Fritsch and Carlson (1980), Dougherty et al (1989)

```r
x. <- c(7.09, 8.09, 8.19, 8.7, 9.2, 10, 12, 15, 20)
f <- c(0, 2.76429e-5, 4.37498e-2, 0.169183, 0.469428, 0.943740,
0.998636, 0.999919, 0.999994)
s0 <- splinefun(x., f)
s1 <- splinefun(x., f, method = "monoH.FC")
s2 <- splinefun(x., f, method = "hyman")
plot(x., f, ylim = c(-0.2, 1.2))
curve(s0(x), add = TRUE, col = 2, n = 1001) -> m0
curve(s1(x), add = TRUE, col = 3, n = 1001)
curve(s2(x), add = TRUE, col = 4, n = 1001)
legend("right",
paste0("splinefun( \"", c("fmm", "monoH.FC", "hyman"), \" \")"),
col = 2:4, lty = 1, bty = "n")
```

## they seem identical, but are not quite:

```r
xx <- m0$x
plot(xx, s1(xx) - s2(xx), type = "l", col = 2, lwd = 2,
main = "Difference monoH.FC - hyman"); abline(h = 0, lty = 3)
x <- xx[xx < 10.2] ## full range: x <- xx .. does not show enough
col <- adjustcolor(2:4, 0.8)
matplot(x, cbind(s0(x, deriv = 2), s1(x, deriv = 2), s2(x, deriv = 2))^2,
lwd = 2, col = col, type = "l", ylab = quote({{f*second}(x)}^2),
main = expression({{f*second}(x)}^2 ~ "for the three 'splines'")
legend("topright",
paste0("splinefun( \"", c("fmm", "monoH.FC", "hyman"), \" \")"),
lwd = 2, col = col, lty = 1:3, bty = "n")
```

## --> "hyman" has slightly smaller Integral f'(x)² dx than "FC",
## here, and both are 'much worse' than the regular fmm spline.

---

**SSasymp**  
**Self-Starting Nls Asymptotic Regression Model**

### Description

This `selfStart` model evaluates the asymptotic regression function and its gradient. It has an initial attribute that will evaluate initial estimates of the parameters `Asym`, `R0`, and `lrc` for a given set of data.

Note that `SSweibull()` generalizes this asymptotic model with an extra parameter.
**Usage**

SSasymp(input, Asym, R0, lrc)

**Arguments**

- **input**: a numeric vector of values at which to evaluate the model.
- **Asym**: a numeric parameter representing the horizontal asymptote on the right side (very large values of input).
- **R0**: a numeric parameter representing the response when input is zero.
- **lrc**: a numeric parameter representing the natural logarithm of the rate constant.

**Value**

A numeric vector of the same length as `input`. It is the value of the expression `Asym+(R0-Asym)*exp(-exp(lrc)*input)`. If all of the arguments `Asym`, `R0`, and `lrc` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

`nls`, `selfStart`

**Examples**

```r
Lob.329 <- Loblolly[Loblolly$Seed == "329",]
SSasymp( Lob.329$age, 100, -8.5, -3.2 ) # response only
local({
  Asym <- 100 ; resp0 <- -8.5 ; lrc <- -3.2
  SSasymp( Lob.329$age, Asym, resp0, lrc ) # response _and_ gradient
})
getInitial(height ~ SSasymp( age, Asym, resp0, lrc), data = Lob.329)
# Initial values are in fact the converged values
fm1 <- nls(height ~ SSasymp( age, Asym, resp0, lrc), data = Lob.329)
summary(fm1)
## Visualize the SSasymp() model parametrization:

xx <- seq(-.3, 5, length.out = 101)
## Asym + (R0-Asym) * exp(-exp(lrc)* x) :
yy <- 5 - 4 * exp(-xx / exp(3/4))
stopifnot( all.equal(yy, SSasymp(xx, Asym = 5, R0 = 1, lrc = -3/4)) )
require(graphics)
op <- par(mar = c(0, .2, 4.1, 0))
plot(xx, yy, type = "l", axes = FALSE, ylim = c(0,5.2), xlim = c(-.3, 5),
xlab = "", ylab = "", lwd = 2,
    main = quote("Parameters in the SSasymp model 
usr <- par("usr")
arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
```
SSasympOff

Self-Starting Nls Asymptotic Regression Model with an Offset

Description

This selfStart model evaluates an alternative parametrization of the asymptotic regression function and the gradient with respect to those parameters. It has an initial attribute that creates initial estimates of the parameters Asym, lrc, and c0.

Usage

SSasympOff(input, Asym, lrc, c0)

Arguments

input a numeric vector of values at which to evaluate the model.
Asym a numeric parameter representing the horizontal asymptote on the right side (very large values of input).
lrc a numeric parameter representing the natural logarithm of the rate constant.
c0 a numeric parameter representing the input for which the response is zero.

Value

a numeric vector of the same length as input. It is the value of the expression Asym*(1 - \exp(-\exp(lrc)*(input - c0))). If all of the arguments Asym, lrc, and c0 are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart; example(SSasympOff) gives graph showing the SSasympOff parametrization.
Examples

CO2.Qn1 <- CO2[CO2$Plant == "Qn1",]
SSasympOff(CO2.Qn1$conc, 32, -4, 43) # response only
local({
  Asym <- 32; lrc <- -4; c0 <- 43
  SSasympOff(CO2.Qn1$conc, Asym, lrc, c0) # response and gradient
})
getInitial(uptake ~ SSasympOff(conc, Asym, lrc, c0), data = CO2.Qn1)
## Initial values are in fact the converged values
fm1 <- nls(uptake ~ SSasympOff(conc, Asym, lrc, c0), data = CO2.Qn1)
summary(fm1)
## Visualize the SSasympOff() model parametrization:
xx <- seq(0.25, 8, by=1/16)
yy <- 5 * (1 - exp(-(xx - 3/4)*0.4))
stopifnot(all.equal(yy, SSasympOff(xx, Asym = 5, lrc = log(0.4), c0 = 3/4)))
require(graphics)
op <- par(mar = c(0, 0, 4.0, 0))
plot(xx, yy, type = "l", axes = FALSE, ylim = c(-.5,6), xlim = c(-1, 8),
xlab = "", ylab = "", lwd = 2,
main = "Parameters in the SSasympOff model")
usr <- par("usr")
arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
text(-0.1, usr[4], "y", adj = c(1, 1))
abline(h = 5, lty = 3)
arrows(-0.8, c(2.1, 2.9),
-0.8, c(0 , 5 ), length = 0.1, angle = 25)
text (-0.8, 2.5, quote(phi[1]))
segments(3/4, -.2, 3/4, 1.6, lty = 2)
text (3/4, c(-.3, 1.7), quote(phi[3]))
arrows(c(1.1, 1.4), -.15,
c(3/4, 7/4), -.15, length = 0.07, angle = 25)
text(3/4 + 1/2, -.15, quote(1))
segments(c(3/4, 7/4, 7/4), c(0, 0, 2), # 5 * exp(log(0.4)) = 2
c(7/4, 7/4, 3/4), c(0, 2, 0), lty = 2, lwd = 2)
text(7/4 +.1, 2./2, quote(phi[1]*exp(phi[2])), adj = c(0, .5))
par(op)

SSasympOrig

Self-Starting Nls Asymptotic Regression Model through the Origin

Description

This \texttt{selfStart} model evaluates the asymptotic regression function through the origin and its gradient. It has an initial attribute that will evaluate initial estimates of the parameters \texttt{Asym} and \texttt{lrc} for a given set of data.

Usage

\texttt{SSasympOrig(input, Asym, lrc)}
**SSasympOrig**

**Arguments**

- `input` a numeric vector of values at which to evaluate the model.
- `Asym` a numeric parameter representing the horizontal asymptote.
- `lrc` a numeric parameter representing the natural logarithm of the rate constant.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression `Asym*(1 - \exp(-\exp(lrc)*input))`. If all of the arguments `Asym` and `lrc` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

`nls`, `selfStart`

**Examples**

```r
Lob.329 <- Loblolly[Loblolly$Seed == "329", ]
SSasympOrig(Lob.329$age, 100, -3.2) # response only
local({
  Asym <- 100;
  lrc <- -3.2
  SSasympOrig(Lob.329$age, Asym, lrc) # response and gradient
})
getInitial(height ~ SSasympOrig(age, Asym, lrc), data = Lob.329)
# Initial values are in fact the converged values
fm1 <- nls(height ~ SSasympOrig(age, Asym, lrc), data = Lob.329)
summary(fm1)
## Visualize the SSasympOrig() model parametrization:
xx <- seq(0, 5, length.out = 101)
yy <- 5 * (1 - \exp(-xx * log(2)))
stopifnot(all.equal(yy, SSasympOrig(xx, Asym = 5, lrc = log(log(2)))))
require(graphics)
par(mar = c(0, 0, 3.5, 0))
plot(xx, yy, type = "l", axes = FALSE, ylim = c(0, 5), xlim = c(-1/4, 5),
     xlab = "", ylab = "", lwd = 2,
     main = quote("Parameters in the SSasympOrig model-- f(\phi(x))"))
grid
xaxis labels: t[0.5]
```

.Execute the code
Description

This selfStart model evaluates the biexponential model function and its gradient. It has an initial attribute that creates initial estimates of the parameters \( A1, lrc1, A2, \) and \( lrc2 \).

Usage

\( \text{SSbiexp}(\text{input}, A1, lrc1, A2, lrc2) \)

Arguments

input a numeric vector of values at which to evaluate the model.

A1 a numeric parameter representing the multiplier of the first exponential.

lrc1 a numeric parameter representing the natural logarithm of the rate constant of the first exponential.

A2 a numeric parameter representing the multiplier of the second exponential.

lrc2 a numeric parameter representing the natural logarithm of the rate constant of the second exponential.

Value

a numeric vector of the same length as input. It is the value of the expression

\[ A1 \exp(-\exp(lrc1) \times \text{input}) + A2 \exp(-\exp(lrc2) \times \text{input}). \]

If all of the arguments \( A1, lrc1, A2, \) and \( lrc2 \) are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart

Examples

\begin{verbatim}
Indo.1 <- Indometh[Indometh$Subject == 1,]
SSbiexp( Indo.1$time, 3, 1, 0.6, -1.3 ) # response only
A1 <- 3; lrc1 <- 1; A2 <- 0.6; lrc2 <- -1.3
SSbiexp( Indo.1$time, A1, lrc1, A2, lrc2 ) # response and gradient
print(getInitial(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = Indo.1),
digits = 5)
# Initial values are in fact the converged values
fm1 <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = Indo.1)
summary(fm1)
\end{verbatim}
## Show the model components visually

```r
require(graphics)
xx <- seq(0, 5, length.out = 101)
y1 <- 3.5 * exp(-4*xx)
y2 <- 1.5 * exp(-xx)
plot(xx, y1 + y2, type = "l", lwd=2, ylim = c(-0.2,6), xlim = c(0, 5),
     main = "Components of the SSbiexp model")
lines(xx, y1, lty = 2, col="tomato"); abline(v=0, h=0, col="gray40")
lines(xx, y2, lty = 3, col="blue2")
legend("topright", c("y1+y2", "y1 = 3.5 * exp(-4*x)", "y2 = 1.5 * exp(-x)")
     , lty=1:3, col=c("black","tomato","blue2"), bty="n")
axis(2, pos=0, at = c(3.5, 1.5), labels = c("A1","A2"), las=2)
```

## and how you could have got their sum via SSbiexp():
```
ySS <- SSbiexp(xx, 3.5, log(4), 1.5, log(1))
```

```r
## Show a no-noise example
datN <- data.frame(time = (0:600)/64)
datN$conc <- predict(fm1, newdata=datN)
plot(conc ~ time, data=datN) # perfect, no noise
```

```r
## Fails by default (scaleOffset=0) on most platforms (also after increasing maxiter !)
## Not run:

```r
nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = datN, trace=TRUE)
```

```r
## End(Not run)

```r
fmX1 <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = datN, control = list(scaleOffset=1))
fmX  <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = datN,
            control = list(scaleOffset=1, printEval=TRUE, tol=1e-11, nDcentral=TRUE), trace=TRUE)
all.equal(coef(fm1), coef(fmX1), tolerance=0) # ... rel.diff.: 1.57e-6
all.equal(coef(fm1), coef(fmX), tolerance=0) # ... rel.diff.: 1.03e-12
```

```r
## IGNORE_RDIFF_END
```

```r
stopifnot(all.equal(coef(fm1), coef(fmX1), tolerance = 1e-15))
```

```r
## SSD
SSD
```

### SSD Matrix and Estimated Variance Matrix in Multivariate Models

#### Description

Functions to compute matrix of residual sums of squares and products, or the estimated variance matrix for multivariate linear models.

#### Usage

```
# S3 method for class 'mlm'
SSD(object, ...)

# S3 methods for class 'SSD' and 'mlm'
estVar(object, ...)
```
Arguments

object object of class "mlm", or "SSD" in the case of estVar.
...
Unused

Value

SSD() returns a list of class "SSD" containing the following components

SSD The residual sums of squares and products matrix
df Degrees of freedom
call Copied from object

estVar returns a matrix with the estimated variances and covariances.

See Also

mauchly.test, anova.mlm

Examples

# Lifted from Baron+Li:
# "Notes on the use of R for psychology experiments and questionnaires"
# Maxwell and Delaney, p. 497
reacttime <- matrix(c(
420, 420, 480, 480, 600, 780,
420, 480, 480, 360, 480, 600,
480, 480, 540, 660, 780, 780,
420, 540, 540, 480, 780, 900,
540, 660, 540, 660, 720, 720,
360, 420, 360, 360, 480, 540,
480, 480, 600, 540, 720, 840,
480, 600, 660, 540, 720, 900,
540, 600, 540, 480, 720, 780,
480, 420, 540, 540, 660, 780),
ncol = 6, byrow = TRUE,
dimnames = list(subj = 1:10,
cond = c("deg0NA", "deg4NA", "deg8NA",
"deg0NP", "deg4NP", "deg8NP")))

mlmfit <- lm(reacttime ~ 1)
SSD(mlmfit)
estVar(mlmfit)
**Usage**

SSfol(Dose, input, lKe, lKa, lCl)

**Arguments**

- **Dose**: a numeric value representing the initial dose.
- **input**: a numeric vector at which to evaluate the model.
- **lKe**: a numeric parameter representing the natural logarithm of the elimination rate constant.
- **lKa**: a numeric parameter representing the natural logarithm of the absorption rate constant.
- **lCl**: a numeric parameter representing the natural logarithm of the clearance.

**Value**

a numeric vector of the same length as `input`, which is the value of the expression

\[
\frac{Dose \times \exp(lKe+lKa-lCl) \times (\exp(-\exp(lKe)\times input) - \exp(-\exp(lKa)\times input))}{\exp(lKa) - \exp(lKe)}
\]

If all of the arguments `lKe`, `lKa`, and `lCl` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

nls, selfStart

**Examples**

```r
Theoph.1 <- Theoph[ Theoph$Subject == 1, ]
with(Theoph.1, SSfol(Dose, Time, -2.5, 0.5, -3)) # response only
with(Theoph.1, local({ lKe <- -2.5; lKa <- 0.5; lCl <- -3
SSfol(Dose, Time, lKe, lKa, lCl) # response and gradient }))
getInitial(conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data = Theoph.1)
# Initial values are in fact the converged values
fm1 <- nls(conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data = Theoph.1)
summary(fm1)
```
SSfpl  Self-Starting Nls Four-Parameter Logistic Model

Description

This selfStart model evaluates the four-parameter logistic function and its gradient. It has an initial attribute computing initial estimates of the parameters A, B, xmid, and scal for a given set of data.

Usage

SSfpl(input, A, B, xmid, scal)

Arguments

input  a numeric vector of values at which to evaluate the model.
A  a numeric parameter representing the horizontal asymptote on the left side (very small values of input).
B  a numeric parameter representing the horizontal asymptote on the right side (very large values of input).
xmid  a numeric parameter representing the input value at the inflection point of the curve. The value of SSfpl will be midway between A and B at xmid.
scal  a numeric scale parameter on the input axis.

Value

a numeric vector of the same length as input. It is the value of the expression A+(B-A)/(1+exp((xmid-input)/scal)). If all of the arguments A, B, xmid, and scal are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

José Pinheiro and Douglas Bates

See Also

nls, selfStart

Examples

Chick.1 <- ChickWeight[ChickWeight$Chick == 1, ]
SSfpl(Chick.1$Time, 13, 368, 14, 6)  # response only
local({
  A <- 13; B <- 368; xmid <- 14; scal <- 6
  SSfpl(Chick.1$Time, A, B, xmid, scal)  # response _and_ gradient
})
print(getInitial(weight ~ SSfpl(Time, A, B, xmid, scal), data = Chick.1),
      digits = 5)
## Initial values are in fact the converged values
fm1 <- nls(weight ~ SSfpl(Time, A, B, xmid, scal), data = Chick.1)
summary(fm1)
## Visualizing the SSfpl() parametrization

```r
xx <- seq(-0.5, 5, length.out = 101)
yy <- 1 + 4 / (1 + exp((2-xx)))  # == SSfpl(xx, *) :
stopifnot( all.equal(yy, SSfpl(xx, A = 1, B = 5, xmid = 2, scal = 1)) )
require(graphics)
op <- par(mar = c(0, 0, 3.5, 0))
plot(xx, yy, type = "l", axes = FALSE, ylim = c(0,6), xlim = c(-1, 5),
xlab = "", ylab = "", lwd = 2,
main = "Parameters in the SSfpl model")

usr <- par("usr")
arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
text( -0.1, usr[4], "y", adj = c(1, 1))
abline(h = c(1, 5), lty = 3)
arrows(-0.8, c(2.1, 2.9),
     -0.8, c(0, 5 ), length = 0.1, angle = 25)
text (-0.8, 2.5, quote(phi[1]))
arrows(-0.3, c(1/4, 3/4),
     -0.3, c(0, 1 ), length = 0.07, angle = 25)
text (-0.3, 0.5, quote(phi[2]))
text(2, -.1, quote(phi[3]))
segments(c(2,3,3), c(0,3,4), # SSfpl(x = xmid = 2) = 3
        c(2,3,2), c(3,4,3), lty = 2, lwd = 0.75)
arrows(c(2.2, 2.7), 3,
      c(2.0, 3 ), 3, length = 0.08, angle = 25)
text( 2.5, 3, quote(phi[4])); text(3.1, 3.5, "1")
par(op)
```

### Description

This selfStart model evaluates the Gompertz growth model and its gradient. It has an initial attribute that creates initial estimates of the parameters Asym, b2, and b3.

### Usage

```r
SSgompertz(x, Asym, b2, b3)
```

### Arguments

- **x**: a numeric vector of values at which to evaluate the model.
- **Asym**: a numeric parameter representing the asymptote.
- **b2**: a numeric parameter related to the value of the function at \( x = 0 \)
- **b3**: a numeric parameter related to the scale the \( x \) axis.

### Value

A numeric vector of the same length as input. It is the value of the expression \( \text{Asym} \ast \exp(-b2 \ast b3 \ast x) \). If all of the arguments Asym, b2, and b3 are names of objects the gradient matrix with respect to these names is attached as an attribute named gradient.
SSlogis

Self-Starting Nls Logistic Model

Description

This selfStart model evaluates the logistic function and its gradient. It has an initial attribute that creates initial estimates of the parameters Asym, xmid, and scal. In R 3.4.2 and earlier, that init function failed when min(input) was exactly zero.

Usage

SSlogis(input, Asym, xmid, scal)

Arguments

input a numeric vector of values at which to evaluate the model.
Asym a numeric parameter representing the asymptote.
xmid a numeric parameter representing the x value at the inflection point of the curve. The value of SSlogis will be Asym/2 at xmid.
scal a numeric scale parameter on the input axis.

Value

a numeric vector of the same length as input. It is the value of the expression Asym/(1+exp((xmid-input)/scal)). If all of the arguments Asym, xmid, and scal are names of objects the gradient matrix with respect to these names is attached as an attribute named gradient.
**SSlogis**

**Author(s)**
José Pinheiro and Douglas Bates

**See Also**
`nls`, `selfStart`

**Examples**

```r
Chick.1 <- ChickWeight[ChickWeight$Chick == 1, ]
SSlogis(Chick.1$Time, 368, 14, 6)  # response only
local({
  Asym <- 368; xmid <- 14; scal <- 6
  SSlogis(Chick.1$Time, Asym, xmid, scal)  # response _and_ gradient
})
getInitial(weight ~ SSlogis(Time, Asym, xmid, scal), data = Chick.1)
  ## Initial values are in fact the converged one here, "Number of iter...: 0" :
  fm1 <- nls(weight ~ SSlogis(Time, Asym, xmid, scal), data = Chick.1)
  summary(fm1)
  ## but are slightly improved here:
  fm2 <- update(fm1, control=nls.control(tol = 1e-9, warnOnly=TRUE), trace = TRUE)
  all.equal(coef(fm1), coef(fm2))  # "Mean relative difference: 9.6e-6"
str(fm2$convInfo)  # 3 iterations
```

dwlg1 <- data.frame(Prop = c(rep(0,5), 2, 5, rep(9, 9)), end = 1:16)
iPar <- getInitial(Prop ~ SSlogis(end, Asym, xmid, scal), data = dwlg1)
  ## failed in R <= 3.4.2 (because of the '0's in 'Prop')
stopifnot(all.equal(tolerance = 1e-6, iPar, c(Asym = 9.0678, xmid = 6.79331, scal = 0.499934)))

```r
## Visualize the SSlogis() model parametrization:
xx <- seq(-0.75, 5, by=1/32)
yy <- 5 / (1 + exp((2-xx)/0.6))  # == SSlogis(xx, *):
stopifnot(all.equal(yy, SSlogis(xx, Asym = 5, xmid = 2, scal = 0.6)))
require(graphics)
par(mar = c(0.5, 0, 3.5, 0))
plot(xx, yy, type = "l", axes = FALSE, ylim = c(0,6), xlim = c(-1, 5),
     xlab = "", ylab = "", lwd = 2,
     main = "Parameters in the SSlogis model")
usr <- par("usr")
arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
text(-0.1, usr[4], "y", adj = c(1, 1))
abline(h = 5, lty = 3)
arrows(-0.8, c(2.1, 2.9),
     -0.8, c(0, 5 ), length = 0.1, angle = 25)
text (-0.8, 2.5, quote(phi[1][]))
segments(c(2.2,6,2.6), c(0, 2.5,3.5), # NB. SSlogis(x = xmid = 2) = 2.5
c(2.2,6 ,2 ), c(2.5,3.5,2.5), lty = 2, lwd = 0.75)
text(2, -.1, quote(phi[2][]))
arrows(c(2.2, 2.4), 2.5,
     c(2.0, 2.6), 2.5, length = 0.08, angle = 25)
text( 2.3, 2.5, quote(phi[3])); text(2.7, 3, "1")
```
Self-Starting Nls Michaelis-Menten Model

Description

This `selfStart` model evaluates the Michaelis-Menten model and its gradient. It has an initial attribute that will evaluate initial estimates of the parameters $V_m$ and $K$.

Usage

```r
SSmicmen(input, Vm, K)
```

Arguments

- `input`: a numeric vector of values at which to evaluate the model.
- `Vm`: a numeric parameter representing the maximum value of the response.
- `K`: a numeric parameter representing the input value at which half the maximum response is attained. In the field of enzyme kinetics this is called the Michaelis parameter.

Value

A numeric vector of the same length as `input`. It is the value of the expression $V_m \times \text{input} / (K + \text{input})$. If both the arguments `Vm` and `K` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

Author(s)

José Pinheiro and Douglas Bates

See Also

`nls`, `selfStart`

Examples

```r
PurTrt <- Puromycin[Puromycin$state == "treated", ]
SSmicmen(PurTrt$conc, 200, 0.05) # response only
local({
  Vm <- 200; K <- 0.05
  SSmicmen(PurTrt$conc, Vm, K) # response _and_ gradient
})
print(getInitial(rate ~ SSmicmen(conc, Vm, K), data = PurTrt), digits = 3)
## Initial values are in fact the converged values
fm1 <- nls(rate ~ SSmicmen(conc, Vm, K), data = PurTrt)
summary(fm1)
## Alternative call using the subset argument
fm2 <- nls(rate ~ SSmicmen(conc, Vm, K), data = Puromycin, subset = state == "treated")
summary(fm2) # The same indeed:
stopifnot(all.equal(coef(summary(fm1)), coef(summary(fm2))))
```
## Visualize the SSmicmen() Michaelis-Menton model parametrization:

```r
xx <- seq(0, 5, length.out = 101)
yy <- 5 * xx/(1+xx)
stopifnot(all.equal(yy, SSmicmen(xx, Vm = 5, K = 1)))
require(graphics)
op <- par(mar = c(0, 0, 3.5, 0))
plot(xx, yy, type = "l", lwd = 2, ylim = c(-1/4,6), xlim = c(-1, 5),
     ann = FALSE, axes = FALSE, main = "Parameters in the SSmicmen model")
usr <- par("usr")
arrows(usr[1], 0, usr[2], 0, length = 0.1, angle = 25)
arrows(0, usr[3], 0, usr[4], length = 0.1, angle = 25)
text(usr[2] - 0.2, 0.1, "x", adj = c(1, 0))
text(-0.1, usr[4], "y", adj = c(1, 1))
abline(h = 5, lty = 3)
arrows(-0.8, c(2.1, 2.9),
      -0.8, c(0, 5 ), length = 0.1, angle = 25)
text( -0.8, 2.5, quote(phi[1]))
segments(1, 0, 1, 2.7, lty = 2, lwd = 0.75)
text(1, 2.7, quote(phi[2]))
par(op)
```

---

### SSweibull

**Self-Starting Nls Weibull Growth Curve Model**

**Description**

This `selfStart` model evaluates the Weibull model for growth curve data and its gradient. It has an initial attribute that will evaluate initial estimates of the parameters `Asym`, `Drop`, `lrc`, and `pwr` for a given set of data.

**Usage**

```r
SSweibull(x, Asym, Drop, lrc, pwr)
```

**Arguments**

- **x**: a numeric vector of values at which to evaluate the model.
- **Asym**: a numeric parameter representing the horizontal asymptote on the right side (very small values of `x`).
- **Drop**: a numeric parameter representing the change from `Asym` to the `y` intercept.
- **lrc**: a numeric parameter representing the natural logarithm of the rate constant.
- **pwr**: a numeric parameter representing the power to which `x` is raised.

**Details**

This model is a generalization of the `SSasymp` model in that it reduces to `SSasymp` when `pwr` is unity.
Value

A numeric vector of the same length as \( x \). It is the value of the expression
\[
\text{Asym} \cdot \text{Drop} \cdot \exp(-\exp(\text{lrc}) \cdot x^{\text{pwr}}).
\]
If all of the arguments \( \text{Asym} \), \( \text{Drop} \), \( \text{lrc} \), and \( \text{pwr} \) are names of objects, the gradient matrix with respect to these names is attached as an attribute named \text{gradient}.

Author(s)

Douglas Bates

References


See Also

\textit{nls}, \textit{selfStart}, \textit{SSasymp}

Examples

\begin{verbatim}
Chick.6 <- subset(ChickWeight, (Chick == 6) & (Time > 0))
SSweibull(Chick.6$Time, 160, 115, -5.5, 2.5)  # response only
local({
  Asym <- 160; Drop <- 115; lrc <- -5.5; pwr <- 2.5
  SSweibull(Chick.6$Time, Asym, Drop, lrc, pwr)  # response _and_ gradient
})
## IGNORE_RDIFF_BEGIN
getInitial(weight ~ SSweibull(Time, Asym, Drop, lrc, pwr), data = Chick.6)
## IGNORE_RDIFF_END
## Initial values are in fact the converged values
fm1 <- nls(weight ~ SSweibull(Time, Asym, Drop, lrc, pwr), data = Chick.6)
summary(fm1)
## Data and Fit:
plot(weight ~ Time, Chick.6, xlim = c(0, 21), main = "SSweibull() fit to Chick.6")
ux <- par("usr")[1:2]; x <- seq(ux[1], ux[2], length.out=250)
lines(x, do.call(SSweibull, c(list(x=x), coef(fm1))), col = "red", lwd=2)
As <- coef(fm1)["Asym"]; abline(v = 0, h = c(As, As - coef(fm1)["Drop"]), lty = 3)
\end{verbatim}

Description

Extract and encode the times the first and last observations were taken. Provided only for compatibility with S version 2.

Usage

\begin{verbatim}
start(x, ...)
end(x, ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \text{start} \quad \text{a univariate or multivariate time-series, or a vector or matrix.}
  \item \text{...} \quad \text{extra arguments for future methods.}
\end{itemize}
Details

These are generic functions, which will use the \texttt{tsp} attribute of \texttt{x} if it exists. Their default methods decode the start time from the original time units, so that for a monthly series \texttt{1995.5} is represented as \texttt{c(1995, 7)}. For a series of frequency \texttt{f}, time \texttt{n+i/f} is presented as \texttt{c(n, i+1)} (even for \texttt{i = 0} and \texttt{f = 1}).

Warning

The representation used by \texttt{start} and \texttt{end} has no meaning unless the frequency is supplied.

See Also
\texttt{ts}, \texttt{time}, \texttt{tsp}.

\begin{tabular}{ll}
\texttt{stat.anova} & \textit{GLM Anova Statistics} \\
\end{tabular}

Description

This is a utility function, used in \texttt{lm} and \texttt{glm} methods for \texttt{anova(..., test ! = NULL)} and should not be used by the average user.

Usage

\begin{verbatim}
stat.anova(table, test = c("Rao","LRT", "Chisq", "F", "Cp"),
            scale, df.scale, n)
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{table} \hspace*{1cm} numeric matrix as results from \texttt{anova.glm(..., test = NULL)}.
\item \texttt{test} \hspace*{1cm} a character string, partially matching one of "Rao", "LRT", "Chisq", "F" or "Cp".
\item \texttt{scale} \hspace*{1cm} a residual mean square or other scale estimate to be used as the denominator in an F test.
\item \texttt{df.scale} \hspace*{1cm} degrees of freedom corresponding to \texttt{scale}.
\item \texttt{n} \hspace*{1cm} number of observations.
\end{itemize}

Value

A matrix which is the original \texttt{table}, augmented by a column of test statistics, depending on the \texttt{test} argument.

References


See Also
\texttt{anova.lm}, \texttt{anova.glm}. 

\texttt{stat.anova}
Examples

```r
##-- Continued from '?glm':
print(ag <- anova(glm.D93))
stat.anova(ag$table, test = "Cp",
           scale = sum(resid(glm.D93, "pearson")^2)/4,
           df.scale = 4, n = 9)
```

Description

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as the next release.

Details

There are currently no deprecated functions in this package.

See Also

`Deprecated`

---

step

Choose a model by AIC in a Stepwise Algorithm

Description

Select a formula-based model by AIC.

Usage

```r
step(object, scope, scale = 0,
     direction = c("both", "backward", "forward"),
     trace = 1, keep = NULL, steps = 1000, k = 2, ...)
```

Arguments

- `object` an object representing a model of an appropriate class (mainly "lm" and "glm"). This is used as the initial model in the stepwise search.
- `scope` defines the range of models examined in the stepwise search. This should be either a single formula, or a list containing components `upper` and `lower`, both formulae. See the details for how to specify the formulae and how they are used.
- `scale` used in the definition of the AIC statistic for selecting the models, currently only for `lm`, `aov` and `glm` models. The default value, 0, indicates the scale should be estimated: see `extractAIC`.
direction

the mode of stepwise search, can be one of "both", "backward", or "forward", with a default of "both". If the scope argument is missing the default for direction is "backward". Values can be abbreviated.

trace

if positive, information is printed during the running of step. Larger values may give more detailed information.

keep

a filter function whose input is a fitted model object and the associated AIC statistic, and whose output is arbitrary. Typically keep will select a subset of the components of the object and return them. The default is not to keep anything.

steps

the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early.

k

do the multiple of the number of degrees of freedom used for the penalty. Only k = 2 gives the genuine AIC: k = log(n) is sometimes referred to as BIC or SBC.

... any additional arguments to extractAIC.

Details

step uses add1 and drop1 repeatedly; it will work for any method for which they work, and that is determined by having a valid method for extractAIC. When the additive constant can be chosen so that AIC is equal to Mallows’ Cp, this is done and the tables are labelled appropriately.

The set of models searched is determined by the scope argument. The right-hand-side of its lower component is always included in the model, and right-hand-side of the model is included in the upper component. If scope is a single formula, it specifies the upper component, and the lower model is empty. If scope is missing, the initial model is used as the upper model.

Models specified by scope can be templates to update object as used by update.formula. So using . in a scope formula means ‘what is already there’, with .^2 indicating all interactions of existing terms.

There is a potential problem in using glm fits with a variable scale, as in that case the deviance is not simply related to the maximized log-likelihood. The "glm" method for function extractAIC makes the appropriate adjustment for a gaussian family, but may need to be amended for other cases. (The binomial and poisson families have fixed scale by default and do not correspond to a particular maximum-likelihood problem for variable scale.)

Value

the stepwise-selected model is returned, with up to two additional components. There is an "anova" component corresponding to the steps taken in the search, as well as a "keep" component if the keep argument was supplied in the call. The "Resid. Dev" column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood: it will be a deviance only in cases where a saturated model is well-defined (thus excluding lm, aov and survreg fits, for example).

Warning

The model fitting must apply the models to the same dataset. This may be a problem if there are missing values and R’s default of na.action = na.omit is used. We suggest you remove the missing values first.

Calls to the function nobs are used to check that the number of observations involved in the fitting process remains unchanged.
Note

This function differs considerably from the function in S, which uses a number of approximations and does not in general compute the correct AIC.

This is a minimal implementation. Use stepAIC in package MASS for a wider range of object classes.

Author(s)

B. D. Ripley: step is a slightly simplified version of stepAIC in package MASS (Venables & Ripley, 2002 and earlier editions).

The idea of a step function follows that described in Hastie & Pregibon (1992); but the implementation in R is more general.

References


See Also

stepAIC in MASS, add1, drop1

Examples

## following on from example(lm)

step(lm.D9)

summary(lm1 <- lm(Fertility ~ ., data = swiss))

slm1 <- step(lm1)

summary(slm1)

slm1$anova

---

stepfun

Step Functions - Creation and Class

Description

Given the vectors \((x_1, \ldots, x_n)\) and \((y_0, y_1, \ldots, y_n)\) (one value more!), \texttt{stepfun}(x, y, ...) returns an interpolating ‘step’ function, say \texttt{fn}. I.e., \(fn(t) = c_i\) (constant) for \(t \in (x_i, x_{i+1})\) and at the abscissa values, if (by default) \texttt{right = FALSE}, \(fn(x_i) = y_i\) and for \texttt{right = TRUE}, \(fn(x_i) = y_{i-1}\), for \(i = 1, \ldots, n\).

The value of the constant \(c_i\) above depends on the ‘continuity’ parameter \(f\). For the default, \texttt{right = FALSE}, \(f = 0\), \texttt{fn} is a \texttt{cadlag} function, i.e., continuous from the right, limits from the left, so that the function is piecewise constant on intervals that include their left endpoint. In general, \(c_i\) is interpolated in between the neighbouring \(y\) values, \(c_i = (1 - f)y_i + f \cdot y_{i+1}\). Therefore, for non-0 values of \(f\), \texttt{fn} may no longer be a proper step function, since it can be discontinuous from both sides, unless \texttt{right = TRUE}, \(f = 1\) which is left-continuous (i.e., constant pieces contain their right endpoint).
Usage

```r
stepfun(x, y, f = as.numeric(right), ties = "ordered",
       right = FALSE)
```

```r
is.stepfun(x)
knots(Fn, ...)
as.stepfun(x, ...)
```

```r
## S3 method for class 'stepfun'
print(x, digits = getOption("digits") - 2, ...)
```

```r
## S3 method for class 'stepfun'
summary(object, ...)
```

Arguments

- **x**: numeric vector giving the knots or jump locations of the step function for `stepfun()`. For the other functions, `x` is as object below.
- **y**: numeric vector one longer than `x`, giving the heights of the function values between the `x` values.
- **f**: a number between 0 and 1, indicating how interpolation outside the given `x` values should happen. See `approxfun`.
- **ties**: Handling of tied `x` values. Either a function or the string "ordered". See `approxfun`.
- **right**: logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
- **Fn, object**: an R object inheriting from "stepfun".
- **digits**: number of significant digits to use, see `print`.
- **...**: potentially further arguments (required by the generic).

Value

A function of class "stepfun", say `fn`.

There are methods available for summarizing ("summary(.)"), representing ("print(.)") and plotting ("plot(.)", see `plot.stepfun") "stepfun" objects.

The environment of `fn` contains all the information needed:

- "x","y" the original arguments
- "n" number of knots (x values)
- "f" continuity parameter
- "yleft","yright" the function values outside the knots
- "method" (always == "constant", from `approxfun(.)`.

The knots are also available via `knots(fn)`.
Note

The objects of class "stepfun" are not intended to be used for permanent storage and may change structure between versions of R (and did at R 3.0.0). They can usually be re-created by

```
  eval(attr(old_obj, "call"), environment(old_obj))
```

since the data used is stored as part of the object’s environment.

Author(s)

Martin Maechler, <maechler@stat.math.ethz.ch> with some basic code from Thomas Lumley.

See Also

ecdf for empirical distribution functions as special step functions and plot.stepfun for plotting step functions.

approxfun and splinefun.

Examples

```
y0 <- c(1., 2., 4., 3.)
sfun0 <- stepfun(1:3, y0, f = 0)
sfun.2 <- stepfun(1:3, y0, f = 0.2)
sfun1 <- stepfun(1:3, y0, f = 1)
sfun1c <- stepfun(1:3, y0, right = TRUE) # hence f=1
sfun0
summary(sfun0)
summary(sfun.2)

## look at the internal structure:
unclass(sfun0)
ls(envir = environment(sfun0))

x0 <- seq(0.5, 3.5, by = 0.25)
rbind(x = x0, f.f0 = sfun0(x0), f.f02 = sfun.2(x0),
     f.f1 = sfun1(x0), f.f1c = sfun1c(x0))

## Identities :
stopifnot(identical(y0[-1], sfun0 (1:3)), # right = FALSE
          identical(y0[-4], sfun1c(1:3))) # right = TRUE
```

---

### stl

**Seasonal Decomposition of Time Series by Loess**

**Description**

Decompose a time series into seasonal, trend and irregular components using loess, acronym STL.
Usage

```r
stl(x, s.window, s.degree = 0,
    t.window = NULL, t.degree = 1,
    l.window = nextodd(period), l.degree = t.degree,
    s.jump = ceiling(s.window/10),
    t.jump = ceiling(t.window/10),
    l.jump = ceiling(l.window/10),
    robust = FALSE,
    inner = if(robust) 1 else 2,
    outer = if(robust) 15 else 0,
    na.action = na.fail)
```

Arguments

- **x**: univariate time series to be decomposed. This should be an object of class "ts" with a frequency greater than one.
- **s.window**: either the character string "periodic" or the span (in lags) of the loess window for seasonal extraction, which should be odd and at least 7, according to Cleveland et al. This has no default.
- **s.degree**: degree of locally-fitted polynomial in seasonal extraction. Should be zero or one.
- **t.window**: the span (in lags) of the loess window for trend extraction, which should be odd. If NULL, the default, `nextodd(ceiling((1.5*period) / (1-(1.5/s.window))))`, is taken.
- **t.degree**: degree of locally-fitted polynomial in trend extraction. Should be zero or one.
- **l.window**: the span (in lags) of the loess window of the low-pass filter used for each subseries. Defaults to the smallest odd integer greater than or equal to `frequency(x)` which is recommended since it prevents competition between the trend and seasonal components. If not an odd integer its given value is increased to the next odd one.
- **l.degree**: degree of locally-fitted polynomial for the subseries low-pass filter. Must be 0 or 1.
- **s.jump, t.jump, l.jump**: integers at least one to increase speed of the respective smoother. Linear interpolation happens between every *, jumppth value.
- **robust**: logical indicating if robust fitting be used in the `loess` procedure.
- **inner**: integer; the number of ‘inner’ (backfitting) iterations; usually very few (2) iterations suffice.
- **outer**: integer; the number of ‘outer’ robustness iterations.
- **na.action**: action on missing values.

Details

The seasonal component is found by `loess` smoothing the seasonal sub-series (the series of all January values, ...); if `s.window = "periodic"` smoothing is effectively replaced by taking the mean. The seasonal values are removed, and the remainder smoothed to find the trend. The overall level is removed from the seasonal component and added to the trend component. This process is iterated a few times. The remainder component is the residuals from the seasonal plus trend fit.

Several methods for the resulting class "stl" objects, see, `plot.stl`.
Value

*stl* returns an object of class "*stl" with components

- **time.series**: a multiple time series with columns seasonal, trend and remainder.
- **weights**: the final robust weights (all one if fitting is not done robustly).
- **call**: the matched call.
- **win**: integer (length 3 vector) with the spans used for the "s", "t", and "l" smoothers.
- **deg**: integer (length 3) vector with the polynomial degrees for these smoothers.
- **jump**: integer (length 3) vector with the 'jumps' (skips) used for these smoothers.
- **ni**: number of inner iterations
- **no**: number of outer robustness iterations

Note

This is similar to but not identical to the *stl* function in S-PLUS. The remainder component given by S-PLUS is the sum of the trend and remainder series from this function.

Author(s)

B.D. Ripley; Fortran code by Cleveland et al (1990) from 'netlib'.

References


See Also

- `plot.stl` for *stl* methods; `loess` in package stats (which is not actually used in *stl*).
- `StructTS` for different kind of decomposition.

Examples

```r
require(graphics)

plot(stl(nottem, "per"))
plot(stl(nottem, s.window = 7, t.window = 50, t.jump = 1))

plot(stllc <- stl(log(co2), s.window = 21))
summary(stllc)
## linear trend, strict period.
plot(stl(log(co2), s.window = "per", t.window = 1000))

## Two STL plotted side by side :
  stdm <- stl(mdeaths, s.window = "per") # non-robust
summary(stmR <- stl(mdeaths, s.window = "per", robust = TRUE))
op <- par(mar = c(0, 4, 0, 3), oma = c(5, 0, 4, 0), mfcol = c(4, 2))
plot(stdm, set.pars = NULL, labels = NULL, main = "stl(mdeaths, s.w = \"per\")")
plot(stmR, set.pars = NULL)
# mark the 'outliers' :
```

```
stlmethods

Methods for STL Objects

Description

Methods for objects of class stl, typically the result of stl. The plot method does a multiple figure plot with some flexibility.

There are also (non-visible) print and summary methods.

Usage

## S3 method for class 'stl'
plot(x, labels = colnames(X),
     set.pars = list(mar = c(0, 6, 0, 6), oma = c(6, 0, 4, 0),
                    tck = -0.01, mfrow = c(nplot, 1)),
     main = NULL, range.bars = TRUE, ...,
     col.range = "light gray")

Arguments

x stl object.
labels character of length 4 giving the names of the component time-series.
set.pars settings for par(.) when setting up the plot.
main plot main title.
range.bars logical indicating if each plot should have a bar at its right side which are of equal heights in user coordinates.
... further arguments passed to or from other methods.
col.range colour to be used for the range bars, if plotted. Note this appears after ... and so cannot be abbreviated.

See Also

plot.ts and stl, particularly for examples.
**StructTS**  
*Fit Structural Time Series*

**Description**
Fit a structural model for a time series by maximum likelihood.

**Usage**
```r
StructTS(x, type = c("level", "trend", "BSM"), init = NULL, fixed = NULL, optim.control = NULL)
```

**Arguments**
- `x`: a univariate numeric time series. Missing values are allowed.
- `type`: the class of structural model. If omitted, a BSM is used for a time series with `frequency(x) > 1`, and a local trend model otherwise. Can be abbreviated.
- `init`: initial values of the variance parameters.
- `fixed`: optional numeric vector of the same length as the total number of parameters. If supplied, only `NA` entries in `fixed` will be varied. Probably most useful for setting variances to zero.
- `optim.control`: List of control parameters for `optim`. Method "L-BFGS-B" is used.

**Details**
*Structural time series* models are (linear Gaussian) state-space models for (univariate) time series based on a decomposition of the series into a number of components. They are specified by a set of error variances, some of which may be zero.

The simplest model is the *local level* model specified by `type = "level"`. This has an underlying level \( \mu_t \) which evolves by

\[
\mu_{t+1} = \mu_t + \xi_t, \quad \xi_t \sim N(0, \sigma_{\xi}^2)
\]

The observations are

\[
x_t = \mu_t + \epsilon_t, \quad \epsilon_t \sim N(0, \sigma_{\epsilon}^2)
\]

There are two parameters, \( \sigma_{\xi}^2 \) and \( \sigma_{\epsilon}^2 \). It is an ARIMA(0,1,1) model, but with restrictions on the parameter set.

The *local linear trend model*, `type = "trend"`, has the same measurement equation, but with a time-varying slope in the dynamics for \( \mu_t \), given by

\[
\mu_{t+1} = \mu_t + \nu_t + \xi_t, \quad \xi_t \sim N(0, \sigma_{\xi}^2)
\]

\[
\nu_{t+1} = \nu_t + \zeta_t, \quad \zeta_t \sim N(0, \sigma_{\zeta}^2)
\]

with three variance parameters. It is not uncommon to find \( \sigma_{\zeta}^2 = 0 \) (which reduces to the local level model) or \( \sigma_{\xi}^2 = 0 \), which ensures a smooth trend. This is a restricted ARIMA(0,2,2) model.

The *basic structural model*, `type = "BSM"`, is a local trend model with an additional seasonal component. Thus the measurement equation is

\[
x_t = \mu_t + \gamma_t + \epsilon_t, \quad \epsilon_t \sim N(0, \sigma_{\epsilon}^2)
\]
where \( \gamma_t \) is a seasonal component with dynamics

\[
\gamma_{t+1} = -\gamma_t + \cdots + \gamma_{t-s+2} + \omega_t, \quad \omega_t \sim N(0, \sigma^2_{\omega})
\]

The boundary case \( \sigma^2_{\omega} = 0 \) corresponds to a deterministic (but arbitrary) seasonal pattern. (This is sometimes known as the ‘dummy variable’ version of the BSM.)

**Value**

A list of class "StructTS" with components:

- **coef**
  - the estimated variances of the components.

- **loglik**
  - the maximized log-likelihood. Note that as all these models are non-stationary this includes a diffuse prior for some observations and hence is not comparable to `arima` nor different types of structural models.

- **loglik0**
  - the maximized log-likelihood with the constant used prior to \( R 3.0.0 \), for backwards compatibility.

- **data**
  - the time series \( x \).

- **residuals**
  - the standardized residuals.

- **fitted**
  - a multiple time series with one component for the level, slope and seasonal components, estimated contemporaneously (that is at time \( t \) and not at the end of the series).

- **call**
  - the matched call.

- **series**
  - the name of the series \( x \).

- **code**
  - the convergence code returned by `optim`.

- **model, model0**
  - Lists representing the Kalman Filter used in the fitting. See `KalmanLike`.

- **xtsp**
  - the tsp attributes of \( x \).

**Note**

Optimization of structural models is a lot harder than many of the references admit. For example, the `AirPassengers` data are considered in Brockwell & Davis (1996): their solution appears to be a local maximum, but nowhere near as good a fit as that produced by `StructTS`. It is quite common to find fits with one or more variances zero, and this can include \( \sigma^2_{\epsilon} \).

**References**


**See Also**

- `KalmanLike`, `tsSmooth`; `stl` for different kind of (seasonal) decomposition.
### Examples

```r
## see also JohnsonJohnson, Nile and AirPassengers
require(graphics)

trees <- window(treering, start = 0)
(fit <- StructTS(trees, type = "level"))
plot(trees)
lines(fitted(fit), col = "green")
tsdia(fit)

(fit <- StructTS(log10(UKgas), type = "BSM"))
par(mfrow = c(4, 1)) # to give appropriate aspect ratio for next plot.
plot(log10(UKgas))
plot(cbind(fitted(fit), resids=resid(fit)), main = "UK gas consumption")

## keep some parameters fixed; trace optimizer:
StructTS(log10(UKgas), type = "BSM", fixed = c(0.1,0.001,NA,NA),
          optim.control = list(trace = TRUE))
```

### summary.aov

**Summary an Analysis of Variance Model**

**Description**

Summarize an analysis of variance model.

**Usage**

```r
## S3 method for class 'aov'
summary(object, intercept = FALSE, split,
         expand.split = TRUE, keep.zero.df = TRUE, ...)

## S3 method for class 'aovlist'
summary(object, ...)
```

**Arguments**

- `object` 
  An object of class "aov" or "aovlist".
- `intercept` 
  logical: should intercept terms be included?
- `split` 
  an optional named list, with names corresponding to terms in the model. Each component is itself a list with integer components giving contrasts whose contributions are to be summed.
- `expand.split` 
  logical: should the split apply also to interactions involving the factor?
- `keep.zero.df` 
  logical: should terms with no degrees of freedom be included?
- `...` 
  Arguments to be passed to or from other methods, for `summary.aovlist` including those for `summary.aov`.

**Value**

An object of class c("summary.aov", "listof") or "summary.aovlist" respectively.

For fits with a single stratum the result will be a list of ANOVA tables, one for each response (even if there is only one response): the tables are of class "anova" inheriting from class "data.frame". They have columns "Df", "Sum Sq", "Mean Sq", as well as "F value" and "Pr(>F)" if there are non-zero residual degrees of freedom. There is a row for each term in the model, plus one for "Residuals" if there are any.

For multistratum fits the return value is a list of such summaries, one for each stratum.

**Note**

The use of expand.split = TRUE is little tested: it is always possible to set it to FALSE and specify exactly all the splits required.

**See Also**

aov, summary, model.tables, TukeyHSD

**Examples**

```r
## For a simple example see example(aov)

# Cochran and Cox (1957, p.164)
# 3x3 factorial with ordered factors, each is average of 12.
CC <- data.frame(
  y = c(449, 413, 326, 409, 358, 291, 341, 278, 312)/12,
  P = ordered(gl(3, 3)),
  N = ordered(gl(3, 1, 9))
)
CC.aov <- aov(y ~ N * P, data = CC , weights = rep(12, 9))
summary(CC.aov)

# Split both main effects into linear and quadratic parts.
summary(CC.aov, split = list(N = list(L = 1, Q = 2),
                              P = list(L = 1, Q = 2)))

# Split only the interaction
summary(CC.aov, split = list("N:P" = list(L.L = 1, Q = 2:4)))

# split on just one var
summary(CC.aov, split = list(P = list(lin = 1, quad = 2)))
summary(CC.aov, split = list(P = list(lin = 1, quad = 2)), expand.split = FALSE)
```

---

**summary.glm**  
*Summarizing Generalized Linear Model Fits*

**Description**

These functions are all methods for class glm or summary.glm objects.
## S3 method for class 'glm'
summary(object, dispersion = NULL, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.glm'
print(x, digits = max(3, getOption("digits") - 3), symbolic.cor = x$symbolic.cor, signif.stars = getOption("show.signif.stars"), show.residuals = FALSE, ...)

### Arguments

**object**   
an object of class "glm", usually, a result of a call to glm.

**x**   
an object of class "summary.glm", usually, a result of a call to summary.glm.

**dispersion**   
the dispersion parameter for the family used. Either a single numerical value or NULL (the default), when it is inferred from object (see ‘Details’).

**correlation**   
logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.

**digits**   
the number of significant digits to use when printing.

**symbolic.cor**   
logical. If TRUE, print the correlations in a symbolic form (see symnum) rather than as numbers.

**signif.stars**   
logical. If TRUE, ‘significance stars’ are printed for each coefficient.

**show.residuals**   
logical. If TRUE then a summary of the deviance residuals is printed at the head of the output.

**...**   
further arguments passed to or from other methods.

### Details

print.summary.glm tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives ‘significance stars’ if signif.stars is TRUE. The coefficients component of the result gives the estimated coefficients and their estimated standard errors, together with their ratio. This third column is labelled t ratio if the dispersion is estimated, and z ratio if the dispersion is known (or fixed by the family). A fourth column gives the two-tailed p-value corresponding to the t or z ratio based on a Student t or Normal reference distribution. (It is possible that the dispersion is not known and there are no residual degrees of freedom from which to estimate it. In that case the estimate is NaN.)

Aliased coefficients are omitted in the returned object but restored by the print method.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print summary(object)$correlation directly.

The dispersion of a GLM is not used in the fitting process, but it is needed to find standard errors. If dispersion is not supplied or NULL, the dispersion is taken as 1 for the binomial and Poisson families, and otherwise estimated by the residual Chisquared statistic (calculated from cases with non-zero weights) divided by the residual degrees of freedom.

summary can be used with Gaussian glm fits to handle the case of a linear regression with known error variance, something not handled by summary.lm.
Summary method for class "lm".

Usage

## S3 method for class 'lm'
summary(object, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.lm'
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
Arguments

- **object**: an object of class "lm", usually, a result of a call to lm.
- **x**: an object of class "summary.lm", usually, a result of a call to summary.lm.
- **correlation**: logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
- **digits**: the number of significant digits to use when printing.
- **symbolic.cor**: logical. If TRUE, print the correlations in a symbolic form (see symnum) rather than as numbers.
- **signif.stars**: logical. If TRUE, ‘significance stars’ are printed for each coefficient.
- **...**: further arguments passed to or from other methods.

Details

- print.summary.lm tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives ‘significance stars’ if signif.stars is TRUE.
- Aliased coefficients are omitted in the returned object but restored by the print method.
- Correlations are printed to two decimal places (or symbolically): to see the actual correlations print summary(object)$correlation directly.

Value

- The function summary.lm computes and returns a list of summary statistics of the fitted linear model given in object, using the components (list elements) "call" and "terms" from its argument, plus
- **residuals**: the weighted residuals, the usual residuals rescaled by the square root of the weights specified in the call to lm.
- **coefficients**: a p × 4 matrix with columns for the estimated coefficient, its standard error, t-statistic and corresponding (two-sided) p-value. Aliased coefficients are omitted.
- **aliased**: named logical vector showing if the original coefficients are aliased.
- **sigma**: the square root of the estimated variance of the random error
  \[ \hat{\sigma}^2 = \frac{1}{n - p} \sum_i w_i R_i^2, \]
  where \( R_i \) is the i-th residual, residuals[i].
- **df**: degrees of freedom, a 3-vector \((p, n - p, p^*)\), the first being the number of non-aliased coefficients, the last being the total number of coefficients.
- **fstatistic**: (for models including non-intercept terms) a 3-vector with the value of the F-statistic with its numerator and denominator degrees of freedom.
- **r.squared**: \( R^2 \), the ‘fraction of variance explained by the model’,
  \[ R^2 = 1 - \frac{\sum_i R_i^2}{\sum_i (y_i - y^*)^2}, \]
  where \( y^* \) is the mean of \( y_i \) if there is an intercept and zero otherwise.
- **adj.r.squared**: the above \( R^2 \) statistic ‘adjusted’, penalizing for higher \( p \).
- **cov.unscaled**: a \( p \times p \) matrix of (unscaled) covariances of the \( \hat{\beta}_j, j = 1, \ldots, p \).
- **correlation**: the correlation matrix corresponding to the above cov.unscaled, if correlation = TRUE is specified.
- **symbolic.cor**: (only if correlation is true.) The value of the argument symbolic.cor.
- **na.action**: from object, if present there.
See Also

The model fitting function \texttt{lm}, \texttt{summary}.

Function \texttt{coef} will extract the matrix of coefficients with standard errors, t-statistics and p-values.

Examples

```r
##-- Continuing the lm(.) example:
coef(lm.D90) # the bare coefficients
sld90 <- summary(lm.D90 <- lm(weight ~ group -1)) # omitting intercept
coef(sld90) # much more

## model with *aliased* coefficient:
lm.D9. <- lm(weight ~ group + I(group != "Ctl"))
Sm.D9. <- summary(lm.D9.)
Sm.D9. # shows the NA NA NA NA line
stopifnot(length(cc <- coef(lm.D9.)) == 3, is.na(cc[3]),
  dim(coef(Sm.D9.)) == c(2,4), Sm.D9.$df == c(2, 18, 3))
```

\texttt{summary.manova} \hspace{1cm} \textit{Summary Method for Multivariate Analysis of Variance}

Description

A summary method for class "manova".

Usage

```r
## S3 method for class 'manova'
summary(object,
  test = c("Pillai", "Wilks", "Hotelling-Lawley", "Roy"),
  intercept = FALSE, tol = 1e-7, ...)
```

Arguments

- \texttt{object} An object of class "manova" or an \texttt{aov} object with multiple responses.
- \texttt{test} The name of the test statistic to be used. Partial matching is used so the name can be abbreviated.
- \texttt{intercept} logical. If \texttt{TRUE}, the intercept term is included in the table.
- \texttt{tol} tolerance to be used in deciding if the residuals are rank-deficient: see \texttt{qr}.
- \texttt{...} further arguments passed to or from other methods.

Details

The \texttt{summary.manova} method uses a multivariate test statistic for the summary table. Wilks’ statistic is most popular in the literature, but the default Pillai–Bartlett statistic is recommended by Hand and Taylor (1987).

The table gives a transformation of the test statistic which has approximately an F distribution. The approximations used follow S-PLUS and SAS (the latter apart from some cases of the Hotelling-Lawley statistic), but many other distributional approximations exist: see Anderson (1984) and
Krzanowski and Marriott (1994) for further references. All four approximate F statistics are the same when the term being tested has one degree of freedom, but in other cases that for the Roy statistic is an upper bound.

The tolerance tol is applied to the QR decomposition of the residual correlation matrix (unless some response has essentially zero residuals, when it is unscaled). Thus the default value guards against very highly correlated responses: it can be reduced but doing so will allow rather inaccurate results and it will normally be better to transform the responses to remove the high correlation.

Value

An object of class "summary.manova". If there is a positive residual degrees of freedom, this is a list with components

- **row.names**: The names of the terms, the row names of the stats table if present.
- **SS**: A named list of sums of squares and product matrices.
- **Eigenvalues**: A matrix of eigenvalues.
- **stats**: A matrix of the statistics, approximate F value, degrees of freedom and P value.

otherwise components row.names, SS and Df (degrees of freedom) for the terms (and not the residuals).

References


See Also

- manova, aov

Examples

```r
## Example on producing plastic film from Krzanowski (1998, p. 381)
tear <- c(6.5, 6.2, 5.8, 6.5, 6.5, 6.9, 7.2, 6.9, 6.1, 6.3, 6.7, 6.6, 7.2, 7.1, 6.8, 7.1, 7.0, 7.2, 7.5, 7.6)
gloss <- c(9.5, 9.9, 9.6, 9.6, 9.2, 9.1, 10.0, 9.9, 9.5, 9.4, 9.1, 9.3, 8.3, 8.4, 8.5, 9.2, 8.8, 9.7, 10.1, 9.2)
opacity <- c(4.4, 6.4, 3.0, 4.1, 0.8, 5.7, 2.0, 3.9, 1.9, 5.7, 2.8, 4.1, 3.8, 1.6, 3.4, 8.4, 5.2, 6.9, 2.7, 1.9)
Y <- cbind(tear, gloss, opacity)
rate <- gl(2,10, labels = c("Low", "High"))
additive <- gl(2, 5, length = 20, labels = c("Low", "High"))

Y <- cbind(tear, gloss, opacity)
rate <- gl(2,10, labels = c("Low", "High"))
additive <- gl(2, 5, length = 20, labels = c("Low", "High"))

fit <- manova(Y ~ rate * additive)
summary.aov(fit) # univariate ANOVA tables
summary(fit, test = "Wilks") # ANOVA table of Wilks' lambda
summary(fit) # same F statistics as single-df terms
```
Summary

**Summary.nls**  

**Summary.nls**  

**Summarizing Non-Linear Least-Squares Model Fits**

**Description**

Summary method for class "nls".

**Usage**

```r
## S3 method for class 'nls'
summary(object, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.nls'
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
```

**Arguments**

- `object`: an object of class "nls".
- `x`: an object of class "summary.nls", usually the result of a call to `summary.nls`.
- `correlation`: logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
- `digits`: the number of significant digits to use when printing.
- `symbolic.cor`: logical. If TRUE, print the correlations in a symbolic form (see `symNum`) rather than as numbers.
- `signif.stars`: logical. If TRUE, 'significance stars' are printed for each coefficient.
- `...`: further arguments passed to or from other methods.

**Details**

The distribution theory used to find the distribution of the standard errors and of the residual standard error (for t ratios) is based on linearization and is approximate, maybe very approximate.

`print.summary.nls` tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if `signif.stars` is TRUE.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print `summary(object)$correlation` directly.

**Value**

The function `summary.nls` computes and returns a list of summary statistics of the fitted model given in `object`, using the component "formula" from its argument, plus

- `residuals`: the weighted residuals, the usual residuals rescaled by the square root of the weights specified in the call to `nls`.
- `coefficients`: a p x 4 matrix with columns for the estimated coefficient, its standard error, t-statistic and corresponding (two-sided) p-value.
The square root of the estimated variance of the random error

\[ \hat{\sigma}^2 = \frac{1}{n-p} \sum_i R_i^2, \]

where \( R_i \) is the \( i \)-th weighted residual.

df
degrees of freedom, a 2-vector \((p, n-p)\). (Here and elsewhere \( n \) omits observations with zero weights.)

cov.unscaled an \( p \times p \) matrix of (unscaled) covariances of the parameter estimates.
correlation the correlation matrix corresponding to the above cov.unscaled, if correlation = TRUE is specified and there are a non-zero number of residual degrees of freedom.
symbolic.cor (only if correlation is true.) The value of the argument symbolic.cor.

See Also

The model fitting function nls, summary.

Function coef will extract the matrix of coefficients with standard errors, t-statistics and p-values.
supsmu

See Also

princomp

Examples

summary(pc.cr <- princomp(USArrests, cor = TRUE))
## The signs of the loading columns are arbitrary
print(summary(princomp(USArrests, cor = TRUE),
            loadings = TRUE, cutoff = 0.2), digits = 2)

supsmu

Friedman’s SuperSmoother

Description

Smooth the (x, y) values by Friedman’s ‘super smoother’.

Usage

supsmu(x, y, wt =, span = "cv", periodic = FALSE, bass = 0, trace = FALSE)

Arguments

x x values for smoothing
y y values for smoothing
wt case weights, by default all equal
span the fraction of the observations in the span of the running lines smoother, or
   “cv” to choose this by leave-one-out cross-validation.
periodic if TRUE, the x values are assumed to be in [0, 1] and of period 1.
bass controls the smoothness of the fitted curve. Values of up to 10 indicate increas-
   ing smoothness.
trace logical, if true, prints one line of info “per spar”, notably useful for "cv".

Details

supsmu is a running lines smoother which chooses between three spans for the lines. The running
lines smoothers are symmetric, with k/2 data points each side of the predicted point, and values of
k as 0.5 * n, 0.2 * n and 0.05 * n, where n is the number of data points. If span is specified, a
single smoother with span span * n is used.

The best of the three smoothers is chosen by cross-validation for each prediction. The best spans are
then smoothed by a running lines smoother and the final prediction chosen by linear interpolation.

The FORTRAN code says: “For small samples (n < 40) or if there are substantial serial correlations
between observations close in x-value, then a pre-specified fixed span smoother (span > 0) should
be used. Reasonable span values are 0.2 to 0.4.”

Cases with non-finite values of x, y or wt are dropped, with a warning.
Value

A list with components

x the input values in increasing order with duplicates removed.
y the corresponding y values on the fitted curve.

References


See Also

ppr

Examples

require(graphics)

with(cars, {
  plot(speed, dist)
  lines(supsmu(speed, dist))
  lines(supsmu(speed, dist, bass = 7), lty = 2)
})

Description

Symbolically encode a given numeric or logical vector or array. Particularly useful for visualization of structured matrices, e.g., correlation, sparse, or logical ones.

Usage

symnum(x, cutpoints = c(0.3, 0.6, 0.8, 0.9, 0.95),
       symbols = if(numeric.x) c(" ", ",", ",", "+", ",x", ",B")
                     else c("", ",!"),
       legend = length(symbols) >= 3,
       na = ",?", eps = 1e-5, numeric.x = is.numeric(x),
       corr = missing(cutpoints) && numeric.x,
       show.max = if(corr) ",1", show.min = NULL,
       abbr.colnames = has.colnames,
       lower.triangular = corr && is.numeric(x) && is.matrix(x),
       diag.lower.tri = corr && !is.null(show.max))
symnum

Arguments

x numeric or logical vector or array.
cutpoints numeric vector whose values cutpoints[j] = c_j (after augmentation, see corr below) are used for intervals.
symbols character vector, one shorter than (the augmented, see corr below) cutpoints. symbols[j] = s_j are used as ‘code’ for the (half open) interval (c_j, c_{j+1}]. When numeric.x is FALSE, i.e., by default when argument x is logical, the default is c(".", "|") (graphical 0 / 1 s).
legend logical indicating if a "legend" attribute is desired.
na character or logical. How NAs are coded. If na == FALSE, NA s are coded invisibly, including the "legend" attribute below, which otherwise mentions NA coding.
eps absolute precision to be used at left and right boundary.
numeric.x logical indicating if x should be treated as numbers, otherwise as logical.
corr logical. If TRUE, x contains correlations. The cutpoints are augmented by 0 and 1 and abs(x) is coded.
show.max if TRUE, or of mode character, the maximal cutpoint is coded especially.
show.min if TRUE, or of mode character, the minimal cutpoint is coded especially.
abbr.colnames logical, integer or NULL indicating how column names should be abbreviated (if they are); if NULL (or FALSE and x has no column names), the column names will all be empty, i.e., ""; otherwise if abbr.colnames is false, they are left unchanged. If TRUE or integer, existing column names will be abbreviated to abbreviate(x, minlength = abbr.colnames).
lower.triangular logical. If TRUE and x is a matrix, only the lower triangular part of the matrix is coded as non-blank.
diag.lower.tri logical. If lower.triangular and this are TRUE, the diagonal part of the matrix is shown.

Value

An atomic character object of class noquote and the same dimensions as x.

If legend is TRUE (as by default when there are more than two classes), the result has an attribute "legend" containing a legend of the returned character codes, in the form

\[ c_1 s_1 c_2 s_2 \ldots s_n c_{n+1} \]

where \( c_j = \text{cutpoints}[j] \) and \( s_j = \text{symbols}[j] \).

Note

The optional (mostly logical) arguments all try to use smart defaults. Specifying them explicitly may lead to considerably improved output in many cases.

Author(s)

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See Also

as.character; image
Examples

```r
ii <- setNames(0:8, 0:8)
symnum(ii, cutpoints = 2*(0:4), symbols = c(".", "-", "+", 
"\$")
symnum(ii, cutpoints = 2*(0:4), symbols = c(".", "-", "+", 
"\$"), show.max = TRUE)
symnum(1:12 %% 3 == 0) # --> ";" = TRUE, "." = FALSE for logical

## Pascal's Triangle modulo 2 -- odd and even numbers:
N <- 38
pascal <- t(sapply(0:N, function(n) round(choose(n, 0:N - (N-n)%/%2))))
rownames(pascal) <- rep("", 1+N) # <-- to improve "graphic"
symnum(pascal %% 2, symbols = c(" ", "A"), numeric.x = FALSE)

##-- Symbolic correlation matrices:
symnum(cor(attitude), diag.lower.tri = FALSE)
symnum(cor(attitude), abbr.colnames = NULL)
symnum(cor(attitude), abbr.colnames = FALSE)
symnum(cor(attitude), abbr.colnames = 2)
symnum(cor(rbind(1, rnorm(25), rnorm(25)*2)))
symnum(cor(matrix(rexp(30, 1), 5, 18))) # <<-- PATTERN ! --
symnum(cm1 <- cor(matrix(rnorm(90) , 5, 18))) # < White Noise SMALL n
symnum(cm1, diag.lower.tri = FALSE)
symnum(cm2 <- cor(matrix(rnorm(900), 50, 18))) # < White Noise "BIG" n
symnum(cm2, lower.triangular = FALSE)

## NA's:
Cm <- cor(matrix(rnorm(60), 10, 6)); Cm[3,6] <- NA
symnum(Cm, show.max = NULL)

## Graphical P-values (aka "significance stars"):
pval <- rev(sort(c(outer(1:6, 10^-(1:3)))))
symp <- symnum(pval, corr = FALSE,
cutpoints = c(0, .001,.01,.05, .1, 1),
symbols = c("***","**","*","." ", ")
noquote(cbind(P.val = format(pval), Signif = symp))
```

---

t.test

**Student's t-Test**

**Description**

Performs one and two sample t-tests on vectors of data.

**Usage**

```r
t.test(x, ...)
```

## Default S3 method:
t.test(x, y = NULL,
alternative = c("two.sided", "less", "greater"),
mu = 0, paired = FALSE, var.equal = FALSE,
conf.level = 0.95, ...)
```
## S3 method for class 'formula'
\texttt{t.test(formula, data, subset, na.action, ...)}

### Arguments

- **x**: a (non-empty) numeric vector of data values.
- **y**: an optional (non-empty) numeric vector of data values.
- **alternative**: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
- **mu**: a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
- **paired**: a logical indicating whether you want a paired t-test.
- **var.equal**: a logical variable indicating whether to treat the two variances as being equal. If TRUE then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.
- **conf.level**: confidence level of the interval.
- **formula**: a formula of the form \texttt{lhs \sim rhs} where \texttt{lhs} is a numeric variable giving the data values and \texttt{rhs} either 1 for a one-sample or paired test or a factor with two levels giving the corresponding groups. If \texttt{lhs} is of class "Pair" and \texttt{rhs} is 1, a paired test is done.
- **data**: an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula \texttt{formula}. By default the variables are taken from \texttt{environment(formula)}.
- **subset**: an optional vector specifying a subset of observations to be used.
- **na.action**: a function which indicates what should happen when the data contain NAs. Defaults to getOption("na.action").
- **...**: further arguments to be passed to or from methods.

### Details

- \texttt{alternative = "greater"} is the alternative that \( x \) has a larger mean than \( y \). For the one-sample case: that the mean is positive.

  If \texttt{paired} is \texttt{TRUE} then both \( x \) and \( y \) must be specified and they must be the same length. Missing values are silently removed (in pairs if \texttt{paired} is \texttt{TRUE}). If \texttt{var.equal} is \texttt{TRUE} then the pooled estimate of the variance is used. By default, if \texttt{var.equal} is \texttt{FALSE} then the variance is estimated separately for both groups and the Welch modification to the degrees of freedom is used.

  If the input data are effectively constant (compared to the larger of the two means) an error is generated.

### Value

A list with class "htest" containing the following components:

- **statistic**: the value of the t-statistic.
- **parameter**: the degrees of freedom for the t-statistic.
- **p.value**: the p-value for the test.
conf.int  
a confidence interval for the mean appropriate to the specified alternative hypothesis.
estimate  
the estimated mean or difference in means depending on whether it was a one-sample test or a two-sample test.
null.value  
the specified hypothesized value of the mean or mean difference depending on whether it was a one-sample test or a two-sample test.
stderr  
the standard error of the mean (difference), used as denominator in the t-statistic formula.
alternative  
a character string describing the alternative hypothesis.
method  
a character string indicating what type of t-test was performed.
data.name  
a character string giving the name(s) of the data.

See Also

prop.test

Examples

```r
require(graphics)

t.test(1:10, y = c(7:20))  # P = .00001855
t.test(1:10, y = c(7:20, 200))  # P = .1245  -- NOT significant anymore

## Classical example: Student’s sleep data
plot(extra ~ group, data = sleep)
## Traditional interface
with(sleep, t.test(extra[group == 1], extra[group == 2]))

## Formula interface

t.test(extra ~ group, data = sleep)

## Formula interface to one-sample test
t.test(extra ~ 1, data = sleep)

## Formula interface to paired test
## The sleep data are actually paired, so could have been in wide format:
sleep2 <- reshape(sleep, direction = "wide",
                  idvar = "ID", timevar = "group")
t.test(Pair(extra.1, extra.2) ~ 1, data = sleep2)
```

TDist  

The Student t Distribution

Description

Density, distribution function, quantile function and random generation for the t distribution with df degrees of freedom (and optional non-centrality parameter ncp).
Usage

dt(x, df, ncp, log = FALSE)
pt(q, df, ncp, lower.tail = TRUE, log.p = FALSE)
qt(p, df, ncp, lower.tail = TRUE, log.p = FALSE)
rt(n, df, ncp)

Arguments

x, q
vector of quantiles.

p
vector of probabilities.

n
number of observations. If length(n) > 1, the length is taken to be the number required.

df
degrees of freedom (> 0, maybe non-integer). df = Inf is allowed.

ncp
non-centrality parameter δ; currently except for rt(), only for abs(ncp) <= 37.62. If omitted, use the central t distribution.

log, log.p
logical; if TRUE, probabilities p are given as log(p).

lower.tail
logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).

Details

The \( t \) distribution with \( df = \nu \) degrees of freedom has density

\[
f(x) = \frac{\Gamma((\nu + 1)/2)}{\sqrt{\pi \nu} \Gamma(\nu/2)} (1 + x^2/\nu)^{-(\nu+1)/2}\]

for all real \( x \). It has mean 0 (for \( \nu > 1 \)) and variance \( \nu/(\nu-2) \) (for \( \nu > 2 \)).

The general non-central \( t \) with parameters \((\nu, \delta) = (df, ncp)\) is defined as the distribution of \( T_{\nu}(\delta) := (U + \delta)/\sqrt{V/\nu} \) where \( U \) and \( V \) are independent random variables, \( U \sim \mathcal{N}(0,1) \) and \( V \sim \chi^2_{\nu} \) (see Chisquare).

The most used applications are power calculations for \( t \)-tests:
Let \( T = \frac{\bar{X} - \mu_0}{S/\sqrt{n}} \) where \( \bar{X} \) is the mean and \( S \) the sample standard deviation (sd) of \( X_1, X_2, \ldots, X_n \) which are i.i.d. \( \mathcal{N}(\mu, \sigma^2) \) Then \( T \) is distributed as non-central \( t \) with \( df = n-1 \) degrees of freedom and non-centrality parameter \( ncp = (\mu - \mu_0)\sqrt{n}/\sigma \).

The \( t \) distribution’s cumulative distribution function (cdf), \( F_\nu(t) \) fulfills \( F_\nu(t) = \frac{1}{2} \text{I}_x(\frac{\nu}{2}, \frac{1}{2}) \), for \( t \leq 0 \), and \( F_\nu(t) = 1 - \frac{1}{2} \text{I}_x(\frac{\nu}{2}, \frac{1}{2}) \), for \( t \geq 0 \), where \( x := (\nu + t^2)^1/2 \), and \( \text{I}_x(a, b) \) is the incomplete beta function, in R this is \text{pbeta}(x, a, b) \).

Value

dt gives the density, pt gives the distribution function, qt gives the quantile function, and rt generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

The length of the result is determined by \( n \) for \( rt \), and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than \( n \) are recycled to the length of the result. Only the first elements of the logical arguments are used.
Note

Supplying ncp = 0 uses the algorithm for the non-central distribution, which is not the same algorithm used if ncp is omitted. This is to give consistent behaviour in extreme cases with values of ncp very near zero.

The code for non-zero ncp is principally intended to be used for moderate values of ncp: it will not be highly accurate, especially in the tails, for large values.

Source

The central dt is computed via an accurate formula provided by Catherine Loader (see the reference in dbinom).

For the non-central case of dt, C code contributed by Claus Ekstrøm based on the relationship (for $x \neq 0$) to the cumulative distribution.

For the central case of pt, a normal approximation in the tails, otherwise via pbeta.

For the non-central case of pt based on a C translation of


This computes the lower tail only, so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant.

For central qt, a C translation of


altered to take account of


The non-central case is done by inversion.

References


See Also

Distributions for other standard distributions, including df for the F distribution.

Examples

require(graphics)

1 - pt(1:5, df = 1)
qt(.975, df = c(1:10,20,50,100,1000))

tt <- seq(0, 10, length.out = 21)
ncp <- seq(0, 6, length.out = 31)
ptn <- outer(tt, ncp, function(t, d) pt(t, df = 3, ncp = d))
t.tit <- "Non-central t - Probabilities"
image(tt, ncp, ptn, zlim = c(0,1), main = t.tit)
termplot

Plot Regression Terms

description
Plots regression terms against their predictors, optionally with standard errors and partial residuals added.

usage
termplot(model, data = NULL, envir = environment(formula(model)), partial.resid = FALSE, rug = FALSE, 
terms = NULL, se = FALSE, xlabs = NULL, ylabs = NULL, main = NULL, 
col.term = 2, lwd.term = 1.5, 
col.se = "orange", lty.se = 2, lwd.se = 1, 
col.res = "gray", cex = 1, pch = par("pch"), 
col.smth = "darkred", lty.smth = 2, span.smth = 2/3, 
ask = dev.interactive() && nb.fig < n.tms, 
use.factor.levels = TRUE, smooth = NULL, ylim = "common", 
plot = TRUE, transform.x = FALSE, ...)

arguments
model fitted model object
data data frame in which variables in model can be found
envir environment in which variables in model can be found
partial.resid logical; should partial residuals be plotted?
rug add rugplots (jittered 1-d histograms) to the axes?
termplot

The model object must have a predict method that accepts type = "terms", e.g., glm in the stats package, coxph and survreg in the survival package.

For the partial.resid = TRUE option model must have a residuals method that accepts type = "partial", which lm and glm do.

The data argument should rarely be needed, but in some cases termplot may be unable to reconstruct the original data frame. Using na.action=na.exclude makes these problems less likely.

Nothing sensible happens for interaction terms, and they may cause errors.

The plot = FALSE option is useful when some special action is needed, e.g. to overlay the results of two different models or to plot confidence bands.

terms which terms to plot (default NULL means all terms); a vector passed to predict(..., type = "terms", terms = *).

se plot pointwise standard errors?
xlabs vector of labels for the x axes
ylabs vector of labels for the y axes
main logical, or vector of main titles; if TRUE, the model's call is taken as main title, NULL or FALSE mean no titles.
col.term, lwd.term color and line width for the 'term curve', see lines.
col.se, lty.se, lwd.se color, line type and line width for the 'twice-standard-error curve' when se = TRUE.
col.res, cex, pch color, plotting character expansion and type for partial residuals, when partial.resid = TRUE, see points.
ask logical; if TRUE, the user is asked before each plot, see par(ask=.).
use.factor.levels Should x-axis ticks use factor levels or numbers for factor terms?
smooth NULL or a function with the same arguments as panel.smooth to draw a smooth through the partial residuals for non-factor terms
lty.smth, col.smth, span.smth Passed to smooth
ylim an optional range for the y axis, or "common" when a range sufficient for all the plot will be computed, or "free" when limits are computed for each plot.
plot if set to FALSE plots are not produced: instead a list is returned containing the data that would have been plotted.
transform.x logical vector; if an element (recycled as necessary) is TRUE, partial residuals for the corresponding term are plotted against transformed values. The model response is then a straight line, allowing a ready comparison against the data or against the curve obtained from smooth=panel.smooth.

Details

... other graphical parameters.
Value

For plot = FALSE, a list with one element for each plot which would have been produced. Each element of the list is a data frame with variables x, y, and optionally the pointwise standard errors se. For continuous predictors x will contain the ordered unique values and for a factor it will be a factor containing one instance of each level. The list has attribute "constant" copied from the predicted terms object.

Otherwise, the number of terms, invisibly.

See Also

For (generalized) linear models, `plot.lm` and `predict.glm`.

Examples

```r
require(graphics)

had.splines <- "package:splines" %in% search()
if(!had.splines) rs <- require(splines)
x <- 1:100
z <- factor(rep(LETTERS[1:4], 25))
y <- rnorm(100, sin(x/10)+as.numeric(z))
model <- glm(y ~ ns(x, 6) + z)
par(mfrow = c(2,2)) ## 2 x 2 plots for same model :
termplot(model, main = paste("termplot( ", deparse(model$call)," ...)"))
termplot(model, rug = TRUE)
termplot(model, partial.resid = TRUE, se = TRUE, main = TRUE)
termplot(model, partial.resid = TRUE, smooth = panel.smooth, span.smth = 1/4)
if(!had.splines && rs) detach("package:splines")

if(requireNamespace("MASS", quietly = TRUE)) {
  hills.lm <- lm(log(time) ~ log(climb)+log(dist), data = MASS::hills)
termplot(hills.lm, partial.resid = TRUE, smooth = panel.smooth,
       terms = "log(dist)", main = "Original")
termplot(hills.lm, transform.x = TRUE,
       partial.resid = TRUE, smooth = panel.smooth,
       terms = "log(dist)", main = "Transformed")
}
```

Terms

<table>
<thead>
<tr>
<th>Model Terms</th>
</tr>
</thead>
<tbody>
<tr>
<td>a list with one element for each plot which would have been produced. Each element of the list is a data frame with variables x, y, and optionally the pointwise standard errors se. For continuous predictors x will contain the ordered unique values and for a factor it will be a factor containing one instance of each level. The list has attribute &quot;constant&quot; copied from the predicted terms object.</td>
</tr>
</tbody>
</table>

Description

The function `terms` is a generic function which can be used to extract terms objects from various kinds of R data objects.

Usage

```r
terms(x, ...)
```
Arguments

- **x**: object used to select a method to dispatch.
- **...**: further arguments passed to or from other methods.

Details

There are methods for classes "aovlist", and "terms" "formula" (see `terms.formula`): the default method just extracts the terms component of the object, or failing that a "terms" attribute (as used by `model.frame`).

There are `print` and `labels` methods for class "terms": the latter prints the term labels (see `terms.object`).

Value

An object of class c("terms", "formula") which contains the terms representation of a symbolic model. See `terms.object` for its structure.

References


See Also

`terms.object`, `terms.formula`, `lm`, `glm`, `formula`.

---

### Construct a terms Object from a Formula

**Description**

This function takes a formula and some optional arguments and constructs a terms object. The terms object can then be used to construct a `model.matrix`.

**Usage**

```r
## S3 method for class 'formula'
terms(x, specials = NULL, abb = NULL, data = NULL, neg.out = TRUE,
      keep.order = FALSE, simplify = FALSE, ..., 
      allowDotAsName = FALSE)
```

**Arguments**

- **x**: a formula.
- **specials**: which functions in the formula should be marked as special in the terms object? A character vector or NULL.
- **abb**: Not implemented in R; deprecated.
- **data**: a data frame from which the meaning of the special symbol . can be inferred. It is used only if there is a . in the formula.
- **neg.out**: Not implemented in R; deprecated.
keep.order  a logical value indicating whether the terms should keep their positions. By default, when FALSE, the terms are reordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on. Effects of a given order are kept in the order specified.

simplify  should the formula be expanded and simplified, the pre-1.7.0 behaviour?

...  further arguments passed to or from other methods.

allowDotAsName  normally . in a formula refers to the remaining variables contained in data. Exceptionally, . can be treated as a name for non-standard uses of formulae.

Details

Not all of the options work in the same way that they do in S and not all are implemented.

Value

A terms object is returned. It is the re-ordered formula (unless keep.order = TRUE) with several attributes, see terms.object for details. In all cases variables within an interaction term in the formula are re-ordered by the ordering of the "variables" attribute, which is the order in which the variables occur in the formula.

See Also

terms, terms.object, also for examples.

terms.object

Description of Terms Objects

Description

An object of class terms holds information about a model. Usually the model was specified in terms of a formula and that formula was used to determine the terms object.

Value

The object itself is simply the result of terms.formula(<formula>). It has a number of attributes and they are used to construct the model frame:

factors  An integer matrix of variables by terms showing which variables appear in which terms. The entries are

0  if the variable does not occur in the term,

1  if it does occur and should be coded by contrasts, and

2  if it occurs and should be coded via dummy variables for all levels (as when a lower-order term is missing).

Note that variables in main effects always receive 1, even if the intercept is missing (in which case the first one should be coded with dummy variables). If there are no terms other than an intercept and offsets, this is integer(0).

term.labels  A character vector containing the labels for each of the terms in the model, except for offsets. Note that these are after possible re-ordering of terms. Non-syntactic names will be quoted by backticks: this makes it easier to re-construct the formula from the term labels.
variables

A call to list of the variables in the model.

intercept

Either 0, indicating no intercept is to be fit, or 1 indicating that an intercept is to be fit.

order

A vector of the same length as term.labels indicating the order of interaction for each term.

response

The index of the variable (in variables) of the response (the left hand side of the formula). Zero, if there is no response.

offset

If the model contains offset terms there is an offset attribute indicating which variable(s) are offsets.

specials

If a specials argument was given to terms.formula there is a specials attribute, a pairlist of vectors (one for each specified special function) giving numeric indices of the arguments of the list returned as the variables attribute which contain these special functions.

dataClasses

optional. A named character vector giving the classes (as given by .MFclass) of the variables used in a fit.

predvars

optional. An expression to help in computing predictions at new covariate values; see makepredictcall.

The object has class c("terms", "formula").

Note

These objects are different from those found in S. In particular there is no formula attribute: instead the object is itself a formula. (Thus, the mode of a terms object is different.)

Examples of the specials argument can be seen in the aov and coxph functions, the latter from package survival.

See Also

terms.formula.

Examples

## use of specials (as used for gam() in packages mgcv and gam)
(tf <- terms(y ~ x + x:z + s(x), specials = "s"))
## Note that the "factors" attribute has variables as row names
## and term labels as column names, both as character vectors.
attr(tf, "labels") # index 's' variable(s)
rownames(attr(tf, "factors"))[attr(tf, "specials")$s]

## we can keep the order by
terms(y ~ x + x:z + s(x), specials = "s", keep.order = TRUE)
Description

time creates the vector of times at which a time series was sampled.
cycle gives the positions in the cycle of each observation.
frequency returns the number of samples per unit time and deltat the time interval between observations (see ts).

Usage

time(x, ...)
## Default S3 method:
time(x, offset = 0, ts.eps = getOption("ts.eps"), ...)

cycle(x, ...)
frequency(x, ...)
deltat(x, ...)

Arguments

x a univariate or multivariate time-series, or a vector or matrix.
offset can be used to indicate when sampling took place in the time unit. 0 (the default) indicates the start of the unit, 0.5 the middle and 1 the end of the interval.
ts.eps time series comparison tolerance, used in time() to determine if values close than ts.eps to an integer should be round()ed to it in order to preserve the “year”.
... extra arguments for future methods.

Details

These are all generic functions, which will use the tsp attribute of x if it exists. time and cycle have methods for class ts that coerce the result to that class.
time() round()s values close to an integer, i.e., closer than ts.eps, since R 4.3.0. For previous behaviour, you can call it with ts.eps = 0.

References


See Also

ts, start, tsp, window.
date for clock time, system.time for CPU usage.
Examples

require(graphics)
cycle(presidents)  # a simple series plot
plot(as.vector(time(presidents)), as.vector(presidents), type = "l")

create Toeplitz Matrix

toeplitz

Description

In its simplest use, \texttt{toeplitz()} forms a symmetric Toeplitz matrix given its first column (or row). For the general case, asymmetric and non-square Toeplitz matrices are formed either by specifying the first column and row separately,

T1 <- toeplitz(col, row)

or by

T <- toeplitz2(x, nr, nc)

where only one of \(\langle\text{nr}, \text{nc}\rangle\) needs to be specified. In the latter case, the simple equivalence \(T_{i,j} = x_{i-j+n_c}\) is fulfilled where \(n_c = \text{ncol}(T)\).

Usage

toeplitz (x, r = NULL, symmetric = \text{is.null}(r))
toeplitz2(x, nrow = \text{length}(x) + 1 - ncol, ncol = \text{length}(x) + 1 - nrow)

Arguments

x for \text{toeplitz}(x, *): the first column of the Toeplitz matrix; for \text{toeplitz2}(x, *) it is the upper-and-left border of the Toeplitz matrix, i.e., from top-right to bottom-left, such that \(T[i,j] = x[i-j + ncol]\).

r the first row of the target Toeplitz matrix; only needed in asymmetric cases.
symmetric optional \text{logical} indicating if the matrix should be symmetric.
nrow, ncol the number of rows and columns; only one needs to be specified.

Value

The \(n \times m\) Toeplitz matrix \(T\); for

\text{toeplitz()}: \text{dim}(T) = (n, m) and \(m = \text{length}(x)\) and \(n = m\) in the symmetric case or \(n = \text{length}(r)\) otherwise.

\text{toeplitz2()}: \text{dim}(T) = c(nrow, ncol).

Author(s)

A. Trapletti and Martin Maechler (speedup and asymmetric extensions)
Examples

```r
x <- 1:5
toeplitz(x)

T2 <- toeplitz2(c(13:12, 1:5), 5, 3)# this is the same matrix:
stopifnot(identical(T., T2))

# Matrix of character (could also have logical, raw, complex ..) {also warning}:
noquote(toeplitz(letters[1:4], LETTERS[20:26]))

## A convolution/smoother weight matrix :
# m <- 17
k <- length(wts <- c(76, 99, 60, 20, 1))
n <- m-k+1
## Convolution
W <- toeplitz2(c(rep(0, m-k), wts, rep(0, m-k)), ncol=n)

## scale W to have column sums 1:
W. <- W / sum(wts)
all.equal(rep(1, ncol(W.)), colSums(W.), check.attributes = FALSE)
```

## ts

**Time-Series Objects**

**Description**

The function `ts` is used to create time-series objects.

`as.ts` and `is.ts` coerce an object to a time-series and test whether an object is a time series.

**Usage**

```r
ts(data = NA, start = 1, end = numeric(), frequency = 1, deltat = 1, ts.eps = getOption("ts.eps"),
```
class = if(nseries > 1) c("mts", "ts", "matrix", "array") else "ts",
names = )
as.ts(x, ...)
is.ts(x)
is.mts(x)

Arguments

data a vector or matrix of the observed time-series values. A data frame will be coerced to a numeric matrix via data.matrix. (See also 'Details'.)
start the time of the first observation. Either a single number or a vector of two numbers (the second of which is an integer), which specify a natural time unit and a (1-based) number of samples into the time unit. See the examples for the use of the second form.
end the time of the last observation, specified in the same way as start.
frequency the number of observations per unit of time.
deltat the fraction of the sampling period between successive observations; e.g., 1/12 for monthly data. Only one of frequency or deltat should be provided.
ts.eps time series comparison tolerance. Frequencies are considered equal if their absolute difference is less than ts.eps.
class class to be given to the result, or none if NULL or "none". The default is "ts" for a single series, or c("mts", "ts", "matrix", "array") for multiple series.
names a character vector of names for the series in a multiple series: defaults to the colnames of data, or "Series 1", "Series 2", ....
x an arbitrary R object.
... arguments passed to methods (unused for the default method).

Details

The function ts is used to create time-series objects. These are vectors or matrices which inherit from class "ts" (and have additional attributes) which represent data which has been sampled at equispaced points in time. In the matrix case, each column of the matrix data is assumed to contain a single (univariate) time series. Time series must have at least one observation, and although they need not be numeric there is very limited support for non-numeric series.

Class "ts" has a number of methods. In particular arithmetic will attempt to align time axes, and subsetting to extract subsets of series can be used (e.g., EuStockMarkets[, "DAX"]). However, subsetting the first (or only) dimension will return a matrix or vector, as will matrix subsetting. Subassignment can be used to replace values but not to extend a series (see window). There is a method for t that transposes the series as a matrix (a one-column matrix if a vector) and hence returns a result that does not inherit from class "ts".

Argument frequency indicates the sampling frequency of the time series, with the default value 1 indicating one sample in each unit time interval. For example, one could use a value of 7 for frequency when the data are sampled daily, and the natural time period is a week, or 12 when the data are sampled monthly and the natural time period is a year. Values of 4 and 12 are assumed in (e.g.) print methods to imply a quarterly and monthly series respectively. frequency need not be a whole number: for example, frequency = 0.2 would imply sampling once every five time units.

as.ts is generic. Its default method will use the tsp attribute of the object if it has one to set the start and end times and frequency.
is.ts() tests if an object is a time series, i.e., inherits from "ts" and is of positive length.
is.mts(x) tests if an object x is a multivariate time series, i.e., fulfills is.ts(x), is.matrix(x) and inherits from class "mts".

References

See Also
tsp, frequency, start, end, time, window; print.ts, the print method for time series objects;
plot.ts, the plot method for time series objects.

For other definitions of 'time series' (e.g., time-ordered observations) see the CRAN task view at https://CRAN.R-project.org/view=TimeSeries.

Examples
require(graphics)
ts(1:10, frequency = 4, start = c(1959, 2)) # 2nd Quarter of 1959
print( ts(1:10, frequency = 7, start = c(12, 2)), calendar = TRUE)
# print.ts(.)
## Using July 1954 as start date:
gnp <- ts(cumsum(1 + round(rnorm(100), 2)),
           start = c(1954, 7), frequency = 12)
plot(gnp) # using 'plot.ts' for time-series plot

## Multivariate
z <- ts(matrix(rnorm(300), 100, 3), start = c(1961, 1), frequency = 12)
class(z)
is.mts(z)
head(z) # as "matrix"
plot(z)
plot(z, plot.type = "single", lty = 1:3)

## A phase plot:
plot(nhtemp, lag(nhtemp, 1), cex = .8, col = "blue",
     main = "Lag plot of New Haven temperatures")
Arguments

- **x**: an object of class "ts" containing the values to be differenced.
- **lag**: an integer indicating which lag to use.
- **differences**: an integer indicating the order of the difference.
- **object**: a univariate or multivariate time series.
- **...**: further arguments to be passed to or from methods.

Details

The `na.omit` method omits initial and final segments with missing values in one or more of the series. 'Internal' missing values will lead to failure.

Value

For the `na.omit` method, a time series without missing values. The class of `object` will be preserved.

See Also

`diff`, `na.omit`, `na.fail`, `na.contiguous`.

---

### ts.plot

*Plot Multiple Time Series*

Description

Plot several time series on a common plot. Unlike `plot.ts` the series can have a different time bases, but they should have the same frequency.

Usage

```r
ts.plot(..., gpars = list())
```

Arguments

- **...**: one or more univariate or multivariate time series.
- **gpars**: list of named graphics parameters to be passed to the plotting functions. Those commonly used can be supplied directly in `...`.

Value

None.

Note

Although this can be used for a single time series, `plot` is easier to use and is preferred.

See Also

`plot.ts`
Examples

```r
require(graphics)

ts.plot(ldeaths, mdeaths, fdeaths,
  gpars=list(xlab="year", ylab="deaths", lty=c(1:3)))
```

---

**Description**

Bind time series which have a common frequency. `ts.union` pads with NAs to the total time coverage, `ts.intersect` restricts to the time covered by all the series.

**Usage**

```r
ts.intersect(..., dframe = FALSE)
ts.union(..., dframe = FALSE)
```

**Arguments**

- `...` two or more univariate or multivariate time series, or objects which can coerced to time series.
- `dframe` logical; if TRUE return the result as a data frame.

**Details**

As a special case, `...` can contain vectors or matrices of the same length as the combined time series of the time series present, as well as those of a single row.

**Value**

A time series object if `dframe` is FALSE, otherwise a data frame.

**See Also**

`cbind`

**Examples**

```r
ts.union(mdeaths, fdeaths)
cbind(mdeaths, fdeaths) # same as the previous line
ts.intersect(window(mdeaths, 1976), window(fdeaths, 1974, 1978))
sales1 <- ts.union(BJsales, lead = BJsales.lead)
ts.intersect(sales1, lead3 = lag(BJsales.lead, -3))
```
tsdiag  Diagnostic Plots for Time-Series Fits

Description

A generic function to plot time-series diagnostics.

Usage

```r
tsdia(object, gof.lag, ...)
```

Arguments

- **object**: a fitted time-series model
- **gof.lag**: the maximum number of lags for a Portmanteau goodness-of-fit test
- **...**: further arguments to be passed to particular methods

Details

This is a generic function. It will generally plot the residuals, often standardized, the autocorrelation function of the residuals, and the p-values of a Portmanteau test for all lags up to `gof.lag`.

The methods for `arima` and `StructTS` objects plots residuals scaled by the estimate of their (individual) variance, and use the Ljung–Box version of the portmanteau test.

Value

None. Diagnostics are plotted.

See Also

- `arima`, `StructTS`, `Box.test`

Examples

```r
require(graphics)
fit <- arima(lh, c(1,0,0))
tsdiag(fit)

## see also examples(arima)
(fit <- StructTS(log10(JohnsonJohnson), type = "BSM"))
tsdiag(fit)
```
Description

`tsp` returns the `tsp` attribute (or `NULL`). It is included for compatibility with S version 2. `tsp<-` sets the `tsp` attribute. `hasTsp` ensures `x` has a `tsp` attribute, by adding one if needed.

Usage

```
tsp(x)
tsp(x) <- value
hasTsp(x)
```

Arguments

- `x`: a vector or matrix or univariate or multivariate time-series.
- `value`: a numeric vector of length 3 or `NULL`.

Details

The `tsp` attribute gives the start time in time units, the end time and the frequency (the number of observations per unit of time, e.g. 12 for a monthly series).

Assignments are checked for consistency.

Assigning `NULL` which removes the `tsp` attribute and any "ts" (or "mts") class of `x`.

Value

An object which differs from `x` only in the `tsp` attribute (unless `NULL` is assigned).

`hasTsp` adds, if needed, an attribute with a start time and frequency of 1 and end time `NROW(x)`.

References


See Also

`ts`, `time`, `start`.
**tsSmooth**

*Use Fixed-Interval Smoothing on Time Series*

**Description**

Performs fixed-interval smoothing on a univariate time series via a state-space model. Fixed-interval smoothing gives the best estimate of the state at each time point based on the whole observed series.

**Usage**

```r
tsSmooth(object, ...)
```

**Arguments**

- `object` a time-series fit. Currently only class "StructTS" is supported
- `...` possible arguments for future methods.

**Value**

A time series, with as many dimensions as the state space and results at each time point of the original series. (For seasonal models, only the current seasonal component is returned.)

**Author(s)**

B. D. Ripley

**References**


**See Also**

- `KalmanSmooth`, `StructTS`
- For examples consult `AirPassengers`, `JohnsonJohnson` and `Nile`.

---

**Tukey**

*The Studentized Range Distribution*

**Description**

Functions of the distribution of the studentized range, $R/s$, where $R$ is the range of a standard normal sample and $df \times s^2$ is independently distributed as chi-squared with $df$ degrees of freedom, see `pchisq`.

**Usage**

```r
ptukey(q, nmeans, df, nranges = 1, lower.tail = TRUE, log.p = FALSE)
qtukey(p, nmeans, df, nranges = 1, lower.tail = TRUE, log.p = FALSE)
```
Tukey

Arguments

- **q**: vector of quantiles.
- **p**: vector of probabilities.
- **nmeans**: sample size for range (same for each group).
- **df**: degrees of freedom for \( s \) (see below).
- **nranges**: number of groups whose maximum range is considered.
- **log.p**: logical; if TRUE, probabilities \( p \) are given as \( \log(p) \).
- **lower.tail**: logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).

Details

If \( n_g = \text{nranges} \) is greater than one, \( R \) is the maximum of \( n_g \) groups of \( n\text{means} \) observations each.

Value

`ptukey` gives the distribution function and `qtukey` its inverse, the quantile function.

The length of the result is the maximum of the lengths of the numerical arguments. The other numerical arguments are recycled to that length. Only the first elements of the logical arguments are used.

Note

A Legendre 16-point formula is used for the integral of `ptukey`. The computations are relatively expensive, especially for `qtukey` which uses a simple secant method for finding the inverse of `ptukey`. `qtukey` will be accurate to the 4th decimal place.

Source

`qtukey` is in part adapted from Odeh and Evans (1974).

References


See Also

*Distributions* for standard distributions, including `pnorm` and `qnorm` for the corresponding functions for the normal distribution.

Examples

```r
if(interactive())
  curve(ptukey(x, nm = 6, df = 5), from = -1, to = 8, n = 101)
(ptt <- ptukey(0:10, 2, df = 5))
(qtt <- qtukey(.95, 2, df = 2:11))
## The precision may be not much more than about 8 digits:
summary(abs(.95 - ptukey(qtt, 2, df = 2:11)))
```
TukeyHSD

Compute Tukey Honest Significant Differences

Description

Create a set of confidence intervals on the differences between the means of the levels of a factor with the specified family-wise probability of coverage. The intervals are based on the Studentized range statistic, Tukey’s ‘Honest Significant Difference’ method.

Usage

TukeyHSD(x, which, ordered = FALSE, conf.level = 0.95, ...)

Arguments

- **x**: A fitted model object, usually an `aov` fit.
- **which**: A character vector listing terms in the fitted model for which the intervals should be calculated. Defaults to all the terms.
- **ordered**: A logical value indicating if the levels of the factor should be ordered according to increasing average in the sample before taking differences. If ordered is true then the calculated differences in the means will all be positive. The significant differences will be those for which the lower end point is positive.
- **conf.level**: A numeric value between zero and one giving the family-wise confidence level to use.
- **...**: Optional additional arguments. None are used at present.

Details

This is a generic function: the description here applies to the method for fits of class "aov".

When comparing the means for the levels of a factor in an analysis of variance, a simple comparison using t-tests will inflate the probability of declaring a significant difference when it is not in fact present. This because the intervals are calculated with a given coverage probability for each interval but the interpretation of the coverage is usually with respect to the entire family of intervals.

John Tukey introduced intervals based on the range of the sample means rather than the individual differences. The intervals returned by this function are based on this Studentized range statistics.

The intervals constructed in this way would only apply exactly to balanced designs where there are the same number of observations made at each level of the factor. This function incorporates an adjustment for sample size that produces sensible intervals for mildly unbalanced designs.

If which specifies non-factor terms these will be dropped with a warning: if no terms are left this is an error.

Value

A list of class c("multicomp", "TukeyHSD"), with one component for each term requested in which. Each component is a matrix with columns diff giving the difference in the observed means, lwr giving the lower end point of the interval, upr giving the upper end point and p adj giving the p-value after adjustment for the multiple comparisons.

There are print and plot methods for class "TukeyHSD". The plot method does not accept xlab, ylab or main arguments and creates its own values for each plot.


**Uniform**

**Author(s)**
Douglas Bates

**References**

**See Also**
aov, qtukey, model.tables, glht in package multcomp.

**Examples**

```r
require(graphics)

summary(fm1 <- aov(breaks ~ wool + tension, data = warpbreaks))
TukeyHSD(fm1, "tension", ordered = TRUE)
plot(TukeyHSD(fm1, "tension"))
```

---

**The Uniform Distribution**

**Description**
These functions provide information about the uniform distribution on the interval from min to max. 
dunif gives the density, punif gives the distribution function qunif gives the quantile function and 
runif generates random deviates.

**Usage**

```r
dunif(x, min = 0, max = 1, log = FALSE)
punif(q, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
qunif(p, min = 0, max = 1, lower.tail = TRUE, log.p = FALSE)
runif(n, min = 0, max = 1)
```

**Arguments**

- `x, q` vector of quantiles.
- `p` vector of probabilities.
- `n` number of observations. If length(n) > 1, the length is taken to be the number required.
- `min, max` lower and upper limits of the distribution. Must be finite.
- `log, log.p` logical; if TRUE, probabilities p are given as log(p).
- `lower.tail` logical; if TRUE (default), probabilities are $P[X \leq x]$, otherwise, $P[X > x]$.  

---
Details

If \( \min \) or \( \max \) are not specified they assume the default values of 0 and 1 respectively.

The uniform distribution has density

\[
f(x) = \frac{1}{\max - \min}
\]

for \( \min \leq x \leq \max \).

For the case of \( u := \min == \max \), the limit case of \( X \equiv u \) is assumed, although there is no density in that case and \( \text{dunif} \) will return NaN (the error condition).

\( \text{runif} \) will not generate either of the extreme values unless \( \max = \min \) or \( \max - \min \) is small compared to \( \min \), and in particular not for the default arguments.

Value

dunif gives the density, punif gives the distribution function, qunif gives the quantile function, and runif generates random deviates.

The length of the result is determined by \( n \) for \( \text{runif} \), and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than \( n \) are recycled to the length of the result. Only the first elements of the logical arguments are used.

Note

The characteristics of output from pseudo-random number generators (such as precision and periodicity) vary widely. See \texttt{Random.seed} for more information on R’s random number generation algorithms.

References


See Also

\texttt{RNG} about random number generation in R.

\texttt{Distributions} for other standard distributions.

Examples

\begin{verbatim}
> u <- runif(20)

## The following relations always hold:
> punif(u) == u
dunif(u) == 1

> var(runif(10000)) # ~ = 1/12 = .08333
\end{verbatim}
uniroot

One Dimensional Root (Zero) Finding

Description

The function `uniroot` searches the interval from `lower` to `upper` for a root (i.e., zero) of the function `f` with respect to its first argument.

Setting `extendInt` to a non-"no" string, means searching for the correct interval = `c(lower,upper)` if `sign(f(x))` does not satisfy the requirements at the interval end points; see the 'Details' section.

Usage

`uniroot(f, interval, ..., lower = min(interval), upper = max(interval), f.lower = f(lower, ...), f.upper = f(upper, ...), extendInt = c("no", "yes", "downX", "upX"), check.conv = FALSE, tol = .Machine$double.eps^0.25, maxiter = 1000, trace = 0)`

Arguments

- `f` the function for which the root is sought.
- `interval` a vector containing the end-points of the interval to be searched for the root.
- `...` additional named or unnamed arguments to be passed to `f`
- `lower, upper` the lower and upper end points of the interval to be searched.
- `f.lower, f.upper` the same as `f(upper)` and `f(lower)`, respectively. Passing these values from the caller where they are often known is more economical as soon as `f()` contains non-trivial computations.
- `extendInt` character string specifying if the interval `c(lower,upper)` should be extended or directly produce an error when `f()` does not have differing signs at the end-points. The default, "no", keeps the search interval and hence produces an error. Can be abbreviated.
- `check.conv` logical indicating whether a convergence warning of the underlying `uniroot` should be caught as an error and if non-convergence in `maxiter` iterations should be an error instead of a warning.
- `tol` the desired accuracy (convergence tolerance).
- `maxiter` the maximum number of iterations.
- `trace` integer number; if positive, tracing information is produced. Higher values giving more details.

Details

Note that arguments after `...` must be matched exactly.

Either `interval` or both `lower` and `upper` must be specified: the upper endpoint must be strictly larger than the lower endpoint. The function values at the endpoints must be of opposite signs (or zero), for `extendInt="no"`, the default. Otherwise, if `extendInt="yes"`, the interval is extended on both sides, in search of a sign change, i.e., until the search interval `[l, u]` satisfies \( f(l) \cdot f(u) \leq 0 \).
If it is known how \( f \) changes sign at the root \( x_0 \), that is, if the function is increasing or decreasing there, extendInt can (and typically should) be specified as "upX" (for "upward crossing") or "downX", respectively. Equivalently, define \( S := \pm 1 \), to require \( S = \text{sign}(f(x_0 + \epsilon)) \) at the solution. In that case, the search interval \([l, u]\) possibly is extended to be such that \( S \cdot f(l) \leq 0 \) and \( S \cdot f(u) \geq 0 \).

\( \text{uniroot()} \) uses Fortran subroutine \textit{zeroin} (from Netlib) based on algorithms given in the reference below. They assume a continuous function (which then is known to have at least one root in the interval).

Convergence is declared either if \( f(x) = 0 \) or the change in \( x \) for one step of the algorithm is less than \( \text{tol} \) (plus an allowance for representation error in \( x \)).

If the algorithm does not converge in \( \text{maxiter} \) steps, a warning is printed and the current approximation is returned.

\( f \) will be called as \( f(x, \ldots) \) for a numeric value of \( x \).

The argument passed to \( f \) has special semantics and used to be shared between calls. The function should not copy it.

### Value

A list with at least five components: \texttt{root} and \texttt{f.root} give the location of the root and the value of the function evaluated at that point. \texttt{iter} and \texttt{estim.prec} give the number of iterations used and an approximate estimated precision for \texttt{root}. (If the root occurs at one of the endpoints, the estimated precision is \texttt{NA}.) \texttt{init.it} contains the number of initial extendInt iterations if there were any and is \texttt{NA} otherwise. In the case of such extendInt iterations, \texttt{iter} contains the sum of these and the \texttt{zeroin} iterations.

Further components may be added in the future.

### Source

Based on ‘zeroin.c’ in \url{https://netlib.org/c/brent.shar}.

### References


### See Also

\texttt{polyroot} for all complex roots of a polynomial; \texttt{optimize, nlm}.

### Examples

```r
require(utils) # for str

## some platforms hit zero exactly on the first step:
## if so the estimated precision is 2/3.
f <- function (x, a) x - a
str(xmin <- uniroot(f, c(0, 1), tol = 0.0001, a = 1/3))

## handheld calculator example: fixed point of \( \cos(.) \):  
uniroot(function(x) cos(x) - x, lower = -pi, upper = pi, tol = 1e-9)$root

str(uniroot(function(x) x*(x^2-1) + .5, lower = -2, upper = 2,  
tol = 0.0001))
```
uniroot

str(uniroot(function(x) x*(x^2-1) + .5, lower = -2, upper = 2, 
tol = 1e-10))

## Find the smallest value x for which exp(x) > 0 (numerically):
$r <- uniroot(function(x) 1e80*exp(x) - 1e-300, c(-1000, 0), tol = 1e-15)
str(r, digits.d = 15) # around -745, depending on the platform.

exp(r$root) # = 0, but not for r$root * 0.999...
mexp <- r$root * (1 - 10*.Machine$double.eps)
exp(mexp) # typically denormalized

###--- uniroot() with new interval extension + checking features:  ---------------

f1 <- function(x) (121 - x^2)/(x^2+1)
f2 <- function(x) exp(-x)*(x - 12)

try(uniroot(f1, c(0,10)))
try(uniroot(f2, c(0, 2)))

## error: f() .. end points not of opposite sign

## where as 'extendInt="yes"'  simply first enlarges the search interval:
u1 <- uniroot(f1, c(0,10),extendInt="yes", trace=1)
u2 <- uniroot(f2, c(0,2), extendInt="yes", trace=2)
stopifnot(all.equal(u1$root, 11, tolerance = 1e-5),
  all.equal(u2$root, 12, tolerance = 6e-6))

## The *danger* of interval extension:
## No way to find a zero of a positive function, but
## numerically, f(-|M|) becomes zero :
u3 <- uniroot(exp, c(0,2), extendInt="yes", trace=TRUE)

## Nonsense example (must give an error):
tools::assertCondition( uniroot(function(x) 1, 0:1, extendInt="yes"),
  "error", verbose=TRUE)

## Convergence checking :
sinc <- function(x) ifelse(x == 0, 1, sin(x)/x)
curve(sinc, -6,18); abline(h=0,v=0, lty=3, col=adjustcolor("gray", 0.8))
uniroot(sinc, c(0,5), extendInt="yes", maxiter=4) #-> "just" a warning

## now with check.conv=TRUE, must signal a convergence error :
uniroot(sinc, c(0,5), extendInt="yes", maxiter=4, check.conv=TRUE)

### Weibull cumulative hazard (example origin, Ravi Varadhan):
cumhaz <- function(t, a, b) b * (t/b)^a
froot <- function(x, u, a, b) cumhaz(x, a, b) - u

n <- 1000
u <- -log(runif(n))
a <- 1/2
b <- 1

## Find failure times
ru <- sapply(u, function(x)
  uniroot(froot, u=x, a=a, b=b, interval= c(1.e-14, 1e04),
  extendInt="yes")$root)
ru2 <- sapply(u, function(x)
  uniroot(froot, u=x, a=a, b=b, interval= c(0.01, 10),
  extendInt="yes")$root)
stopifnot(all.equal(ru, ru2, tolerance = 6e-6))

r1 <- uniroot(froot, u= 0.99, a=a, b=b, interval= c(0.01, 10),
  extendInt="up")
stopifnot(all.equal(0.99, cumhaz(r1$root, a=a, b=b)))

## An error if 'extendInt' assumes "wrong zero-crossing direction":
uniroot(froot, u= 0.99, a=a, b=b, interval= c(0.1, 10), extendInt="down")

---

**update**

*Update and Re-fit a Model Call*

**Description**

update will update and (by default) re-fit a model. It does this by extracting the call stored in the object, updating the call and (by default) evaluating that call. Sometimes it is useful to call update with only one argument, for example if the data frame has been corrected.

“Extracting the call” in update() and similar functions uses getCall() which itself is a (S3) generic function with a default method that simply gets x$call.

Because of this, update() will often work (via its default method) on new model classes, either automatically, or by providing a simple getCall() method for that class.

**Usage**

update(object, ...)

## Default S3 method:

update(object, formula., ..., evaluate = TRUE)

call(x, ...)

**Arguments**

object, x

An existing fit from a model function such as lm, glm and many others.

formula.

Changes to the formula – see update.formula for details.

...  

Additional arguments to the call, or arguments with changed values. Use name = NULL to remove the argument name.

evaluate  

If true evaluate the new call else return the call.

**Value**

If evaluate = TRUE the fitted object, otherwise the updated call.
update.formula

References


See Also

update.formula

Examples

```r
oldcon <- options(contrasts = c("contr.treatment", "contr.poly"))
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

lm.D9 <- lm(weight ~ group)
summary(lm.D90 <- update(lm.D9, . ~ . - 1))
options(contrasts = c("contr.helmert", "contr.poly"))
update(lm.D9)
getCall(lm.D90) # "through the origin"

options(oldcon)
```

Description

`update.formula` is used to update model formulae. This typically involves adding or dropping terms, but updates can be more general.

Usage

```r
## S3 method for class 'formula'
update(old, new, ...)
```

Arguments

- `old`: a model formula to be updated.
- `new`: a formula giving a template which specifies how to update.
- `...`: further arguments passed to or from other methods.

Details

Either or both of `old` and `new` can be objects such as length-one character vectors which can be coerced to a formula via `as.formula`.

The function works by first identifying the *left-hand side* and *right-hand side* of the `old` formula. It then examines the new formula and substitutes the *lhs* of the `old` formula for any occurrence of `.` on the left of `new`, and substitutes the *rhs* of the `old` formula for any occurrence of `.` on the right of `new`. The result is then simplified via `terms.formula(simplify = TRUE)`. 

Model Updating

update.formula
### Value

The updated formula is returned. The environment of the result is that of old.

### See Also

terms, model.matrix.

### Examples

```r
update(y ~ x, ~ . + x2) #> y ~ x + x2
update(y ~ x, log(.) ~ . ) #> log(y) ~ x
update(. ~ u+v, res ~ . ) #> res ~ u + v
```

### Description

Performs an F test to compare the variances of two samples from normal populations.

### Usage

```r
var.test(x, ...)
```

#### Default S3 method:
```r
var.test(x, y, ratio = 1,
         alternative = c("two.sided", "less", "greater"),
         conf.level = 0.95, ...)
```

#### S3 method for class 'formula'
```r
var.test(formula, data, subset, na.action, ...)
```

### Arguments

- **x, y**: numeric vectors of data values, or fitted linear model objects (inheriting from class "lm").
- **ratio**: the hypothesized ratio of the population variances of x and y.
- **alternative**: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
- **conf.level**: confidence level for the returned confidence interval.
- **formula**: a formula of the form lhs ~ rhs where lhs is a numeric variable giving the data values and rhs a factor with two levels giving the corresponding groups.
- **data**: an optional matrix or data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
- **subset**: an optional vector specifying a subset of observations to be used.
- **na.action**: a function which indicates what should happen when the data contain NAs. Defaults togetOption("na.action").
- **...**: further arguments to be passed to or from methods.
Details

The null hypothesis is that the ratio of the variances of the populations from which x and y were drawn, or in the data to which the linear models x and y were fitted, is equal to ratio.

Value

A list with class "htest" containing the following components:

- statistic: the value of the F test statistic.
- parameter: the degrees of the freedom of the F distribution of the test statistic.
- p.value: the p-value of the test.
- conf.int: a confidence interval for the ratio of the population variances.
- estimate: the ratio of the sample variances of x and y.
- null.value: the ratio of population variances under the null.
- alternative: a character string describing the alternative hypothesis.
- method: the character string "F test to compare two variances".
- data.name: a character string giving the names of the data.

See Also

- bartlett.test for testing homogeneity of variances in more than two samples from normal distributions;
- ansari.test and mood.test for two rank based (nonparametric) two-sample tests for difference in scale.

Examples

```r
x <- rnorm(50, mean = 0, sd = 2)
y <- rnorm(30, mean = 1, sd = 1)
var.test(x, y) # Do x and y have the same variance?
var.test(lm(x ~ 1), lm(y ~ 1)) # The same.
```

---

**varimax**

*Rotation Methods for Factor Analysis*

Description

These functions 'rotate' loading matrices in factor analysis.

Usage

```r
varimax(x, normalize = TRUE, eps = 1e-5)
promax(x, m = 4)
```

Arguments

- **x**: A loadings matrix, with \( p \) rows and \( k < p \) columns.
- **m**: The power used the target for promax. Values of 2 to 4 are recommended.
- **normalize**: logical. Should Kaiser normalization be performed? If so the rows of \( x \) are re-scaled to unit length before rotation, and scaled back afterwards.
- **eps**: The tolerance for stopping: the relative change in the sum of singular values.
**Details**

These seek a ‘rotation’ of the factors \(x \% \times T\) that aims to clarify the structure of the loadings matrix. The matrix \(T\) is a rotation (possibly with reflection) for varimax, but a general linear transformation for promax, with the variance of the factors being preserved.

**Value**

A list with components

- `loadings` The ‘rotated’ loadings matrix, \(x \% \times \text{rotmat}\), of class "loadings".
- `rotmat` The ‘rotation’ matrix.

**References**


**See Also**

`factanal`, `Harman74.cor`.

**Examples**

```r
## varimax with normalize = TRUE is the default
fa <- factanal(~., 2, data = swiss)
varimax(loadings(fa), normalize = FALSE)
promax(loadings(fa))
```

---

**vcov**

*Calculate Variance-Covariance Matrix for a Fitted Model Object*

**Description**

Returns the variance-covariance matrix of the main parameters of a fitted model object. The “main” parameters of model correspond to those returned by `coef`, and typically do not contain a nuisance scale parameter (\(\sigma\)).

**Usage**

```r
vcov(object, ...)
## S3 method for class 'lm'
vcov(object, complete = TRUE, ...)
## and also for '[summary.]glm' and 'mlm'
## S3 method for class 'aov'
vcov(object, complete = FALSE, ...)
```

```r
.vcov.aliased(aliased, vc, complete = TRUE)
```
Arguments

object  a fitted model object, typically. Sometimes also a summary() object of such a fitted model.

complete for the aov, lm, glm, mlm, and where applicable summary.lm etc methods: logical indicating if the full variance-covariance matrix should be returned also in case of an over-determined system where some coefficients are undefined and coef(.) contains NAs correspondingly. When complete = TRUE, vcov() is compatible with coef() also in this singular case.

... additional arguments for method functions. For the glm method this can be used to pass a dispersion parameter.

aliased a logical vector typically identical to is.na(coef(.)) indicating which coefficients are ‘aliased’.

vc  a variance-covariance matrix, typically “incomplete”, i.e., with no rows and columns for aliased coefficients.

Details

vcov() is a generic function and functions with names beginning in vcov. will be methods for this function. Classes with methods for this function include: lm, mlm, glm, nls, summary.lm, summary.glm, negbin, polr, rlm (in package MASS), multinom (in package nnet) gls, lme (in package nlme), coxph and survreg (in package survival).

(vcov() methods for summary objects allow more efficient and still encapsulated access when both summary(mod) and vcov(mod) are needed.)

.vcov.aliased() is an auxiliary function useful for vcov method implementations which have to deal with singular model fits encoded via NA coefficients: It augments a vcov–matrix vc by NA rows and columns where needed, i.e., when some entries of aliased are true and vc is of smaller dimension than length(aliased).

Value

A matrix of the estimated covariances between the parameter estimates in the linear or non-linear predictor of the model. This should have row and column names corresponding to the parameter names given by the coef method.

When some coefficients of the (linear) model are undetermined and hence NA because of linearly dependent terms (or an “over specified” model), also called “aliased”, see alias, then since R version 3.5.0, vcov() (iff complete = TRUE, i.e., by default for lm etc, but not for aov) contains corresponding rows and columns of NAs, wherever coef() has always contained such NAs.

Weibull

The Weibull Distribution

Description

Density, distribution function, quantile function and random generation for the Weibull distribution with parameters shape and scale.
Usage

dweibull(x, shape, scale = 1, log = FALSE)

pweibull(q, shape, scale = 1, lower.tail = TRUE, log.p = FALSE)

qweibull(p, shape, scale = 1, lower.tail = TRUE, log.p = FALSE)

rweibull(n, shape, scale = 1)

Arguments

x, q  vector of quantiles.

p  vector of probabilities.

n  number of observations. If length(n) > 1, the length is taken to be the number
required.

shape, scale  shape and scale parameters, the latter defaulting to 1.

log, log.p  logical; if TRUE, probabilities p are given as log(p).

lower.tail  logical; if TRUE (default), probabilities are

            \( P[X \leq x] \)

            otherwise, \( P[X > x] \).

Details

The Weibull distribution with shape parameter \( a \) and scale parameter \( \sigma \) has density given by

\[
f(x) = \left(\frac{a}{\sigma}\right)(x/\sigma)^{a-1} \exp\left(-\left(\frac{x}{\sigma}\right)^a\right)
\]

for \( x > 0 \). The cumulative distribution function is \( F(x) = 1 - \exp\left(-\left(\frac{x}{\sigma}\right)^a\right) \) on \( x > 0 \), the mean

is \( E(X) = \sigma \Gamma\left(1 + \frac{1}{a}\right) \), and the \( Var(X) = \sigma^2 \left(\Gamma\left(1 + \frac{2}{a}\right) - \left(\Gamma\left(1 + \frac{1}{a}\right)\right)^2\right) \).

Value

dweibull gives the density, pweibull gives the distribution function, qweibull gives the quantile
function, and rweibull generates random deviates.

Invalid arguments will result in return value NaN, with a warning.

The length of the result is determined by n for rweibull, and is the maximum of the lengths of the
numerical arguments for the other functions.

The numerical arguments other than n are recycled to the length of the result. Only the first elements
of the logical arguments are used.

Note

The cumulative hazard \( H(t) = -\log(1 - F(t)) \) is

\[-pweibull(t, a, b, lower = FALSE, log = TRUE)\]

which is just \( H(t) = \left(\frac{t}{b}\right)^a \).

Source

[dpq]weibull are calculated directly from the definitions. rweibull uses inversion.

References

weighted.mean

Weighted Arithmetic Mean

Description

Compute a weighted mean.

Usage

weighted.mean(x, w, ...)

## Default S3 method:
weighted.mean(x, w, ..., na.rm = FALSE)

Arguments

x
an object containing the values whose weighted mean is to be computed.
w
a numerical vector of weights the same length as x giving the weights to use for elements of x.
...
arguments to be passed to or from methods.
na.rm
a logical value indicating whether NA values in x should be stripped before the computation proceeds.

Details

This is a generic function and methods can be defined for the first argument x: apart from the default methods there are methods for the date-time classes "POSIXct", "POSIXlt", "difftime" and "Date". The default method will work for any numeric-like object for which [, multiplication, division and sum have suitable methods, including complex vectors.

If w is missing then all elements of x are given the same weight, otherwise the weights are normalized to sum to one (if possible: if their sum is zero or infinite the value is likely to be NaN).

Missing values in w are not handled specially and so give a missing value as the result. However, zero weights are handled specially and the corresponding x values are omitted from the sum.

Value

For the default method, a length-one numeric vector.

See Also

Distributions for other standard distributions, including the Exponential which is a special case of the Weibull distribution.

Examples

x <- c(0, rlnorm(50))
all.equal(dweibull(x, shape = 1), dexp(x))
all.equal(pweibull(x, shape = 1, scale = pi), pexp(x, rate = 1/pi))
## Cumulative hazard H():
all.equal(pweibull(x, 2.5, pi, lower.tail = FALSE, log.p = TRUE),
         -(x/pi)^2.5, tolerance = 1e-15)
all.equal(qweibull(x/11, shape = 1, scale = pi), qexp(x/11, rate = 1/pi))
weighted.residuals

Description

Computed weighted residuals from a linear model fit.

Usage

weighted.residuals(obj, drop0 = TRUE)

Arguments

obj

R object, typically of class \texttt{lm} or \texttt{glm}.

drop0

logical. If TRUE, drop all cases with \texttt{weights == 0}.

Details

Weighted residuals are based on the deviance residuals, which for a \texttt{lm} fit are the raw residuals $R_i$ multiplied by $\sqrt{w_i}$, where $w_i$ are the weights as specified in \texttt{lm}'s call.

Dropping cases with weights zero is compatible with \texttt{influence} and related functions.

Value

Numeric vector of length $n'$, where $n'$ is the number of non-0 weights (\texttt{drop0 = TRUE}) or the number of observations, otherwise.

See Also

\texttt{residuals}, \texttt{lm.influence}, etc.

Examples

## following on from example(lm)

all.equal(weighted.residuals(lm.D9), residuals(lm.D9))
x <- 1:10
w <- 0:9
y <- rnorm(x)
weighted.residuals(lmxy <- lm(y ~ x, weights = w))
weighted.residuals(lmxy, drop0 = FALSE)
weights

Extract Model Weights

Description

weights is a generic function which extracts fitting weights from objects returned by modeling functions.

Methods can make use of napredict methods to compensate for the omission of missing values. The default methods do so.

Usage

weights(object, ...)

Arguments

object  
an object for which the extraction of model weights is meaningful.

...  
other arguments passed to methods.

Value

Weights extracted from the object object: the default method looks for component "weights" and if not NULL calls napredict on it.

References


See Also

weights.glm

wilcox.test

Wilcoxon Rank Sum and Signed Rank Tests

Description

Performs one- and two-sample Wilcoxon tests on vectors of data; the latter is also known as ’Mann-Whitney’ test.

Usage

wilcox.test(x, ...)

## Default S3 method:
wilcox.test(x, y = NULL,
    alternative = c("two.sided", "less", "greater"),
    mu = 0, paired = FALSE, exact = NULL, correct = TRUE,
    conf.int = FALSE, conf.level = 0.95,
## Arguments

- **x**: numeric vector of data values. Non-finite (e.g., infinite or missing) values will be omitted.
- **y**: an optional numeric vector of data values: as with x non-finite values will be omitted.
- **alternative**: a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
- **mu**: a number specifying an optional parameter used to form the null hypothesis. See 'Details'.
- **paired**: a logical indicating whether you want a paired test.
- **exact**: a logical indicating whether an exact p-value should be computed.
- **correct**: a logical indicating whether to apply continuity correction in the normal approximation for the p-value.
- **conf.int**: a logical indicating whether a confidence interval should be computed.
- **conf.level**: confidence level of the interval.
- **tol.root**: (when conf.int is true:) a positive numeric tolerance, used in \texttt{uniroot(*, tol=tol.root)} calls.
- **digits.rank**: a number; if finite, \texttt{rank(signif(r, digits.rank))} will be used to compute ranks for the test statistic instead of (the default) \texttt{rank(r)}.
- **formula**: a formula of the form \(lhs \sim rhs\) where \(lhs\) is a numeric variable giving the data values and \(rhs\) either 1 for a one-sample or paired test or a factor with two levels giving the corresponding groups. If \(lhs\) is of class "Pair" and \(rhs\) is 1, a paired test is done.
- **data**: an optional matrix or data frame (or similar: see \texttt{model.frame}) containing the variables in the formula \texttt{formula}. By default the variables are taken from \texttt{environment(formula)}.
- **subset**: an optional vector specifying a subset of observations to be used.
- **na.action**: a function which indicates what should happen when the data contain NAs. Defaults to \texttt{getOption("na.action")}.
- **...**: further arguments to be passed to or from methods.

## Details

The formula interface is only applicable for the 2-sample tests.

If only \(x\) is given, or if both \(x\) and \(y\) are given and paired is \TRUE, a Wilcoxon signed rank test of the null that the distribution of \(x\) (in the one sample case) or of \(x - y\) (in the paired two sample case) is symmetric about \(mu\) is performed.

Otherwise, if both \(x\) and \(y\) are given and paired is \FALSE, a Wilcoxon rank sum test (equivalent to the Mann-Whitney test: see the Note) is carried out. In this case, the null hypothesis is that the distributions of \(x\) and \(y\) differ by a location shift of \(mu\) and the alternative is that they differ by some other location shift (and the one-sided alternative "greater" is that \(x\) is shifted to the right of \(y\)).
By default (if `exact` is not specified), an exact p-value is computed if the samples contain less than 50 finite values and there are no ties. Otherwise, a normal approximation is used.

For stability reasons, it may be advisable to use rounded data or to set `digits.rank = 7`, say, such that determination of ties does not depend on very small numeric differences (see the example).

Optionally (if argument `conf.int` is true), a nonparametric confidence interval and an estimator for the pseudomedian (one-sample case) or for the difference of the location parameters $x - y$ is computed. (The pseudomedian of a distribution $F$ is the median of the distribution of $(u + v)/2$, where $u$ and $v$ are independent, each with distribution $F$. If $F$ is symmetric, then the pseudomedian and median coincide. See Hollander & Wolfe (1973), page 34.) Note that in the two-sample case the estimator for the difference in location parameters does **not** estimate the difference in medians (a common misconception) but rather the median of the difference between a sample from $x$ and a sample from $y$.

If exact p-values are available, an exact confidence interval is obtained by the algorithm described in Bauer (1972), and the Hodges-Lehmann estimator is employed. Otherwise, the returned confidence interval and point estimate are based on normal approximations. These are continuity-corrected for the interval but **not** the estimate (as the correction depends on the alternative).

With small samples it may not be possible to achieve very high confidence interval coverages. If this happens a warning will be given and an interval with lower coverage will be substituted.

When $x$ (and $y$ if applicable) are valid, the function now always returns, also in the `conf.int = TRUE` case when a confidence interval cannot be computed, in which case the interval boundaries and sometimes the estimate now contain NaN.

**Value**

A list with class "htest" containing the following components:

- **statistic** the value of the test statistic with a name describing it.
- **parameter** the parameter(s) for the exact distribution of the test statistic.
- **p.value** the p-value for the test.
- **null.value** the location parameter $\mu$.
- **alternative** a character string describing the alternative hypothesis.
- **method** the type of test applied.
- **data.name** a character string giving the names of the data.
- **conf.int** a confidence interval for the location parameter. (Only present if argument `conf.int = TRUE`.)
- **estimate** an estimate of the location parameter. (Only present if argument `conf.int = TRUE`.)

**Warning**

This function can use large amounts of memory and stack (and even crash R if the stack limit is exceeded) if `exact = TRUE` and one sample is large (several thousands or more).

**Note**

The literature is not unanimous about the definitions of the Wilcoxon rank sum and Mann-Whitney tests. The two most common definitions correspond to the sum of the ranks of the first sample with the minimum value subtracted or not: R subtracts and S-PLUS does not, giving a value which is larger by $m(m + 1)/2$ for a first sample of size $m$. (It seems Wilcoxon’s original paper used the unadjusted sum of the ranks but subsequent tables subtracted the minimum.)
R's value can also be computed as the number of all pairs \((x[i], y[j])\) for which \(y[j]\) is not greater than \(x[i]\), the most common definition of the Mann-Whitney test.

References


See Also

`psignrank`, `pwilcox`.

`wilcox_test` in package `coin` for exact, asymptotic and Monte Carlo conditional p-values, including in the presence of ties.

`kruskal.test` for testing homogeneity in location parameters in the case of two or more samples;

`t.test` for an alternative under normality assumptions [or large samples]

Examples

```r
require(graphics)

## One-sample test.
## Hollander & Wolfe (1973), 29f.
## Hamilton depression scale factor measurements in 9 patients with
## mixed anxiety and depression, taken at the first (x) and second
## (y) visit after initiation of a therapy (administration of a
## tranquilizer).
x <- c(1.83, 0.50, 1.62, 2.48, 1.68, 1.88, 1.55, 3.06, 1.30)
y <- c(0.878, 0.647, 0.598, 2.05, 1.06, 1.29, 1.06, 3.14, 1.29)
wilcox.test(x, y, paired = TRUE, alternative = "greater")
wilcox.test(y - x, alternative = "less") # The same.
wilcox.test(y - x, alternative = "less", 
    exact = FALSE, correct = FALSE) # H&W large sample
    # approximation

## Two-sample test.
## Hollander & Wolfe (1973), 69f.
## Permeability constants of the human chorioamnion (a placental
## membrane) at term (x) and between 12 to 26 weeks gestational
## age (y). The alternative of interest is greater permeability
## of the human chorioamnion for the term pregnancy.
x <- c(0.80, 0.83, 1.89, 1.04, 1.45, 1.38, 1.91, 1.64, 0.73, 1.46)
y <- c(1.15, 0.88, 0.90, 0.74, 1.21)
wilcox.test(x, y, alternative = "g") # greater
wilcox.test(x, y, alternative = "greater", 
    exact = FALSE, correct = FALSE) # H&W large sample
    # approximation
```
wilcoxon.test(rnorm(10), rnorm(10, 2), conf.int = TRUE)

## Formula interface.
boxplot(Ozone ~ Month, data = airquality)
wilcoxon.test(Ozone ~ Month, data = airquality,
subset = Month %in% c(5, 8))

## accuracy in ties determination via 'digits.rank':
wilcoxon.test(4:2, 3:1, paired=TRUE) # Warning: cannot compute exact p-value with ties
wilcoxon.test((4:2)/10, (3:1)/10, paired=TRUE) # no ties => no* warning
wilcoxon.test((4:2)/10, (3:1)/10, paired=TRUE, digits.rank = 9) # same ties as (4:2, 3:1)

---

### Wilcoxon

#### Distribution of the Wilcoxon Rank Sum Statistic

**Description**

Density, distribution function, quantile function and random generation for the distribution of the Wilcoxon rank sum statistic obtained from samples with size \( m \) and \( n \), respectively.

**Usage**

\[
dwilcox(x, m, n, log = FALSE)
pwilcox(q, m, n, lower.tail = TRUE, log.p = FALSE)
qwilcox(p, m, n, lower.tail = TRUE, log.p = FALSE)
rwilcox(nn, m, n)
\]

**Arguments**

- \( x, q \) vector of quantiles.
- \( p \) vector of probabilities.
- \( nn \) number of observations. If \( \text{length}(nn) > 1 \), the length is taken to be the number required.
- \( m, n \) numbers of observations in the first and second sample, respectively. Can be vectors of positive integers.
- \( \text{log}, \text{log.p} \) logical; if TRUE, probabilities \( p \) are given as \( \log(p) \).
- \( \text{lower.tail} \) logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).

**Details**

This distribution is obtained as follows. Let \( x \) and \( y \) be two random, independent samples of size \( m \) and \( n \). Then the Wilcoxon rank sum statistic is the number of all pairs \((x[i], y[j])\) for which \( y[j] \) is not greater than \( x[i] \). This statistic takes values between 0 and \( m \times n \), and its mean and variance are \( m \times n / 2 \) and \( m \times n \times (m + n + 1) / 12 \), respectively.

If any of the first three arguments are vectors, the recycling rule is used to do the calculations for all combinations of the three up to the length of the longest vector.
Value

dwilcox gives the density, pwilcox gives the distribution function, qwilcox gives the quantile function, and rwilcox generates random deviates.
The length of the result is determined by nn for rwilcox, and is the maximum of the lengths of the numerical arguments for the other functions.
The numerical arguments other than nn are recycled to the length of the result. Only the first elements of the logical arguments are used.

Warning

These functions can use large amounts of memory and stack (and even crash R if the stack limit is exceeded and stack-checking is not in place) if one sample is large (several thousands or more).

Note

S-PLUS uses a different (but equivalent) definition of the Wilcoxon statistic: see wilcox.test for details.

Author(s)

Kurt Hornik

Source

These ("d","p","q") are calculated via recursion, based on cwilcox(k, m, n), the number of choices with statistic k from samples of size m and n, which is itself calculated recursively and the results cached. Then dwilcox and pwilcox sum appropriate values of cwilcox, and qwilcox is based on inversion.

rwilcox generates a random permutation of ranks and evaluates the statistic. Note that it is based on the same C code as sample(), and hence is determined by .Random.seed, notably from RNGkind(sample.kind = ..) which changed with R version 3.6.0.

See Also

wilcox.test to calculate the statistic from data, find p values and so on.
Distributions for standard distributions, including dsignrank for the distribution of the one-sample Wilcoxon signed rank statistic.

Examples

```
require(graphics)
x <- -1:(4*6 + 1)
fx <- dwilcox(x, 4, 6)
Fx <- pwilcox(x, 4, 6)

layout(rbind(1,2), widths = 1, heights = c(3,2))
plot(x, fx, type = "h", col = "violet",
     main = "Probabilities (density) of Wilcoxon-Statist.(n=6, m=4)")
plot(x, Fx, type = "s", col = "blue",
     main = "Distribution of Wilcoxon-Statist.(n=6, m=4)")
abline(h = 0:1, col = "gray20", lty = 2)
layout(1) # set back
```
N <- 200
hist(U <- rwilcox(N, m = 4, n = 6), breaks = 0:25 - 1/2,
    border = "red", col = "pink", sub = paste("N =", N))
mtext("N * f(x), f() = true "density"", side = 3, col = "blue")
lines(x, N*fx, type = "h", col = "blue", lwd = 2)
points(x, N*fx, cex = 2)

## Better is a Quantile-Quantile Plot
qqplot(U, qw <- qwilcox((1:N - 1/2)/N, m = 4, n = 6),
    main = paste("Q-Q-Plot of empirical and theoretical quantiles",
        "Wilcoxon Statistic, (m=4, n=6)\n"))
n <- as.numeric(names(print(tU <- table(U))))
text(n+.2, n+.5, labels = tU, col = "red")

window

Time (Series) Windows

Description

window is a generic function which extracts the subset of the object x observed between the times start and end. If a frequency is specified, the series is then re-sampled at the new frequency.

Usage

window(x, ...)
## S3 method for class 'ts'
window(x, ...)
## Default S3 method:
window(x, start = NULL, end = NULL,
    frequency = NULL, deltat = NULL, extend = FALSE, ts.eps = getOption("ts.eps"), ...)

window(x, ...) <- value
## S3 replacement method for class 'ts'
window(x, start, end, frequency, deltat, ...) <- value

Arguments

x a time-series (or other object if not replacing values).
start the start time of the period of interest.
end the end time of the period of interest.
frequency, deltat
    the new frequency can be specified by either (or both if they are consistent).
extend logical. If true, the start and end values are allowed to extend the series. If false, attempts to extend the series give a warning and are ignored.
ts.e.ps time series comparison tolerance. Frequencies are considered equal if their absolute difference is less than ts.e.ps and boundaries (length-1 versions of start and end) are checked with fuzz ts.e.ps/frequency(x).
...
    further arguments passed to or from other methods.
value replacement values.
Details

The start and end times can be specified as for ts. If there is no observation at the new start or end, the immediately following (start) or preceding (end) observation time is used.

The replacement function has a method for ts objects, and is allowed to extend the series (with a warning). There is no default method.

Value

The value depends on the method. window.default will return a vector or matrix with an appropriate tsp attribute.

window.ts differs from window.default only in ensuring the result is a ts object.

If extend = TRUE the series will be padded with NAs if needed.

References


See Also

time, ts.

Examples

window(presidents, 1960, c(1969,4)) # values in the 1960's
window(presidents, deltat = 1) # All Qtr1s
window(presidents, start = c(1945,3), deltat = 1) # All Qtr3s
window(presidents, 1944, c(1979,2), extend = TRUE)

pres <- window(presidents, 1945, c(1949,4)) # values in the 1940's
window(pres, 1945.25, 1945.50) <- c(60, 70)
window(pres, 1944, 1944.75) <- 0 # will generate a warning
window(pres, c(1945,4), c(1949,4), frequency = 1) <- 85:89

pres

xtabs

Cross Tabulation

Description

Create a contingency table (optionally a sparse matrix) from cross-classifying factors, usually contained in a data frame, using a formula interface.

Usage

xtabs(formula = ~., data = parent.frame(), subset, sparse = FALSE,
na.action, addNA = FALSE, exclude = if(laddNA) c(NA, NaN),
drop.unused.levels = FALSE)

## S3 method for class 'xtabs'
print(x, na.print = "", ...)
xtabs

Arguments

- **formula**: a formula object with the cross-classifying variables (separated by \(+\)) on the right hand side (or an object which can be coerced to a formula). Interactions are not allowed. On the left hand side, one may optionally give a vector or a matrix of counts; in the latter case, the columns are interpreted as corresponding to the levels of a variable. This is useful if the data have already been tabulated, see the examples below.

- **data**: an optional matrix or data frame (or similar: see `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.

- **subset**: an optional vector specifying a subset of observations to be used.

- **sparse**: logical specifying if the result should be a sparse matrix, i.e., inheriting from `sparseMatrix`. Only works for two factors (since there are no higher-order sparse array classes yet).

- **na.action**: a function which indicates what should happen when the data contain NAs. If unspecified, and `addNA` is true, this is set to `na.pass`. When it is `na.omit` and `formula` has a left hand side (with counts), `sum(*, na.rm = TRUE)` is used instead of `sum(*)` for the counts.

- **addNA**: logical indicating if NAs should get a separate level and be counted, using `addNA(*, ifany=TRUE)` and setting the default for `na.action` to `na.pass`.

- **exclude**: a vector of values to be excluded when forming the set of levels of the classifying factors.

- **drop.unused.levels**: a logical indicating whether to drop unused levels in the classifying factors. If this is `FALSE` and there are unused levels, the table will contain zero marginals, and a subsequent chi-squared test for independence of the factors will not work.

- **x**: an object of class "xtabs".

- **na.print**: character string (or NULL) indicating how NA are printed. The default ("") does not show NAs clearly, and `na.print = "NA"` maybe advisable instead.

- **...**: further arguments passed to or from other methods.

Details

There is a summary method for contingency table objects created by `table` or `xtabs(*, sparse = FALSE)`, which gives basic information and performs a chi-squared test for independence of factors (note that the function `chisq.test` currently only handles 2-d tables).

If a left hand side is given in `formula`, its entries are simply summed over the cells corresponding to the right hand side; this also works if the lhs does not give counts.

For variables in `formula` which are factors, `exclude` must be specified explicitly; the default exclusions will not be used.

In R versions before 3.4.0, e.g., when `na.action = na.pass`, sometimes zeroes (0) were returned instead of NAs.

Note that when `addNA` is false as by default, and `na.action` is not specified (or set to NULL), in effect `na.action =getOption("na.action", default=na.omit)` is used; see also the examples.
Value

By default, when `sparse = FALSE`, a contingency table in array representation of S3 class c("xtabs", "table"), with a "call" attribute storing the matched call.

When `sparse = TRUE`, a sparse numeric matrix, specifically an object of S4 class `dgTMatrix` from package `Matrix`.

See Also

`table` for traditional cross-tabulation, and `as.data.frame.table` which is the inverse operation of `xtabs` (see the example below).

`sparseMatrix` on sparse matrices in package `Matrix`.

Examples

```r
## 'esoph' has the frequencies of cases and controls for all levels of
## the variables 'agegp', 'alcgp', and 'tobgp'.
xtabs(cbind(ncases, ncontrols) ~ ., data = esoph)
## Output is not really helpful ... flat tables are better:
ftable(xtabs(cbind(ncases, ncontrols) ~ ., data = esoph))
## In particular if we have fewer factors ... 
ftable(xtabs(cbind(ncases, ncontrols) ~ agegp, data = esoph))

## This is already a contingency table in array form.
DF <- as.data.frame(UCBAdmissions)
## Now 'DF' is a data frame with a grid of the factors and the counts
## in variable 'Freq'.
DF
## Nice for taking margins ...
xtabs(Freq ~ Gender + Admit, DF)
## And for testing independence ...
summary(xtabs(Freq ~ ., DF))

## with NA's
DN <- DF; DN[cbind(6:9, c(1:2,4,1))] <- NA
DN # 'Freq' is missing only for (Rejected, Female, B)
tools::assertError(# 'na.fail' should fail :
xtabs(Freq ~ Gender + Admit, DN, na.action=na.fail), verbose=TRUE)
op <- options(na.action = "na.fail") # the "factory" default
(xtabs(Freq ~ Gender + Admit, DN) -> xtD)
noC <- function(O) `attr<-(O, "call", NULL)
ident_noC <- function(x,y) identical(noC(x), noC(y))
stopifnot(exprs = {
  ident_noC(xtD, xtabs(Freq ~ Gender + Admit, DN, na.action = na.omit))
  ident_noC(xtD, xtabs(Freq ~ Gender + Admit, DN, na.action = NULL))
})

xtabs(Freq ~ Gender + Admit, DN, na.action = na.pass)
## The Female:Rejected combination has NA 'Freq' (and NA prints 'invisibly' as "")
(xtNA <- xtabs(Freq ~ Gender + Admit, DN, addNA = TRUE)) # ==> count NAs
## show NA's better via na.print = ".." :
print(xtNA, na.print= "NA")

## Create a nice display for the warp break data.
warpbreaks$replicate <- rep_len(1:9, 54)
```
xtabs

ftable(xtabs(breaks ~ wool + tension + replicate, data = warpbreaks))

### ---- Sparse Examples ----

if(require("Matrix")) withAutoprint({
  ## similar to "nlme"s 'ergoStool':
  d.ergo <- data.frame(Type = paste0("T", rep(1:4, 9*4)),
                        Subj = gl(9, 4, 36*4))
  xtabs(~ Type + Subj, data = d.ergo) # 4 replicates each
  set.seed(15) # a subset of cases:
  xtabs(~ Type + Subj, data = d.ergo[sample(36, 10), ], sparse = TRUE)

  ## Hypothetical two-level setup:
  inner <- factor(sample(letters[1:25], 100, replace = TRUE))
  inout <- factor(sample(LETTERS[1:5], 25, replace = TRUE))
  fr <- data.frame(inner = inner, outer = inout[as.integer(inner)])
  xtabs(~ inner + outer, fr, sparse = TRUE)
})
Chapter 11

The stats4 package

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<th>Statistical Functions using S4 Classes</th>
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**Description**

Statistical Functions using S4 classes.

**Details**

This package contains functions and classes for statistics using the S version 4 class system.

The methods currently support maximum likelihood (function `mle()` returning class "mle"), including methods for `logLik` for use with `AIC`.

**Author(s)**

R Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

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<th>coef-methods</th>
<th>Methods for Function coef in Package stats4</th>
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**Description**

Extract the coefficient vector from "mle" objects.

**Methods**

signature(object = "ANY") Generic function: see `coef`.

signature(object = "mle") Extract the full coefficient vector (including any fixed coefficients) from the fit.

signature(object = "summary.mle") Extract the coefficient vector and standard errors from the summary of the fit.
confint-methods

Methods for Function confint in Package stats4

Description

Generate confidence intervals

Methods

signature(object = "ANY") Generic function: see confint.
signature(object = "mle") First generate profile and then confidence intervals from the profile.
signature(object = "profile.mle") Generate confidence intervals based on likelihood profile.

logLik-methods

Methods for Function logLik in Package stats4

Description

Extract the maximized log-likelihood from "mle" objects.

Methods

signature(object = "ANY") Generic function: see logLik.
signature(object = "mle") Extract log-likelihood from the fit.

Note

The mle method does not know about the number of observations unless nobs was specified on the call and so may not be suitable for use with BIC.

mle

Maximum Likelihood Estimation

Description

Estimate parameters by the method of maximum likelihood.

Usage

mle(minuslogl, start,
     optim = stats::optim,
     method = if(!useLim) "BFGS" else "L-BFGS-B",
     fixed = list(), nobs, lower, upper, ...)
Arguments

minuslogl Function to calculate negative log-likelihood.
start Named list of vectors or single vector. Initial values for optimizer. By default taken from the default arguments of minuslogl
optim Optimizer function. (Experimental)
method Optimization method to use. See optim.
fixed Named list of vectors or single vector. Parameter values to keep fixed during optimization.
nobs optional integer: the number of observations, to be used for e.g. computing BIC.
lower, upper Named lists of vectors or single vectors. Bounds for optim, if relevant.
... Further arguments to pass to optim.

Details

The optim optimizer is used to find the minimum of the negative log-likelihood. An approximate covariance matrix for the parameters is obtained by inverting the Hessian matrix at the optimum. By default, optim from the stats package is used; other optimizers need to be plug-compatible, both with respect to arguments and return values.

The function minuslogl should take one or several arguments, each of which can be a vector. The optimizer optimizes a function which takes a single vector argument, containing the concatenation of the arguments to minuslogl, removing any values that should be held fixed. This function internally unpacks the argument vector, inserts the fixed values and calls minuslogl.

The vector arguments start, fixed, upper, and lower, can be given in both packed and unpacked form, either as a single vector or as a list of vectors. In the latter case, you only need to specify those list elements that are actually affected. For vector arguments, including those inside lists, use a default marker for those values that you don’t want to set: NA for fixed and start, and +Inf, -Inf for upper, and lower.

Value

An object of class mle-class.

Note

Notice that the mll argument should calculate -log L (not -2 log L). It is for the user to ensure that the likelihood is correct, and that asymptotic likelihood inference is valid.

See Also

mle-class

Examples

## Avoid printing to unwarranted accuracy
od <- options(digits = 5)

## Simulated EC50 experiment with count data
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)

## Easy one-dimensional MLE:
nLL <- function(lambda) -sum(stats::dpois(y, lambda, log = TRUE))
fit0 <- mle(nLL, start = list(lambda = 5), nobs = NROW(y))
## sanity check --- notice that "nobs" must be input
## (not guaranteed to be meaningful for any likelihood)
stopifnot(nobs(fit0) == length(y))

# For 1D, this is preferable:
fit1 <- mle(nLL, start = list(lambda = 5), nobs = NROW(y),
   method = "Brent", lower = 1, upper = 20)

## This needs a constrained parameter space: most methods will accept NA
ll <- function(ymax = 15, xhalf = 6) {
   if(ymax > 0 && xhalf > 0)
      -sum(stats::dpois(y, lambda = ymax/(1+x/xhalf), log = TRUE))
   else NA
}
(fit <- mle(ll, nobs = length(y)))
mle(ll, fixed = list(xhalf = 6))

## Alternative using bounds on optimization
ll2 <- function(ymax = 15, xhalf = 6)
   -sum(stats::dpois(y, lambda = ymax/(1+x/xhalf), log = TRUE))
mle(ll2, lower = rep(0, 2))

AIC(fit)
BIC(fit)

summary(fit)
logLik(fit)
vcov(fit)
plot(profile(fit), absVal = FALSE)
confint(fit)

## Use bounded optimization
## The lower bounds are really > 0,
## but we use >=0 to stress-test profiling
(fit2 <- mle(ll2, lower = c(0, 0)))
plot(profile(fit2), absVal = FALSE)

## A better parametrization:
ll3 <- function(lymax = log(15), lxhalf = log(6))
   -sum(stats::dpois(y, lambda = exp(lymax)/(1+x/exp(lxhalf)), log = TRUE))
(fit3 <- mle(ll3))
plot(profile(fit3), absVal = FALSE)
exp(confint(fit3))

# Regression tests for bounded cases (this was broken in R 3.3)
fit4 <- mle(ll, lower = c(0, 4)) # has max on boundary

## direct check that fixed= and constraints work together
mle(ll, lower = c(0, 4), fixed=list(ymax=23)) # has max on boundary

## Linear regression using MLE
x <- 1:10
y <- c(0.48, 2.24, 2.22, 5.15, 4.64, 5.53, 7, 8.8, 7.67, 9.23)

LM_mll <- function(formula, data = environment(formula))
{
  y <- model.response(model.frame(formula, data))
  X <- model.matrix(formula, data)
  b0 <- numeric(NCOL(X))
  names(b0) <- colnames(X)
  function(b=b0, sigma=1)
    -sum(dnorm(y, X %*% b, sigma, log=TRUE))
}

mll <- LM_mll(y ~ x)

summary(lm(y~x))  # for comparison -- notice variance bias in MLE
summary(mle(mll, lower=c(-Inf,-Inf, 0.01))))
summary(mle(mll, lower=list(sigma = 0.01))))  # alternative specification

confint(mle(mll, lower=list(sigma = 0.01)))
plot(profile(mle(mll, lower=list(sigma = 0.01))))

Binom_mll <- function(x, n)
{
  force(x); force(n) ## beware lazy evaluation
  function(p=.5) -dbinom(x, n, p, log=TRUE)
}

## Likelihood functions for different x.
## This code goes wrong, if force(x) is not used in Binom_mll:
curve(Binom_mll(0, 10)(p), xname="p", ylim=c(0, 10))
mll_list <- list(10)
for (x in 1:10)
  mll_list[[x]] <- Binom_mll(x, 10)
for (mll in mll_list)
  curve(mll(p), xname="p", add=TRUE)

mll <- Binom_mll(4,10)
mle(mll, lower = 1e-16, upper = 1-1e-16)  # limits must be inside (0,1)

## Boundary case: This works, but fails if limits are set closer to 0 and 1
mll <- Binom_mll(0, 10)
mle(mll, lower=.005, upper=.995)

## Not run:
## We can use limits closer to the boundaries if we use the
## drop-in replacement optimr() from the optimx package.

mle(mll, lower = 1e-16, upper = 1-1e-16, optim=optimx::optimr)

## End(Not run)

options(od)
**mle-class**  
*Class “mle” for Results of Maximum Likelihood Estimation*

**Description**

This class encapsulates results of a generic maximum likelihood procedure.

**Objects from the Class**

Objects can be created by calls of the form `new("mle", ...)`, but most often as the result of a call to `mle`.

**Slots**

- **call**: Object of class "language". The call to `mle`.
- **coef**: Object of class "numeric". Estimated parameters.
- **fullcoef**: Object of class "numeric". Full parameter set of fixed and estimated parameters.
- **fixed**: Object of class "numeric". Fixed parameter values (NA for non-fixed parameters).
- **vcov**: Object of class "matrix". Approximate variance-covariance matrix.
- **min**: Object of class "numeric". Minimum value of objective function.
- **details**: a "list", as returned from `optim`.
- **minuslogl**: Object of class "function". The negative loglikelihood function.
- **nobs**: "integer" of length one. The number of observations (often NA, when not set in call explicitly).
- **method**: Object of class "character". The optimization method used.

**Methods**

- **confint** signature(object = "mle"): Confidence intervals from likelihood profiles.
- **logLik** signature(object = "mle"): Extract maximized log-likelihood.
- **profile** signature(fitted = "mle"): Likelihood profile generation.
- **nobs** signature(object = "mle"): Number of observations, here simply accessing the `nobs` slot mentioned above.
- **show** signature(object = "mle"): Display object briefly.
- **summary** signature(object = "mle"): Generate object summary.
- **update** signature(object = "mle"): Update fit.
- **vcov** signature(object = "mle"): Extract variance-covariance matrix.
Description

Plot profile likelihoods for "mle" objects.

Usage

## S4 method for signature 'profile.mle,missing'
plot(x, levels, conf = c(99, 95, 90, 80, 50)/100, nseg = 50,
     absVal = TRUE, ...)

Arguments

x an object of class "profile.mle"
levels levels, on the scale of the absolute value of a t statistic, at which to interpolate
       intervals. Usually conf is used instead of giving levels explicitly.
conf a numeric vector of confidence levels for profile-based confidence intervals on
       the parameters.
nseg an integer value giving the number of segments to use in the spline interpolation
       of the profile t curves.
absVal a logical value indicating whether or not the plots should be on the scale of the
       absolute value of the profile t. Defaults to TRUE.
...
other arguments to the plot function can be passed here.

Methods

signature(x = "ANY", y = "ANY") Generic function: see plot.
signature(x = "profile.mle", y = "missing") Plot likelihood profiles for x.

profile-methods

Methods for Function profile in Package stats4

Description

Profile likelihood for "mle" objects.

Usage

## S4 method for signature 'mle'
profile(fitted, which = 1:p, maxsteps = 100, alpha = 0.01,
       zmax = sqrt(qchisq(1 - alpha, 1L)), del = zmax/5,
       trace = FALSE, ...)
profile.mle-class

Arguments

- **fitted**: Object to be profiled
- **which**: Optionally select subset of parameters to profile.
- **maxsteps**: Maximum number of steps to bracket \( z_{\text{max}} \).
- **alpha**: Significance level corresponding to \( z_{\text{max}} \), based on a Scheffe-style multiple testing interval. Ignored if \( z_{\text{max}} \) is specified.
- **zmax**: Cutoff for the profiled value of the signed root-likelihood.
- **del**: Initial stepsize on root-likelihood scale.
- **trace**: Logical. Print intermediate results.
- **...**: Currently unused.

Details

The profiling algorithm tries to find an approximately evenly spaced set of at least five parameter values (in each direction from the optimum) to cover the root-likelihood function. Some care is taken to try and get sensible results in cases of high parameter curvature. Notice that it may not always be possible to obtain the cutoff value, since the likelihood might level off.

Value

An object of class "profile.mle", see "profile.mle-class".

Methods

- `signature(fitted = "ANY")`: Generic function: see `profile`.
- `signature(fitted = "mle")`: Profile the likelihood in the vicinity of the optimum of an "mle" object.

profile.mle-class  Class "profile.mle"; Profiling information for "mle" object

Description

Likelihood profiles along each parameter of likelihood function

Objects from the Class

Objects can be created by calls of the form `new("profile.mle", ...)`, but most often by invoking `profile` on an "mle" object.

Slots

- **profile**: Object of class "list". List of profiles, one for each requested parameter. Each profile is a data frame with the first column called \( z \) being the signed square root of the -2 log likelihood ratio, and the others being the parameters with names prefixed by `par.vals`.
- **summary**: Object of class "summary.mle". Summary of object being profiled.
Methods

**confint** signature(object = "profile.mle"): Use profile to generate approximate confidence intervals for parameters.

**plot** signature(x = "profile.mle", y = "missing"): Plot profiles for each parameter.

See Also

`mle, mle-class, summary.mle-class`

---

Description

Show objects of classes `mle` and `summary.mle`

Methods

signature(object = "mle") Print simple summary of `mle` object. Just the coefficients and the call.

signature(object = "summary.mle") Shows call, table of coefficients and standard errors, and $-2 \log L$.

---

Description

Summarize objects

Methods

signature(object = "ANY") Generic function

signature(object = "mle") Generate a summary as an object of class "summary.mle", containing estimates, asymptotic SE, and value of $-2 \log L$. 
Class "summary.mle", Summary of "mle" Objects

Description

Extract of "mle" object

Objects from the Class

Objects can be created by calls of the form `new("summary.mle", ...)`, but most often by invoking `summary` on an "mle" object. They contain values meant for printing by `show`.

Slots

call: Object of class "language" The call that generated the "mle" object.
coef: Object of class "matrix". Estimated coefficients and standard errors
m2logL: Object of class "numeric". Minus twice the log likelihood.

Methods

`show` signature(object = "summary.mle"): Pretty-prints object
`coef` signature(object = "summary.mle"): Extracts the contents of the coef slot

See Also

`summary, mle, mle-class`

Methods for Function `update` in Package `stats4`

Description

Update "mle" objects.

Usage

```r
## S4 method for signature 'mle'
update(object, ..., evaluate = TRUE)
```

Arguments

- **object**  
  An existing fit.
- **...**  
  Additional arguments to the call, or arguments with changed values. Use `name = NULL` to remove the argument `name`.
- **evaluate**  
  If true evaluate the new call else return the call.
Methods

signature(object = "ANY") Generic function: see update.
signature(object = "mle") Update a fit.

Examples

x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 8, 5, 4, 8)
l1 <- function(ymax = 15, xhalf = 6)
  -sum(stats::dpois(y, lambda = ymax/(1+x/xhalf), log = TRUE))
fit <- mle(l1)
## note the recorded call contains ..1, a problem with S4 dispatch
update(fit, fixed = list(xhalf = 3))
Chapter 12

The tcltk package

---

tcltk-package  

*Tcl/Tk Interface*

**Description**

Interface and language bindings to Tcl/Tk GUI elements.

**Details**

This package provides access to the platform-independent Tcl scripting language and Tk GUI elements. See TkWidgets for a list of supported widgets, TkWidgetcmds for commands to work with them, and references in those files for more.

The Tcl/Tk documentation is in the system man pages.

For a complete list of functions, use `ls("package:tcltk")`.

Note that Tk will not be initialized if there is no `DISPLAY` variable set, but Tcl can still be used. This is most useful to allow the loading of a package which depends on tcltk in a session that does not actually use it (e.g., during installation).

**Author(s)**

R Core Team

Maintainer: R Core Team <R-core@r-project.org>

---

TclInterface  

*Low-level Tcl/Tk Interface*

**Description**

These functions and variables provide the basic glue between R and the Tcl interpreter and Tk GUI toolkit. Tk windows may be represented via R objects. Tcl variables can be accessed via objects of class `tclVar` and the C level interface to Tcl objects is accessed via objects of class `tclObj`.

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Usage

.Tcl(...)  
.Tcl.objv(objv)  
.Tcl.args(...)  
.Tcl.args.objv(...)  
.Tcl.callback(...)  
.Tk.ID(win)  
.Tk.newwin(ID)  
.Tk.subwin(parent)  
.TkRoot  
.TkUp

tkdestroy(win)  
is.tkwin(x)

tclvalue(x)  
tclvalue(x) <- value

tclVar(init = "")  
## S3 method for class 'tclVar'  
as.character(x, ...)  
## S3 method for class 'tclVar'  
tclvalue(x)  
## S3 replacement method for class 'tclVar'  
tclvalue(x) <- value

tclArray()  
## S3 method for class 'tclArray'  
x[[...]]  
## S3 replacement method for class 'tclArray'  
x[[...]] <- value  
## S3 method for class 'tclArray'  
x$i  
## S3 replacement method for class 'tclArray'  
x$i <- value

## S3 method for class 'tclArray'  
names(x)  
## S3 method for class 'tclArray'  
length(x)

tclObj(x)  
tclObj(x) <- value  
## S3 method for class 'tclVar'  
tclObj(x)  
## S3 replacement method for class 'tclVar'  
tclObj(x) <- value

as.tclObj(x, drop = FALSE)  
is.tclObj(x)

## S3 method for class 'tclObj'
as.character(x, ...)  
## S3 method for class 'tclObj'
as.integer(x, ...)  
## S3 method for class 'tclObj'
as.double(x, ...)  
## S3 method for class 'tclObj'
as.logical(x, ...)  
## S3 method for class 'tclObj'
as.raw(x, ...)  
## S3 method for class 'tclObj'
tclvalue(x)

## Default S3 method:
tclvalue(x)
## Default S3 replacement method:
tclvalue(x) <- value

addTclPath(path = ".")
tclRequire(package, warn = TRUE)
tclVersion()

Arguments

- **objv**: a named vector of Tcl objects
- **win**: a window structure
- **x**: an object
- **i**: character or (unquoted) name
- **drop**: logical. Indicates whether a single-element vector should be made into a simple Tcl object or a list of length one
- **value**: For tclvalue assignments, a character string. For tclObj assignments, an object of class tclObj
- **ID**: a window ID
- **parent**: a window which becomes the parent of the resulting window
- **path**: path to a directory containing Tcl packages
- **package**: a Tcl package name
- **warn**: logical. Warn if not found?
- **...**: Additional arguments. See below.
- **init**: initialization value

Details

Many of these functions are not intended for general use but are used internally by the commands that create and manipulate Tk widgets and Tcl objects. At the lowest level .Tcl sends a command as a text string to the Tcl interpreter and returns the result as an object of class tclObj (see below). A newer variant .Tcl.objv accepts arguments in the form of a named list of tclObj objects.

.Tcl.args converts an R argument list of tag = value pairs to the Tcl -option value style, thus enabling a simple translation between the two languages. To send a value with no preceding option flag to Tcl, just use an untagged argument. In the rare case one needs an option with no subsequent
value tag = NULL can be used. Most values are just converted to character mode and inserted in the
command string, but window objects are passed using their ID string, and callbacks are passed via
the result of .Tcl.callback. Tags are converted to option flags simply by prepending a -
.Tcl.args.objv serves a similar purpose as .Tcl.args but produces a list of tclObj objects
suitable for passing to .Tcl.objv. The names of the list are converted to Tcl option style internally
by .Tcl.objv.

Callbacks can be either atomic callbacks handled by .Tcl.callback or expressions. An expression
is treated as a list of atomic callbacks, with the following exceptions: if an element is a name, it
is first evaluated in the callers frame, and likewise if it is an explicit function definition; the break
expression is translated directly to the Tcl counterpart. .Tcl.callback converts R functions and
unevaluated calls to Tcl command strings. The argument must be either a function closure or an
object of mode "call" followed by an environment. The return value in the first case is of the
form R_call 0x4094d4 in which the hexadecimal number is the memory address of the function.
In the second case it will be of the form R_call_lang 0x8a95904 0x819bfd0. For expressions, a
sequence of similar items is generated, separated by semicolons.

.Tcl.args takes special precautions to ensure that functions or calls will continue to exist at the specified address by assigning the
callback into the relevant window environment (see below).

Tk windows are represented as objects of class tkwin which are lists containing a ID field and an
eenv field which is an R environments, enclosed in the global environment. The value of the ID
field is identical to the Tk window name. The env environment contains a parent variable and a
num.subwin variable. If the window obtains sub-windows and callbacks, they are added as variables
to the environment. .TkRoot is the top window with ID ".": this window is not displayed in order
to avoid ill effects of closing it via window manager controls. The parent variable is undefined for
.TkRoot.

.Tk.ID extracts the ID of a window, .Tk.newwin creates a new window environment with a given
ID and .Tk.subwin creates a new window which is a sub-window of a given parent window.

.TkUp is a logical flag to indicate whether the Tk widget system is active; if FALSE, only the Tcl
interpreter is available.

.ttkdestroy destroys a window and also removes the reference to a window from its parent.

is.tkwin can be used to test whether a given object is a window environment.

tc1Var creates a new Tcl variable and initializes it to init. An R object of class tc1Var is created
to represent it. Using as.character on the object returns the Tcl variable name. Accessing the Tcl
variable from R is done using the tclvalue function, which can also occur on the left-hand side of
assignments. If tclvalue is passed an argument which is not a tc1Var object, then it will assume
that it is a character string explicitly naming global Tcl variable. Tcl variables created by tc1Var
are uniquely named and automatically unset by the garbage collector when the representing object
is no longer in use.

tc1Array creates a new Tcl array and initializes it to the empty array. An R object of class tc1Array
and inheriting from class tc1Var is created to represent it. You can access elements of the Tcl
array using indexing with [[] or $, which also allow replacement forms. Notice that Tcl arrays are
associative by nature and hence unordered; indexing with a numeric index i refers to the element
with the name as.character(i). Multiple indices are pasted together separated by commas to
form a single name. You can query the length and the set of names in an array using methods for
length and names, respectively; these cannot meaningfully be set so assignment forms exist only
to print an error message.

It is possible to access Tcl's 'dual-ported' objects directly, thus avoiding parsing and deparsing of
their string representation. This works by using objects of class tc10bj. The string representation
of such objects can be extracted (but not set) using tclvalue and conversion to vectors of mode
"character", "double", "integer", "logical", and "raw" is performed using the standard co-
ercion functions as.character, etc. Conversely, such vectors can be converted using as.tc10bj.
There is an ambiguity as to what should happen for length one vectors, controlled by the drop argument; there are cases where the distinction matters to Tcl, although mostly it treats them equivalently. Notice that tclvalue and as.character differ on an object whose string representation has embedded spaces, the former is sometimes to be preferred, in particular when applied to the result of tclread, tkgetOpenFile, and similar functions. The as.raw method returns a raw vector or a list of raw vectors and can be used to return binary data from Tcl.

The object behind a tclVar object is extracted using tclObj(x) which also allows an assignment form, in which the right hand side of the assignment is automatically converted using as.tclObj.

There is a print method for tclObj objects; it prints <Tcl> followed by the string representation of the object. Notice that as.character on a tclVar object is the name of the corresponding Tcl variable and not the value.

Tcl packages can be loaded with tclRequire; it may be necessary to add the directory where they are found to the Tcl search path with addTclPath. The return value is a class "tclObj" object if it succeeds, or FALSE if it fails (when a warning is issued). To see the current search path as an R character vector, use

strsplit(tclvalue('auto_path'), " ")[1]

The Tcl version (including patchlevel) is returned as a character string (such as "8.6.3").

Note

Strings containing unbalanced braces are currently not handled well in many circumstances.

See Also

TKWidgets, TkCommands, TkWidgetcmds.

capabilities("tcltk") to see if Tcl/Tk support was compiled into this build of R.

Examples

tclVersion()

.Tcl("format "%s
" "Hello, World!
")
f <- function() cat("HI!
")
## IGNORE_RDIFF_BEGIN
.Tcl.callback(f)
.Tcl.args(text = "Push!", command = f) # NB: Different address
## IGNORE_RDIFF_END

xyzzy <- tclVar(7913)
tclvalue(xyzzy)
tclvalue(xyzzy) <- "foo"
as.character(xyzzy)
tcl("set", as.character(xyzzy))

## Not run:
## These cannot be run by example() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

## End(Not run)
DESCRIPTION

This function controls or reports on the Tcl service mode, i.e., whether Tcl will respond to events.

USAGE

tclServiceMode(on = NULL)

ARGUMENTS

on (logical) Whether event servicing is turned on.

DETAILS

If called with on == NULL (the default), no change is made.

Note that this blocks all Tcl/Tk activity, including for widgets from other packages. It may be better to manage mapping of windows individually.

VALUE

The value of the Tcl service mode before the call.

EXAMPLES

## see demo(tkcanvas) for an example
oldmode <- tclServiceMode(FALSE)
# Do some work to create a nice picture.
# Nothing will be displayed until...
tclServiceMode(oldmode)
## another idea is to use tkwm.withdraw() ... tkwm.deiconify()

TkCommands

Tk non-widget commands

DESCRIPTION

These functions interface to Tk non-widget commands, such as the window manager interface commands and the geometry managers.
Usage

tcl(...)  
tktitle(x)

tktitle(x) <- value

tkbell(...)  
tkbind(...)  
tkbindtags(...)  
tkfocu(...)  
tklower(...)  
tkraise(...)

=tkclipboard.append(...)  
tkclipboard.clear(...)

tkevent.add(...)  
tkevent.delete(...)  
tkevent.generate(...)  
tkevent.info(...)

tkfont.actual(...)  
tkfont.configure(...)  
tkfont.create(...)  
tkfont.delete(...)  
tkfont.families(...)  
tkfont.measure(...)  
tkfont.metrics(...)  
tkfont.names(...)

=tkgrab(...)  
tkgrab.current(...)  
tkgrab.release(...)  
tkgrab.set(...)  
tkgrab.status(...)

=tkimage.create(...)  
tkimage.delete(...)  
tkimage.height(...)  
tkimage.inuse(...)  
tkimage.names(...)  
tkimage.type(...)  
tkimage.types(...)  
tkimage.width(...)

## NB: some widgets also have a selection.clear command,  
## hence the "X".

=tkXselection.clear(...)  
tkXselection.get(...)  
tkXselection.handle(...)  
tkXselection.own(...)
tkwait.variable(...)  
tkwait.visibility(...)  
tkwait.window(...)  

## winfo actually has a large number of subcommands,  
## but it's rarely used,  
## so use tkwinfo("atom", ...) etc. instead.

tkwinfo(...)  

# Window manager interface

tkwm.aspect(...)  
tkwm.client(...)  
tkwm.colormapwindows(...)  
tkwm.command(...)  
tkwm.deiconify(...)  
tkwm.focusmodel(...)  
tkwm.frame(...)  
tkwm.geometry(...)  
tkwm.grid(...)  
tkwm.group(...)  
tkwm.iconbitmap(...)  
tkwm.iconify(...)  
tkwm.iconmask(...)  
tkwm.iconname(...)  
tkwm.iconposition(...)  
tkwm.iconwindow(...)  
tkwm.maxsize(...)  
tkwm.minsize(...)  
tkwm.overrideredirect(...)  
tkwm.positionfrom(...)  
tkwm.protocol(...)  
tkwm.resizable(...)  
tkwm.sizefrom(...)  
tkwm.state(...)  
tkwm.title(...)  
tkwm.transient(...)  
tkwm.withdraw(...)  

### Geometry managers

tkgrid(...)  
tkgrid.bbox(...)  
tkgrid.columnconfigure(...)  
tkgrid.configure(...)  
tkgrid.forget(...)  
tkgrid.info(...)  
tkgrid.location(...)  
tkgrid.propagate(...)
TkCommands

Tkgrid.rowconfigure(...)
Tkgrid.remove(...)
Tkgrid.size(...)
Tkgrid.slaves(...)

Tkpack(...)
Tkpack.configure(...)
Tkpack.forget(...)
Tkpack.info(...)
Tkpack.propagate(...)
Tkpack.slaves(...)

Tkplace(...)
Tkplace.configure(...)
Tkplace.forget(...)
Tkplace.info(...)
Tkplace.slaves(...)

## Standard dialogs
TkgetOpenFile(...)
TkgetSaveFile(...)
TkchooseDirectory(...)
TkmessageBox(...)
Tkdialog(...)
Tkpopup(...)

## File handling functions
Tclfile.tail(...)
Tclfile.dir(...)
Tclopen(...)
Tclclose(...)
Tclputs(...)
Tclread(...)

Arguments
x A window object
value For tktitle assignments, a character string.
... Handled via .Tcl.args

Details
tcl provides a generic interface to calling any Tk or Tcl command by simply running .Tcl.args.objv on the argument list and passing the result to .Tcl.objv. Most of the other commands simply call tcl with a particular first argument and sometimes also a second argument giving the subcommand.

tktitle and its assignment form provides an alternate interface to Tk's wm title

There are far too many of these commands to describe them and their arguments in full. Please refer to the Tcl/Tk documentation for details. With a few exceptions, the pattern is that Tk subcommands like pack.configure are converted to function names like tkpack.configure, and Tcl subcommands are like tclfile.dir.
tkpager

Page file using Tk text widget

Description

This plugs into `file.show`, showing files in separate windows.

Usage

tkpager(file, header, title, delete.file)

Arguments

- `file` character vector containing the names of the files to be displayed
- `header` headers to use for each file
- `title` common title to use for the window(s). Pasted together with the `header` to form actual window title.
- `delete.file` logical. Should file(s) be deleted after display?

Note

The "\b_" string used for underlining is currently quietly removed. The font and background colour are currently hardcoded to Courier and gray90.

See Also

`file.show`
tkProgressBar

Progress Bars via Tk

Description

Put up a Tk progress bar widget.

Usage

tkProgressBar(title = "R progress bar", label = "", min = 0, max = 1, initial = 0, width = 300)

getTkProgressBar(pb)

setTkProgressBar(pb, value, title = NULL, label = NULL)

## S3 method for class 'tkProgressBar'

close(con, ...)

Arguments

title, label character strings, giving the window title and the label on the dialog box respectively.

min, max (finite) numeric values for the extremes of the progress bar.

initial, value initial or new value for the progress bar.

width the width of the progress bar in pixels: the dialog box will be 40 pixels wider (plus frame).

pb, con an object of class "tkProgressBar".

... for consistency with the generic.

Details

tkProgressBar will display a widget containing a label and progress bar.

setTkProgressBar will update the value and for non-NULL values, the title and label (provided there was one when the widget was created). Missing (NA) and out-of-range values of value will be (silently) ignored.

The progress bar should be closed when finished with.

This will use the ttk::progressbar widget for Tk version 8.5 or later, otherwise R’s copy of BWidget’s progressbar.

Value

For tkProgressBar an object of class "tkProgressBar".

For getTkProgressBar and setTkProgressBar, a length-one numeric vector giving the previous value (invisibly for setTkProgressBar).

See Also

txtProgressBar
Examples

```r
pb <- tkProgressBar("test progress bar", "Some information in %", 0, 100, 50)
Sys.sleep(0.5)
u <- c(0, sort(runif(20, 0, 100)), 100)
for(i in u) {
  Sys.sleep(0.1)
  info <- sprintf("%d%% done", round(i))
  setTkProgressBar(pb, i, sprintf("test (%s)", info), info)
}
Sys.sleep(5)
close(pb)
```

tkStartGUI

_Tcl/Tk GUI startup_

**Description**

Starts up the Tcl/Tk GUI

**Usage**

```
tkStartGUI()
```

**Details**

Starts a GUI console implemented via a Tk text widget. This should probably be called at most once per session. Also redefines the file pager (as used by `help()`) to be the Tk pager.

**Note**

`tkStartGUI()` saves its evaluation environment as `.GUIenv`. This means that the user interface elements can be accessed in order to extend the interface. The three main objects are named `Term`, `Menu`, and `Toolbar`, and the various submenus and callback functions can be seen with `ls(envir = .GUIenv)`.

**Author(s)**

Peter Dalgaard

**TkWidgetcmds**

_Tk widget commands_

**Description**

These functions interface to Tk widget commands.
Usage

tkactivate(widget, ...)
tkadd(widget, ...)
tkaddtag(widget, ...)
tkbbox(widget, ...)
tkcanvasx(widget, ...)
tkcanvasy(widget, ...)
tkcget(widget, ...)
tkcompare(widget, ...)
tkconfigure(widget, ...)
tkcoords(widget, ...)
tkcreate(widget, ...)
tkcurselection(widget, ...)
tkdchars(widget, ...)
tkdebug(widget, ...)
tkdelete(widget, ...)
tkdelta(widget, ...)
tkdeselect(widget, ...)
tkdlineinfo(widget, ...)
tkdtag(widget, ...)
tkdump(widget, ...)
tkentrycget(widget, ...)
tkentryconfigure(widget, ...)
tkfind(widget, ...)
tkflash(widget, ...)
tkfraction(widget, ...)
tkget(widget, ...)
tkgettags(widget, ...)
tkicursor(widget, ...)
tkidentify(widget, ...)
tkindex(widget, ...)
tkinsert(widget, ...)
tkinvoke(widget, ...)
tkitembind(widget, ...)
tkitemcget(widget, ...)
tkitemconfigure(widget, ...)
tkitemfocus(widget, ...)
tkitemlower(widget, ...)
tkitemraise(widget, ...)
tkitemscale(widget, ...)
tkmark.gravity(widget, ...)
tkmark.names(widget, ...)
tkmark.next(widget, ...)
tkmark.previous(widget, ...)
tkmark.set(widget, ...)
tkmark.unset(widget, ...)
tkmove(widget, ...)
tknearest(widget, ...)
tkpost(widget, ...)
tkpostcascade(widget, ...)
tkpostscript(widget, ...)
tkscan.mark(widget, ...)

TkWidgetcmds
tkscan.dragto(widget, ...)  
tksearch(widget, ...)  
tksee(widget, ...)  
tkselect(widget, ...)  
tkselection.adjust(widget, ...)  
tkselection.anchor(widget, ...)  
tkselection.clear(widget, ...)  
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tkselection.range(widget, ...)  
tkselection.set(widget, ...)  
tkselection.to(widget, ...)  
tkset(widget, ...)  
tksize(widget, ...)  
tktoggle(widget, ...)  
tktag.add(widget, ...)  
tktag.bind(widget, ...)  
tktag.cget(widget, ...)  
tktag.configure(widget, ...)  
tktag.delete(widget, ...)  
tktag.lower(widget, ...)  
tktag.names(widget, ...)  
tktag.nextrange(widget, ...)  
tktag.prevrange(widget, ...)  
tktag.raise(widget, ...)  
tktag.ranges(widget, ...)  
tktag.remove(widget, ...)  
tktag.widget(widget, ...)  
tkunpost(widget, ...)  
tkwindow.cget(widget, ...)  
tkwindow.configure(widget, ...)  
tkwindow.create(widget, ...)  
tkwindow.names(widget, ...)  
tkxview(widget, ...)  
tkxview.moveto(widget, ...)  
tkxview.scroll(widget, ...)  
tkyposition(widget, ...)  
tkyview(widget, ...)  
tkyview.moveto(widget, ...)  
tkyview.scroll(widget, ...)  

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>widget</td>
<td>The widget this applies to</td>
</tr>
<tr>
<td>...</td>
<td>Handled via .Tcl.args</td>
</tr>
</tbody>
</table>

Details

There are far too many of these commands to describe them and their arguments in full. Please refer to the Tcl/Tk documentation for details. Except for a few exceptions, the pattern is that Tcl widget commands possibly with subcommands like .a.b.selection.clear are converted to function names like `tkselection.clear` and the widget is given as the first argument.
## TkWidgets

### Tkwidgets

Create Tk widgets and associated R objects.

### Usage

```r
tkwidget(parent, type, ...)
tkbutton(parent, ...)
tkcanvas(parent, ...)
tkcheckbutton(parent, ...)
tkentry(parent, ...)
ttkentry(parent, ...)
tkframe(parent, ...)
tklabel(parent, ...)
tklistbox(parent, ...)
tkmenu(parent, ...)
tkmenubutton(parent, ...)
tkmessage(parent, ...)
tkradiobutton(parent, ...)
tkscale(parent, ...)
tkscrollbar(parent, ...)
tktext(parent, ...)
tktoplevel(parent = .TkRoot, ...)
```

### Examples

```r
## Not run:
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
tkpack(txt.w <- tktext(tt))
tkinsert(txt.w, "0.0", "plot(1:10)")

# callback function
eval.txt <- function() eval(str2lang(tclvalue(tkget(txt.w, "0.0", "end"))))
tkpack(but.w <- tkbutton(tt, text = "Submit", command = eval.txt))

## Try pressing the button, edit the text and when finished:
tkdestroy(tt)

## End(Not run)
```

---

<table>
<thead>
<tr>
<th>TkWidgets</th>
<th>Tk widgets</th>
</tr>
</thead>
</table>

### Description

Create Tk widgets and associated R objects.
tkbutton(parent, ...)
ttkcheckbutton(parent, ...)
ttkcombox(parent, ...)
ttkframe(parent, ...)
ttklabel(parent, ...)
ttklabelframe(parent, ...)
ttkmenubutton(parent, ...)
ttknotebook(parent, ...)
ttkpanedwindow(parent, ...)
ttkprogressbar(parent, ...)
ttkradiobutton(parent, ...)
ttkradiobutton(parent, ...)
ttkscale(parent, ...)
ttkscrollbar(parent, ...)
ttkseparator(parent, ...)
ttksizegrip(parent, ...)
ttkspinbox(parent, ...)
ttktreeview(parent, ...)

Arguments

parent: Parent of widget window.
type: string describing the type of widget desired.
... handled via .Tcl.args.

Details

These functions create Tk widgets. `tkwidget` creates a widget of a given type, the others simply call `tkwidget` with the respective type argument.

The functions starting `ttk` are for the themed widget set for Tk 8.5 or later. A tutorial can be found at https://tkdocs.com/.

It is not possible to describe the widgets and their arguments in full. Please refer to the Tcl/Tk documentation.

See Also

TclInterface, TkCommands, TkWidgetcmds

Examples

```r
## Not run:
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
label.widget <- ttklabel(tt, text = "Hello, World!"
button.widget <- ttkbutton(tt, text = "Push",
                           command = function()
cat("OW!\n"))
tkpack(label.widget, button.widget) # geometry manager
                           # see Tk-commands
                           # geometry manager
                           # see Tk-commands

tkdestroy(tt)
```
## test for themed widgets
if(as.character(tcl("info", "tclversion")) >= "8.5") {
    # make use of themed widgets
    # list themes
    themes <- as.character(tcl("ttk::style", "theme", "names"))
    themes
    # select a theme -- for pre-XP windows
    # tcl("ttk::style", "theme", "use", "winnative")
    tcl("ttk::style", "theme", "use", themes[1])
} else {
    # use Tk 8.0 widgets
}

## End(Not run)

---

tk_choose.dir  

Choose a Folder Interactively

**Description**

Use a Tk widget to choose a directory interactively.

**Usage**

```
tk_choose.dir(default = "", caption = "Select directory")
```

**Arguments**

- **default**: which directory to show initially.
- **caption**: the caption on the selection dialog.

**Value**

A length-one character vector, character NA if 'Cancel' was selected.

**See Also**

- `tk_choose.files`

**Examples**

```
if (interactive()) tk_choose.dir(getwd(), "Choose a suitable folder")
```
tk_choose.files

Choose a List of Files Interactively

Description
Use a Tk file dialog to choose a list of zero or more files interactively.

Usage

```r
tk_choose.files(default = "", caption = "Select files",
multi = TRUE, filters = NULL, index = 1)
```

Arguments
- `default` which filename to show initially.
- `caption` the caption on the file selection dialog.
- `multi` whether to allow multiple files to be selected.
- `filters` two-column character matrix of filename filters.
- `index` unused.

Details
Unlike `file.choose`, `tk_choose.files` will always attempt to return a character vector giving a list of files. If the user cancels the dialog, then zero files are returned, whereas `file.choose` would signal an error.

The format of `filters` can be seen from the example. File patterns are specified via extensions, with "*" meaning any file, and "" any file without an extension (a filename not containing a period). (Other forms may work on specific platforms.) Note that the way to have multiple extensions for one file type is to have multiple rows with the same name in the first column, and that whether the extensions are named in file chooser widget is platform-specific. The format may change before release.

Value
A character vector giving zero or more file paths.

Note
A bug in Tk 8.5.0–8.5.4 prevented multiple selections being used.

See Also
- `file.choose`, `tk_choose.dir`

Examples

```r
Filters <- matrix(c("R code", ".R", "R code", ".s",
"Text", ".txt", "All files", "*"),
4, 2, byrow = TRUE)

Filters
if(interactive()) tk_choose.files(filter = Filters)
```
tk_messageBox

Tk Message Box

Description
An implementation of a generic message box using Tk.

Usage
```
tk_messageBox(type = c("ok", "okcancel", "yesno", "yesnocancel", "retrycancel", "abortretryignore"),
               message, caption = "", default = "", ...)
```

Arguments
- **type**: character. The type of dialog box. It will have the buttons implied by its name. Can be abbreviated.
- **message**: character. The information field of the dialog box.
- **caption**: the caption on the widget displayed.
- **default**: character. The name of the button to be used as the default.
- **...**: additional named arguments to be passed to the Tk function of this name. An example is icon = "warning".

Value
A character string giving the name of the button pressed.

See Also
- tkmessageBox for a 'raw' interface.

tk_select.list

Select Items from List

Description
Select item(s) from a character vector using a Tk listbox.

Usage
```
tk_select.list(choices, preselect = NULL, multiple = FALSE,
                title = NULL)
```

Arguments
- **choices**: a character vector of items.
- **preselect**: a character vector, or NULL. If non-null and if the string(s) appear in the list, the item(s) are selected initially.
- **multiple**: logical: can more than one item be selected?
- **title**: optional character string for window title, or NULL for no title.
Details

This is a version of `select.list` implemented as a Tk list box plus OK and Cancel buttons. There will be a scrollbar if the list is too long to fit comfortably on the screen.

The dialog box is modal, so a selection must be made or cancelled before the R session can proceed. Double-clicking on an item is equivalent to selecting it and then clicking OK.

If Tk is version 8.5 or later, themed widgets will be used.

Value

A character vector of selected items. If `multiple` is false and no item was selected (or Cancel was used), "" is returned. If `multiple` is true and no item was selected (or Cancel was used) then a character vector of length 0 is returned.

See Also

`select.list` (a text version except on Windows and the macOS GUI), `menu` (whose `graphics = TRUE` mode uses this on most Unix-alikes).
Chapter 13

The tools package

---

**tools-package**  
*Tools for Package Development*

**Description**

Tools for package development, administration and documentation.

**Details**

This package contains tools for manipulating R packages and their documentation.

For a complete list of functions, use `library(help = "tools")`.

**Author(s)**

Kurt Hornik and Friedrich Leisch

Maintainer: R Core Team <R-core@r-project.org>

---

**.print.via.format**  
*Printing Utilities*

**Description**

`.print.via.format` is a “prototype” `print()` method, useful, at least as a start, by a simple

```r
print.<myS3class> <- .print.via.format
```

**Usage**

`.print.via.format(x, ...)`

**Arguments**

- `x`  
  object to be printed.

- `...`  
  optional further arguments, passed to `format`.
Value

x, invisibly (by invisible()), as print methods should.

See Also

The print generic; its default method print.default (used for many basic implicit classes such as "numeric", "character" and arrays of them, lists etc).

Examples

## The function is simply defined as
function (x, ...) {
  writelines(format(x, ...))
  invisible(x)
}
## is used for simple print methods in R, and as prototype for new methods.

add_datalist

Add a ‘datalist’ File to a Source Package

Description

The data() command with no arguments lists all the datasets available via data in attached packages, and to do so a per-package list is installed. Creating that list at install time can be slow for packages with huge datasets, and can be expedited by a supplying ‘data/datalist’ file.

Usage

add_datalist(pkgpath, force = FALSE, small.size = 1024^2)

Arguments

pkgpath The path to a (source) package.
force logical: can an existing ‘data/datalist’ file be over-written?
small.size number: a ‘data/datalist’ file is created only if the total size of the data files is larger than small.size bytes.

Details

R CMD build will call this function to add a data list to packages with 1MB or more of file in the ‘data’ directory.

It can also be also helpful to give a ‘data/datalist’ file in packages whose datasets have many dependencies, including loading the packages itself (and maybe others).

See Also

data.
The ‘Writing R Extensions’ manual.
assertCondition

**Asserting Error Conditions**

**Description**

When testing code, it is not sufficient to check that results are correct, but also that errors or warnings are signalled in appropriate situations. The functions described here provide a convenient facility for doing so. The three functions check that evaluating the supplied expression produces an error, a warning or one of a specified list of conditions, respectively. If the assertion fails, an error is signalled.

**Usage**

```r
assertError(expr, classes = "error", verbose = FALSE)
assertWarning(expr, classes = "warning", verbose = FALSE)
assertCondition(expr, ..., .exprString = , verbose = FALSE)
```

**Arguments**

- `expr`:
  an unevaluated R expression which will be evaluated via `tryCatch(expr, ..)`.
- `classes, ...`:
  character strings corresponding to the classes of the conditions that would satisfy the assertion; e.g., "error" or "warning". If none are specified, any condition will satisfy the assertion. See the details section.
- `.exprString`:
  The string to be printed corresponding to `expr`. By default, the actual `expr` will be deparsed. Will be omitted if the function is supplied with the actual expression to be tested. If `assertCondition()` is called from another function, with the actual expression passed as an argument to that function, supply the deparsed version.
- `verbose`:
  If TRUE, a message is printed when the condition is satisfied.

**Details**

`assertCondition()` uses the general condition mechanism to check all the conditions generated in evaluating `expr`. The occurrence of any of the supplied condition classes among these satisfies the assertion regardless of what other conditions may be signalled.

`assertError()` is a convenience function for asserting errors; it calls `assertCondition()`.

`assertWarning()` asserts that a warning will be signalled, but not an error, whereas `assertCondition(expr, "warning")` will be satisfied even if an error follows the warning. See the examples.

**Value**

If the assertion is satisfied, a list of all the condition objects signalled is returned, invisibly. See `conditionMessage` for the interpretation of these objects. Note that all conditions signalled during the evaluation are returned, whether or not they were among the requirements.

**Author(s)**

John Chambers and Martin Maechler
See Also

stop, warning; signalCondition, tryCatch.

Examples

assertError(sqrt("abc"))
assertWarning(matrix(1:8, 4,3))

assertCondition( "-1" ) # ok, any condition would satisfy this

try( assertCondition(sqrt(2), "warning" ) )
## .. Failed to get warning in evaluating sqrt(2)
assertCondition(sqrt("abc"), "error") # ok
try( assertCondition(sqrt("abc"), "warning") )# -> error: had no warning
assertCondition(sqrt("abc"), "error")
## identical to assertError() call above

assertCondition(matrix(1:5, 2,3), "warning")
try( assertCondition(matrix(1:8, 4,3), "error") )
## .. Failed to get expected error ....
## either warning or worse:
assertCondition(matrix(1:8, 4,3), "error", "warning") # OK
assertCondition(matrix(1:8, 4,3), "warning") # OK

## when both are signalled:
ff <- function() { warning("my warning"); stop("my error") }
assertCondition(ff(), "warning")
## but assertWarning does not allow an error to follow
try(assertWarning(ff()))
assertCondition(ff(), "error") # ok
assertCondition(ff(), "error", "warning") # ok (quietly, catching warning)

## assert that assertC..() does not assert [and use *one* argument only]
assertCondition( assertCondition(sqrt( 2 ), "warning") )
assertCondition( assertCondition(sqrt("abc"), "warning"), "error")
assertCondition( assertCondition(matrix(1:8, 4,3), "error"),
    "error")

____________________________________________________________________

bibstyle Select or Define a Bibliography Style

Description

This function defines and registers styles for rendering bibentry objects into ‘Rd’ format, for later conversion to text, HTML, etc.

Usage

bibstyle(style, envir, ..., .init = FALSE, .default = TRUE)
getBibstyle(all = FALSE)
Arguments

style  A character string naming the style.
envir  (optional) An environment holding the functions to implement the style.
...    Named arguments to add to the environment.
.init Whether to initialize the environment from the default style "JSS".
.default Whether to set the specified style as the default style.
all    Whether to return the names of all registered styles.

Details

Rendering of bibentry objects may be done using routines modelled after those used by BibTeX. This function allows environments to be created and manipulated to contain those routines.

There are two ways to create a new style environment. The easiest is to set .init = TRUE, in which case the environment will be initialized with a copy of the default "JSS" environment. (This style is modelled after the ‘jss.bst’ style used by the Journal of Statistical Software.) Alternatively, the envir argument can be used to specify a completely new style environment.

To find the name of the default style, use getBibstyle(). To retrieve an existing style without setting it as the default, use bibstyle(style, .default = FALSE). To modify an existing style, specify style and some named entries via .... (Modifying the default "JSS" style is discouraged.) Setting style to NULL or leaving it missing will retrieve the default style, but modifications will not be allowed.

At a minimum, the environment should contain routines to render each of the 12 types of bibliographic entry supported by bibentry as well as several other routines described below. The former must be named formatArticle, formatBook, formatInbook, formatIncollection, formatInProceedings, formatManual, formatMastersthesis, formatMisc, formatPhdthesis, formatProceedings, formatTechreport and formatUnpublished. Each of these takes one argument, a single unclassed entry from the bibentry vector passed to the renderer, and should produce a single element character vector (possibly containing newlines).

The other routines are as follows. sortKeys, a function to produce a sort key to sort the entries, is passed the original bibentry vector and should produce a sortable vector of the same length to define the sort order. Finally, the optional function cite should have the same argument list as utils::cite, and should produce a citation to be used in text.

The format method for "bibentry" objects adds a field named ".index" to each entry after sorting and before formatting. This is a 1-based index within the complete object that can be used in styles that require numbering. Although the "JSS" style doesn’t use numbers, it includes a fmtPrefix() stub function that may be used to display them. See the example below.

Value

bibstyle returns the environment which has been selected or created.
getBibstyle returns the name of the default style, or all style names.

Author(s)

Duncan Murdoch

See Also

bibentry
Examples

```r
refs <-
c(bibentry(bibtype = "manual",
  title = "R: A Language and Environment for Statistical Computing",
  author = person("R Core Team"),
  organization = "R Foundation for Statistical Computing",
  address = "Vienna, Austria",
  year = 2013,
  url = "https://www.R-project.org"),
bibentry(bibtype = "article",
  author = c(person(c("George", "E.", "P."), "Box"),
             person(c("David", "R."), "Cox"),
  year = 1964,
  title = "An Analysis of Transformations",
  journal = "Journal of the Royal Statistical Society, Series B",
  volume = 26, number = 2, pages = "211--243",
  doi = "10.1111/j.2517-6161.1964.tb00553.x"))

bibstyle("unsorted", sortKeys = function(refs) seq_along(refs),
  fmtPrefix = function(paper) paste0("[", paper$.index, "]"),
  .init = TRUE)
print(refs, .bibstyle = "unsorted")
```

**buildVignette**  
*Build One Vignette*

Description  
Run **Sweave** (or other custom weave function), **texi2pdf**, and/or **Stangle** (or other custom tangle function) on one vignette.

This is the workhorse of **R CMD Sweave**.

Usage

```r
buildVignette(file, dir = ".", weave = TRUE, latex = TRUE, tangle = TRUE,
  quiet = TRUE, clean = TRUE, keep = character(),
  engine = NULL, buildPkg = NULL, encoding, ...)
```

Arguments

- **file** character; the vignette source file.
- **dir** character; the working directory in which the intermediate and output files will be produced.
- **weave** logical; should weave be run?
- **latex** logical; should **texi2pdf** be run if weaving produces a `.tex` file?
- **tangle** logical; should tangle be run?
- **quiet** logical; run in quiet mode?
- **clean** logical; whether to remove some newly created, often intermediate, files. See details below.
buildVignettes a list of file names to keep in any case when cleaning. Note that “target” files are kept anyway.

generate NULL or character; name of vignette engine to use. Overrides any \VignetteEngine{} markup in the vignette.

buildPkg NULL or a character vector; optional packages in which to find the vignette engine.

encoding the encoding to assume for the file. If not specified, it will be read if possible from the file’s contents. Note that if the vignette is part of a package, buildVignettes reads the package’s encoding from the ‘DESCRIPTION’ file but this function does not.

... Additional arguments passed to weave and tangle.

Details

This function determines the vignette engine for the vignette (default utils::Sweave), then weaves and/or tangles the vignette using that engine. Finally, if clean is TRUE, newly created intermediate files (non “targets”, where these depend on the engine, etc, and not any in keep) will be deleted. If clean is NA, and weave is true, newly created intermediate output files (e.g., ‘.tex’) will not be deleted even if a ‘.pdf’ file has been produced from them.

If buildPkg is specified, those packages will be loaded before the vignette is processed and will be used as the default packages in the search for a vignette engine, but an explicitly specified package in the vignette source (e.g., using \VignetteEngine{utils::Sweave} to specify the Sweave engine in the utils package) will override it. In contrast, if the engine argument is given, it will override the vignette source.

Value

A character vector naming the files that have been produced.

Author(s)

Henrik Bengtsson and Duncan Murdoch

See Also

buildVignettes for building all vignettes in a package.

---

buildVignettes List and Build Package Vignettes

Description

Run Sweave (or other custom weave function) and texi2pdf on all vignettes of a package, or list the vignettes.
Usage

buildVignettes(package, dir, lib.loc = NULL, quiet = TRUE,
    clean = TRUE, tangle = FALSE, skip = NULL,
    ser_elibs = NULL)

pkgVignettes(package, dir, subdirs = NULL, lib.loc = NULL,
    output = FALSE, source = FALSE, check = FALSE)

Arguments

package a character string naming an installed package. If given, vignette source files are by default looked for in subdirectory 'doc'.
dir a character string specifying the path to a package's root source directory. If given, vignette source files are by default looked for in subdirectory 'vignettes'.
lib.loc a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.
quiet logical. Weave and run texi2pdf in quiet mode.
clean Remove all files generated by the build, even if there were copies there before.
tangle logical. Do tangling as well as weaving.
skip a character vector of names of vignettes (without file extension, matching the names returned from pkgVignettes) which should be skipped, or TRUE to skip those with unavailable `
    VignetteDepends` (from vignetteInfo).
ser_elibs For use from R CMD check.
subdirs a character vector of subdirectories of dir in which to look for vignettes. The first which exists is used. Defaults to "doc" if package is supplied, otherwise "vignettes".
output logical indicating if the output filenames for each vignette should be returned (in component outputs).
source logical indicating if the tangled output filenames for each vignette should be returned (in component sources).
check logical. If TRUE, check whether all files that have vignette-like filenames have an identifiable vignette engine. This may be a false positive if a file is not a vignette but has a filename matching a pattern defined by one of the vignette engines.

Details

buildVignettes is used by R CMD build and R CMD check to (re-)build vignette outputs from their sources.

As from R 3.4.1, both of these functions ignore files that are listed in the ".Rbuildignore" file in dir.

Value

buildVignettes is called for its side effect of creating the outputs of all vignettes, and if tangle = TRUE, extracting the R code.

pkgVignettes returns an object of class "pkgVignettes" if a vignette directory is found, otherwise NULL.
Examples

gVigns <- pkgVignettes("grid")
str(gVigns)

---

Charsets

Conversion Tables between Character Sets

Description

charset_to_Unicode is a matrix of Unicode code points with columns for the common 8-bit encodings.

Adobe_glyphs is a data frame which gives Adobe glyph names for Unicode code points. It has two character columns, "adobe" and "unicode" (a 4-digit hex representation).

Usage

charset_to_Unicode

Adobe_glyphs

Details

charset_to_Unicode is an integer matrix of class c("noquote", "hexmode") so prints in hexadecimal. The mappings are those used by libiconv: there are differences in the way quotes and minus/hyphen are mapped between sources (and the postscript encoding files use a different mapping).

Adobe_glyphs includes all the Adobe glyph names which correspond to single Unicode characters. It is sorted by Unicode code point and within a point alphabetically on the glyph (there can be more than one name for a Unicode code point). The data are in the file ‘R_HOME/share/encodings/Adobe_glyphlist’.

Examples

```r
## find Adobe names for ISOLatin2 chars.
latin2 <- charset_to_Unicode[, "ISOLatin2"]
aUnicode <- as.hexmode(paste0("0x", Adobe_glyphs$unicode))
keep <- aUnicode %in% latin2
aUnicode <- aUnicode[keep]
aAdobe <- Adobe_glyphs[keep, 1]
## first match
aLatin2 <- aAdobe[match(latin2, aUnicode)]
## all matches
bLatin2 <- lapply(1:256, function(x) aAdobe[aUnicode == latin2[x]])
format(bLatin2, justify = "none")
```
checkFF

**Description**

Performs checks on calls to compiled code from R code. Currently only checks whether the interface functions such as `.C` and `.Fortran` are called with a "NativeSymbolInfo" first argument or with argument `PACKAGE` specified, which is highly recommended to avoid name clashes in foreign function calls.

**Usage**

```r
checkFF(package, dir, file, lib.loc = NULL,
       registration = FALSE, check_DUP = FALSE,
       verbose = getOption("verbose"))
```

**Arguments**

- `package` a character string naming an installed package. If given, the installed R code of the package is checked.
- `dir` a character string specifying the path to a package's root source directory. This should contain the subdirectory ‘R’ (for R code). Only used if `package` is not given.
- `file` the name of a file containing R code to be checked. Used if neither `package` nor `dir` are given.
- `lib.loc` a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. The specified library trees are used to search for `package`.
- `registration` a logical. If TRUE, checks the registration information on the call (if available).
- `check_DUP` a logical. If TRUE, `.C` and `.Fortran` calls with `DUP = FALSE` are reported.
- `verbose` a logical. If TRUE, additional diagnostics are printed (and the result is returned invisibly).

**Details**

Note that we can only check if the name argument is a symbol or a character string, not what class of object the symbol resolves to at run-time.

If the package has a namespace which contains a `useDynLib` directive, calls in top-level functions in the package are not reported as their symbols will be preferentially looked up in the DLL named in the first `useDynLib` directive.

This checks that calls with `PACKAGE` specified are to the same package, and reports separately those which are in base packages and those which are in other packages (and if those packages are specified in the ‘DESCRIPTION’ file).

**Value**

An object of class "checkFF".

There are `format` and `print` methods to display the information contained in such objects.
checkMD5sums

See Also

.C., Fortran, Foreign.

Examples

# order is pretty much random
checkFF(package = "stats", verbose = TRUE)

checkMD5sums  Check and Create MD5 Checksum Files

Description

checkMD5sums checks the files against a file 'MD5'.

Usage

checkMD5sums(package, dir)

Arguments

package  the name of an installed package

dir  the path to the top-level directory of an installed package.

Details

The file 'MD5' which is created is in a format which can be checked by md5sum -c MD5 if a suitable
command-line version of md5sum is available. (For Windows, one is supplied in the bundle at
https://cran.r-project.org/bin/windows/Rtools/.)

If dir is missing, an installed package of name package is searched for.

The private function tools:::.installMD5sums is used to create MD5 files in the Windows build.

Value

checkMD5sums returns a logical, NA if there is no 'MD5' file to be checked.

See Also

md5sum
checkPoFiles

Check Translation Files for Inconsistent Format Strings

Description

These functions compare formats embedded in English messages with translated strings to check for consistency. checkPoFile checks one file, while checkPoFiles checks all files for a specified language.

Usage

checkPoFile(f, strictPlural = FALSE)
checkPoFiles(language, dir = ".")

Arguments

f a character string giving a single filepath.
strictPlural whether to compare formats of singular and plural forms in a strict way.
language a character string giving a language code.
dir a path to a directory in which to check files.

Details

Part of R’s internationalization depends on translations of messages in ‘.po’ files. In these files an ‘English’ message taken from the R sources is followed by a translation into another language. Many of these messages are format strings for C or R sprintf and related functions. In these cases, the translation must give a compatible format or an error will be generated when the message is displayed.

The rules for compatibility differ between C and R in several ways. C supports several conversions not supported by R, namely c, u, p, n. It is allowed in C’s sprintf() function to have more arguments than are needed by the format string, but in R the counts must match exactly. R requires types of arguments to match, whereas C will do the display whether it makes sense or not.

These functions compromise on the testing as follows. The additional formats allowed in C are accepted, and all differences in argument type or count are reported. As a consequence some reported differences are not errors.

If the strictPlural argument is TRUE, then argument lists must agree exactly between singular and plural forms of messages; if FALSE, then translations only need to match one or the other of the two forms. When checkPoFiles calls checkPoFile, the strictPlural argument is set to TRUE for files with names starting ‘R-’, and to FALSE otherwise.

Items marked as ‘fuzzy’ in the ‘.po’ file are not processed (as they are ignored by the message compiler).

If a difference is found, the translated string is checked for variant percent signs (e.g., the wide percent sign "\uFF05"). Such signs will not be recognized as format specifiers, and are likely to be errors.

Value

Both functions return an object of S3 class "check_po_files". A print method is defined for this class to display a report on the differences.
checkRd

Author(s)
Duncan Murdoch

References
See the GNU gettext manual for the `.po` file format:

See Also
update_pkg_po() which calls checkPoFile(): xgettext, sprintf.

Examples
## Not run:
checkPoFiles("de", "/path/to/R/src/directory")
## End(Not run)

---

checkRd Check an Rd Object

Description
Check an help file or the output of the parse_Rd function.

Usage
checkRd(Rd, defines = .Platform$OS.type, stages = "render",
       unknownOK = TRUE, listOK = TRUE, ..., def_enc = FALSE)

Arguments
Rd a filename or Rd object to use as input.
defines string(s) to use in #ifdef tests.
stages at which stage ("build", "install", or "render") should \$expr macros be
        executed? See the notes below.
unknownOK unrecognized macros are treated as errors if FALSE, otherwise warnings.
listOK unnecessary non-empty braces (e.g., around text, not as an argument) are treated
        as errors if FALSE, otherwise warnings.
... additional parameters to pass to parse_Rd when Rd is a filename. One that is
        often useful is encoding.
def_enc logical: has the package declared an encoding, so tests for non-ASCII text are
        suppressed?
checkRd performs consistency checks on an Rd file, confirming that required sections are present, etc.

It accepts a filename for an Rd file, and will use parse_Rd to parse it before applying the checks. If so, warnings from parse_Rd are collected, together with those from the internal function prepare_Rd, which does the #ifdef and \Sexpr processing, drops sections that would not be rendered or are duplicated (and should not be) and removes empty sections.

An Rd object is passed through prepare_Rd, but it may already have been (and installed Rd objects have).

Warnings are given a ‘level’: those from prepare_Rd have level 0. These include

- All text must be in a section
- Only one tag name section is allowed: the first will be used
- Section name is unrecognized and will be dropped
- Dropping empty section name

checkRd itself can show

- Tag tag name not recognized
- \tabular format must be simple text
- Unrecognized \tabular format: . . .
- Only a columns allowed in this table
- \docType must be plain text
- Tag tag name is invalid in a block name block
- \method not valid outside a code block
- Tag \method is only valid in \usage
- Tag \dontrun is only valid in \examples
- Invalid email address: . . .
- Invalid URL: . . .
- Must have a tag name
- Only one tag name is allowed
- Tag tag name must not be empty
- Multiple sections named tag name are not allowed
- \item in block name must have non-empty label
- Empty section tag name
- Non-ASCII contents without declared encoding
- Non-ASCII contents in second part of \enc
- Escaped LaTeX specials: . . .
- Tag \ldots is invalid in a code block
- Apparent non-ASCII contents without declared encoding
- Apparent non-ASCII contents in second part of \enc
- Unnecessary braces at . . .

and variations with \method replaced by \S3method or \S4method, and \dontrun replaced by \donttest or \dontshow.

Note that both prepare_Rd and checkRd have tests for an empty section: that in checkRd is stricter (essentially that nothing is output).
Value

This may fail through an R error, but otherwise warnings are collected as returned as an object of class "checkRd", a character vector of messages. This class has a print method which only prints unique messages, and has argument minlevel that can be used to select only more serious messages. (This is set to -1 in R CMD check.)

Possible fatal errors are those from running the parser (e.g., a non-existent file, unclosed quoted string, non-ASCII input without a specified encoding) or from prepare_Rd (multiple \rdversion declarations, invalid \encoding or \docType or \name sections, and missing or duplicate \name or \title sections).

Author(s)

Duncan Murdoch, Brian Ripley

See Also

parse_Rd, Rd2HTML.

checkRdaFiles

Report on Details of Saved Images or Re-saves them

Description

This reports for each of the files produced by save the size, if it was saved in ASCII or XDR binary format, and if it was compressed (and if so in what format).

Usually such files have extension '.rda' or '.RData', hence the name of the function.

Usage

checkRdaFiles(paths)
resaveRdaFiles(paths, compress = c("auto", "gzip", "bzip2", "xz"),
               compression_level, version = NULL)

Arguments

paths A character vector of paths to save files. If this specifies a single directory, it is taken to refer to all '.rda' and '.RData' files in that directory.
compress, compression_level Type and level of compression: see save. Values of compress can be abbreviated.
version The format to be used when re-saving: see save.

Details

compress = "auto" asks R to choose the compression and ignores compression_level. It will try "gzip", "bzip2" and if the "gzip" compressed size is over 10Kb, "xz" and choose the smallest compressed file (but with a 10% bias towards "gzip"). This can be slow.

For back-compatibility, version = NULL is interpreted to mean version 2: however version-3 files will only be saved as version 3.
checkTnF

Value

For checkRdaFiles, a data frame with rows names paths and columns

<table>
<thead>
<tr>
<th>size</th>
<th>numeric: file size in bytes, NA if the file does not exist.</th>
</tr>
</thead>
<tbody>
<tr>
<td>ASCII</td>
<td>logical: true for save(ASCII = TRUE), NA if the format is not that of an R save file.</td>
</tr>
<tr>
<td>compress</td>
<td>character: type of compression. One of &quot;gzip&quot;, &quot;bzip2&quot;, &quot;xz&quot;, &quot;none&quot; or &quot;unknown&quot; (which means that if this is an R save file it is from a later version of R).</td>
</tr>
<tr>
<td>version</td>
<td>integer: positive with the version(s) of the save(), see there on which versions have been default in which versions of R, and NA for non-Rda files.</td>
</tr>
</tbody>
</table>

Examples

```r
## Not run:
## from a package top-level source directory
paths <- sort(Sys.glob(c("data/*.rda", "data/*.RData")))
(res <- checkRdaFiles(paths))
## pick out some that may need attention
bad <- is.na(res$ASCII) | res$ASCII | (res$size > 1e4 & res$compress == "none")
res[bad, ]
## End(Not run)
```

checkTnF

Check R Packages or Code for T/F

Description

Checks the specified R package or code file for occurrences of T or F, and gathers the expression containing these. This is useful as in R T and F are just variables which are set to the logicals TRUE and FALSE by default, but are not reserved words and hence can be overwritten by the user. Hence, one should always use TRUE and FALSE for the logicals.

Usage

```r
checkTnF(package, dir, file, lib.loc = NULL)
```

Arguments

| package | a character string naming an installed package. If given, the installed R code and the examples in the documentation files of the package are checked. R code installed as an image file cannot be checked. |
| dir | a character string specifying the path to a package’s root source directory. This must contain the subdirectory ‘R’ (for R code), and should also contain ‘man’ (for documentation). Only used if package is not given. If used, the R code files and the examples in the documentation files are checked. |
| file | the name of a file containing R code to be checked. Used if neither package nor dir are given. |
| lib.loc | a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package. |
Value

An object of class "checkTnF" which is a list containing, for each file where occurrences of T or F were found, a list with the expressions containing these occurrences. The names of the list are the corresponding file names.

There is a print method for nicely displaying the information contained in such objects.

checkVignettes

Check Package Vignettes

Description

Check all vignettes of a package by running Sweave (or other custom weave function) and/or Stangle (or other custom tangle function) on them. All R source code files found after the tangling step are sourced to check whether all code can be executed without errors.

Usage

checkVignettes(package, dir, lib.loc = NULL,
    tangle = TRUE, weave = TRUE, latex = FALSE,
    workdir = c("tmp", "src", "cur"),
    keepfiles = FALSE)

Arguments

package
    a character string naming an installed package. If given, vignette source files are looked for in subdirectory 'doc'.

dir
    a character string specifying the path to a package’s root source directory. If given, vignette source files are looked for in subdirectory 'vignettes'.

lib.loc
    a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.

tangle
    Perform a tangle and source the extracted code?

weave
    Perform a weave?

latex
    logical: if weave and latex are TRUE and there is no 'Makefile' in the vignettes directory, run the intermediate '.tex' outputs from weaving through texi2pdf.

workdir
    Directory used as working directory while checking the vignettes. If "tmp" then a temporary directory is created, this is the default. If "src" then the directory containing the vignettes itself is used, if "cur" then the current working directory of R is used.

keepfiles
    Delete files in the temporary directory? This option is ignored when workdir != "tmp".
Details

This function first uses pkgVignettes to find the package vignettes, and in particular their vignette engines (see vignetteEngine).

If tangle is true, it then runs Stangle (or other custom tangle function provided by the engine) to produce (one or more) R code files from each vignette, then sources each code file in turn.

If weave is true, the vignettes are run through Sweave (or other custom weave function provided by the engine). If latex is also true and there is no ‘Makefile’ in the vignettes directory, texi2pdf is run on the intermediate ‘.tex’ files from weaving for those vignettes which did not give errors in the previous steps.

Value

An object of class "checkVignettes", which is a list with the error messages found during the tangle, source, weave and latex steps. There is a print method for displaying the information contained in such objects.
Arguments

dir  a character string giving the path to the directory with the source '*.tar.gz' files to be checked.

pfiles (optional) character vector of tarball files to be checked. Useful for choosing a subset of the '*.tar.gz' files in dir.

check_args  a character vector with arguments to be passed to R CMD check, or a list of length two of such character vectors to be used for checking packages and reverse dependencies, respectively.

check_args_db  a named list of character vectors with arguments to be passed to R CMD check, with names the respective package names.

reverse  a list with names partially matching "repos", "which", or "recursive", giving the repositories to use for locating reverse dependencies (a subset of getOption("repos"), the default), the types of reverse dependencies (default: c("Depends", "Imports", "LinkingTo"), with shorthands "most" and "all" as for package_dependencies), and indicating whether to also check reverse dependencies of reverse dependencies and so on (default: FALSE), or NULL (default), in which case no reverse dependencies are checked.

check_env  a character vector of name=value strings to set environment variables for checking, or a list of length two of such character vectors to be used for checking packages and reverse dependencies, respectively.

xvfb  a logical indicating whether to perform checking inside a virtual framebuffer X server (Unix only), or a character vector of Xvfb options for doing so.

Ncpus  the number of parallel processes to use for parallel installation and checking.

clean  a logical indicating whether to remove the downloaded reverse dependency sources.

...  passed to readLines, e.g. for reading log files produced in a different encoding; currently not used by check_packages_in_dir.

all  a logical indicating whether to also summarize the reverse dependencies checked.

full  a logical indicating whether to also give details for checks with non-ok results, or summarize check example timings (if available).

which  see package_dependencies.

old  a character string giving the path to the directory of a previous check_packages_in_dir run.

outputs  a logical indicating whether to analyze changes in the outputs of the checks performed, or only (default) the status of the checks.

sources  a logical indicating whether to also investigate the changes in the source files checked (default: FALSE).

logs  a character vector with the paths of '00check.log' to analyze. Only used if dir was not given.

drop_ok  a logical indicating whether to drop checks with 'ok' status, or a character vector with the 'ok' status tags to drop. The default corresponds to tags 'OK', 'NONE' and 'SKIPPED'.


check_packages_in_dir

Details

check_packages_in_dir allows to conveniently check source package `.tar.gz` files in the given directory `dir`, along with their reverse dependencies as controlled by `reverse`.

The "which" component of `reverse` can also be a list, in which case reverse dependencies are obtained for each element of the list and the corresponding element of the "recursive" component of `reverse` (which is recycled as needed).

If needed, the source `.tar.gz` files of the reverse dependencies to be checked as well are downloaded into `dir` (and removed at the end if `clean` is true). Next, all packages (additionally) needed for checking are installed to the ‘Library’ subdirectory of `dir`. Then, all `.tar.gz` files are checked using the given arguments and environment variables, with outputs and messages to files in the ‘Outputs’ subdirectory of `dir`. The ‘*.Rcheck’ directories with the check results of the reverse dependencies are renamed by prefixing their base names with ‘rdepends_’.

Results and timings can conveniently be summarized using `summarize_check_packages_in_dir_results` and `summarize_check_packages_in_dir_timings`, respectively.

Installation and checking is performed in parallel if `Ncpus` is greater than one: this will use `mclapply` on Unix and `parLapply` on Windows.

check_packages_in_dir returns an object inheriting from class "check_packages_in_dir" which has `print` and `summary` methods.

check_packages_in_dir_changes allows to analyze the effect of changing (some of) the sources. With `dir` and `old` the paths to the directories with the new and old sources, respectively, and the corresponding check results, possible changes in the check results can conveniently be analyzed as controlled via options `outputs` and `sources`. The changes object returned can be subscripted according to change in severity from the old to the new results by using one of "==", "!=" "<", "<=" ", ">=" or ">=" as row index.

check_packages_in_dir_details analyzes check log files to obtain check details as a data frame which can be used for further processing, providing check name, status and output for every check performed and not dropped according to status tag (via variables `Check`, `Status` and `Output`, respectively).

Environment variable `_R_CHECK_ELAPSED_TIMEOUT_` can be used to set a limit on the elapsed time of each check run. See the ‘R Internals’ manual for how the value is interpreted and for other environment variables which can be used for finer-grained control on timeouts within a check run.

Note

This functionality is still experimental: interfaces may change in future versions.

Examples

## Not run:
## Check packages in dir without reverse dependencies:
check_packages_in_dir(dir)
## Check packages in dir and their reverse dependencies using the
## defaults (all repositories in getOption("repos"), all "strong"
## reverse dependencies, no recursive reverse dependencies):
check_packages_in_dir(dir, reverse = list())
## Check packages in dir with their reverse dependencies from CRAN,
## using all strong reverse dependencies and reverse suggests:
check_packages_in_dir(dir,
  reverse = list(repos = getOption("repos")["CRAN"],
                  which = "most"))
## Check packages in dir with their reverse dependencies from CRAN, using '--as-cran' for the former but not the latter:

```r
check_packages_in_dir(dir,
  check_args = c("--as-cran", ""),
  reverse = list(repos = getOption("repos")[["CRAN"]])
)
```

## End(Not run)

---

### Description

Find inconsistencies between actual and documented ‘structure’ of \texttt{R} objects in a package. \texttt{codoc} compares names and optionally also corresponding positions and default values of the arguments of functions. \texttt{codocClasses} and \texttt{codocData} compare slot names of S4 classes and variable names of data sets, respectively.

### Usage

```r
codoc(package, dir, lib.loc = NULL,
  use.values = NULL, verbose = getOption("verbose"))
codocClasses(package, lib.loc = NULL)
codocData(package, lib.loc = NULL)
```

### Arguments

- **package**: a character string naming an installed package.
- **dir**: a character string specifying the path to a package’s root source directory. This must contain the subdirectories ‘\texttt{man}’ with \texttt{R} documentation sources (in Rd format) and ‘\texttt{R}’ with \texttt{R} code. Only used if package is not given.
- **lib.loc**: a character vector of directory names of \texttt{R} libraries, or \texttt{NULL}. The default value of \texttt{NULL} corresponds to all libraries currently known. The specified library trees are used to search for package.
- **use.values**: if \texttt{FALSE}, do not use function default values when comparing code and docs. Otherwise, compare all default values if \texttt{TRUE}, and only the ones documented in the usage otherwise (default).
- **verbose**: a logical. If \texttt{TRUE}, additional diagnostics are printed.

### Details

The purpose of \texttt{codoc} is to check whether the documented usage of function objects agrees with their formal arguments as defined in the \texttt{R} code. This is not always straightforward, in particular as the usage information for methods to generic functions often employs the name of the generic rather than the method.

The following algorithm is used. If an installed package is used, it is loaded (unless it is the \texttt{base} package), after possibly detaching an already loaded version of the package. Otherwise, if the sources are used, the \texttt{R} code files of the package are collected and sourced in a new environment. Then, the usage sections of the Rd files are extracted and parsed ‘as much as possible’ to give the formals documented. For interpreted functions in the code environment, the formals are compared between code and documentation according to the values of the argument \texttt{use.values}. 
If a package has a namespace both exported and unexported objects are checked, as well as registered S3 methods. (In the unlikely event of differences the order is exported objects in the package, registered S3 methods and finally objects in the namespace and only the first found is checked.)

Currently, the R documentation format has no high-level markup for the basic ‘structure’ of classes and data sets (similar to the usage sections for function synopses). Variable names for data frames in documentation objects obtained by suitably editing ‘templates’ created by prompt are recognized by codocData and used provided that the documentation object is for a single data frame (i.e., only has one alias). codocClasses analogously handles slot names for classes in documentation objects obtained by editing shells created by promptClass.

Help files named ‘pkgname-defunct.Rd’ for the appropriate pkgname are checked more loosely, as they may have undocumented arguments.

Value

codoc returns an object of class “codoc”. Currently, this is a list which, for each Rd object in the package where an inconsistency was found, contains an element with a list of the mismatches (which in turn are lists with elements code and docs, giving the corresponding arguments obtained from the function’s code and documented usage).
codocClasses and codocData return objects of class ”codocClasses” and ”codocData”, respectively, with a structure similar to class ”codoc”.

There are print methods for nicely displaying the information contained in such objects.

Note

The default for use.values has been changed from FALSE to NULL, for R versions 1.9.0 and later.

See Also

undoc, QC

---

**compactPDF**

*Compact PDF Files*

**Description**

Re-save PDF files (especially vignettes) more compactly. Support function for R CMD build --compact-vignettes.

**Usage**

```r
compactPDF(paths,
qdpdf = Sys.which(Sys.getenv("R_QPDF", "qdpdf")),
gs_cmd = Sys.getenv("R_GSCMD", ""),
gs_quality = Sys.getenv("GS_QUALITY", "none"),
gsExtras = character(),
verbose = FALSE)
## S3 method for class 'compactPDF'
format(x, ratio = 0.9, diff = 1e4, ...)
```

```r

```
Arguments

paths
A character vector of paths to PDF files, or a length-one character vector naming a directory, when all `.pdf` files in that directory will be used.

qpdf
Character string giving the path to the `qpdf` command. If empty, `qpdf` will not be used.

gs_cmd
Character string giving the path to the GhostScript executable, if that is to be used. On Windows this is the path to `gswin32c.exe` or `gswin64c.exe`. If `""` (the default), the function will try to find a platform-specific path to GhostScript where required.

gs_quality
A character string indicating the quality required: the options are "none" (so GhostScript is not used), "printer" (300dpi), "ebook" (150dpi) and "screen" (72dpi). Can be abbreviated.

gs_extras
An optional character vector of further options to be passed to GhostScript.

verbose
`logical` or non-negative integer indicating if and how much of the compression utilities’ output should be shown.

x
An object of class "compactPDF".

ratio, diff
Limits for reporting: files are only reported whose sizes are reduced both by a factor of `ratio` and by `diff` bytes.

... Further arguments to be passed to or from other methods.

Details

This by default makes use of `qpdf`, available from [https://qpdf.sourceforge.io/](https://qpdf.sourceforge.io/) (including as a Windows binary) and included with the CRAN macOS distribution of R. If `gs_cmd` is non-empty and `gs_quality` != "none", GhostScript will used first, then `qpdf` if it is available. If `gs_quality` != "none" and `gs_cmd` is ""`, an attempt will be made to find a GhostScript executable.

`qpdf` and/or `gs_cmd` are run on all PDF files found, and those which are reduced in size by at least 10% and 10Kb are replaced.

The strategy of our use of `qpdf` is to (losslessly) compress both PDF streams and objects. GhostScript compresses streams and more (including downsampling and compressing embedded images) and consequently is much slower and may lose quality (but can also produce much smaller PDF files). However, quality "ebook" is perfectly adequate for screen viewing and printing on laser printers.

Where PDF files are changed they will become PDF version 1.5 files: these have been supported by Acrobat Reader since version 6 in 2003, so this is very unlikely to cause difficulties.

Stream compression is what most often has large gains. Most PDF documents are generated with object compression, but this does not seem to be the default for MiKTeX’s `pdflatex`. For some PDF files (and especially package vignettes), using GhostScript can dramatically reduce the space taken by embedded images (often screenshots).

Where both GhostScript and `qpdf` are selected (when `gs_quality` != "none" and both executables are found), they are run in that order and the size reductions apply to the total compression achieved.

Value

An object of class `c("compactPDF", "data.frame")`. This has two columns, the old and new sizes in bytes for the files that were changed.

There are `format` and `print` methods: the latter passes `...` to the format method, so will accept `ratio` and `diff` arguments.
CRANtools

Note

The external tools used may change in future releases.
Frequently, updates to GhostScript have produced better compression (up to several times better),
so if possible use the latest version available.

See Also

resaveRdaFiles.
For other tools to compact PDF files, see the ‘Writing R Extensions’ manual.

Description

Tools for obtaining information about current packages in the CRAN package repository, and their
check status.

Usage

CRAN_package_db()

CRAN_check_results(flavors = NULL)
CRAN_check_details(flavors = NULL)
CRAN_check_issues()
summarize_CRAN_check_status(packages,
  results = NULL,
  details = NULL,
  issues = NULL)

Arguments

packages a character vector of package names.
flavors a character vector of CRAN check flavor names, or NULL (default), corresponding
to all available flavors.
results the return value of CRAN_check_results() (default), or a subset of this.
details the return value of CRAN_check_details() (default), or a subset of this.
issues the return value of CRAN_check_issues() (default), or a subset of this.

Details

CRAN_package_db() returns a data frame with character columns containing most ‘DESCRIPTION’
metadata for the current packages in the CRAN package repository, including in particular the
Description and Maintainer information not provided by utils::available.packages().
CRAN_check_results() returns a data frame with the basic CRAN package check results including
timings, with columns Package, Flavor and Status giving the package name, check flavor, and
overall check status, respectively.
CRANtools

CRAN_check_details() returns a data frame inheriting from class "check_details" (which has useful print and format methods) with details on the check results, providing check name, status and output for every non-OK check (via columns Check, Status and Output, respectively). Packages with all-OK checks are indicated via a * Check wildcard name and OK Status.

CRAN_check_issues() returns a character frame with additional check issues (including the memory-access check results made available from https://www.stats.ox.ac.uk/pub/bdr/memtests/) as a character frame with variables Package, Version, kind (an identifier for the issue) and href (a URL with information on the issue).

Value

See ‘Details’. Note that the results are collated on CRAN: currently this is done in a locale which sorts aAbB ....

Which CRAN?

The main functions access a CRAN mirror specified by the environment variable R_CRAN_WEB, defaulting to one specified in the "repos" option. Otherwise the entry in the ‘repositories’ file (see setRepositories) is used: if that specifies @CRAN@ (the default) or does not contain an entry for CRAN then https://CRAN.R-project.org is used.

The mirror to be used is reported by utils::findCRANmirror("web").

Note that these functions access parts of CRAN under ‘web/contrib’ and ‘web/packages’ so if you have specified a mirror of just ‘src/contrib’ for installing packages you will need to set R_CRAN_WEB to point to a full mirror.

Internal functions CRAN_aliases_db, CRAN_archive_db, CRAN_current_db and CRAN_rdxrefs_db (used by R CMD check) use R_CRAN_SRC rather than R_CRAN_WEB.

Examples

## This can be rather slow with a non-local CRAN mirror
## and might fail (slowly) without Internet access in that case.
set.seed(11)  # but the packages chosen will change as soon as CRAN does.
pdb <- CRAN_package_db()
dim(pdb)
## DESCRIPTION fields included:
colnames(pdb)
## Summarize publication dates:
summary(as.Date(pdb$Published))
## Summarize numbers of packages according to maintainer:
summary(lengths(split(pdb$Package, pdb$Maintainer)))
## Packages with ‘LASSO’ in their Description:
pdb$Package[grepl("LASSO", pdb$Description)]

results <- CRAN_check_results()
## Available variables:
names(results)
## Tabulate overall check status according to flavor:
with(results, table(Flavor, Status))

details <- CRAN_check_details()
## Available variables:
names(details)
## Tabulate checks according to their status:
tab <- with(details, table(Check, Status))

## Inspect some installation problems:
bad <- subset(details,
  ((Check == "whether package can be installed") &
   (Status != "OK")))

## Show a random sample of up to 6
head(bad[sample(seq_len(NROW(bad)), NROW(bad)), ])

issues <- CRAN_check_issues()
head(issues)

## Show counts of issues according to kind:
table(issues[, "kind"])

## Summarize CRAN check status for 10 randomly-selected packages
## (reusing the information already read in):
pos <- sample(seq_len(NROW(pdb)), 10L)
summarize_CRAN_check_status(pdb[pos, "Package"],
  results, details, issues)

delimMatch

Delimited Pattern Matching

Description

Match delimited substrings in a character vector, with proper nesting.

Usage

delimMatch(x, delim = c("{", "}"), syntax = "Rd")

Arguments

  x          a character vector.
  delim      a character vector of length 2 giving the start and end delimiters. Future versions might allow for arbitrary regular expressions.
  syntax     currently, always the string "Rd" indicating Rd syntax (i.e., ‘%’ starts a comment extending till the end of the line, and ‘\‘ escapes). Future versions might know about other syntax, perhaps via ‘syntax tables’ allowing to flexibly specify comment, escape, and quote characters.

Value

An integer vector of the same length as x giving the starting position (in characters) of the first match, or −1 if there is none, with attribute "match.length" giving the length (in characters) of the matched text (or −1 for no match).

See Also

  regexpr for ‘simple’ pattern matching.
dependsOnPkgs

Examples

\begin{verbatim}
x <- c("\value{foo}", "function(bar)"
delimMatch(x)
delimMatch(x, c("\", "))
\end{verbatim}

\begin{verbatim}
deps <- c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances")
deps[3:5] # Exclude "Enhances"
\end{verbatim}

\begin{verbatim}
dependsOnPkgs(pkgs, dependencies = "strong",
        recursive = TRUE, lib.loc = NULL,
        installed =
        utils::installed.packages(lib.loc, fields = "Enhances"))
\end{verbatim}

Description

Find ‘reverse’ dependencies of packages, that is those packages which depend on this one, and (optionally) so on recursively.

Usage

\begin{verbatim}
dependsOnPkgs(pkgs, dependencies = "strong",
        recursive = TRUE, lib.loc = NULL,
        installed =
        utils::installed.packages(lib.loc, fields = "Enhances"))
\end{verbatim}

Arguments

\begin{verbatim}
  pkgs    a character vector of package names.
  dependencies    a character vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances", character string "strong" (default) for the first three elements of that vector.
  recursive    logical: should reverse dependencies of reverse dependencies (and so on) be included?
  lib.loc    a character vector of \texttt{R} library trees, or \texttt{NULL} for all known trees (see \texttt{.libPaths}).
  installed    a result of calling \texttt{installed.packages}.
\end{verbatim}

Value

A character vector of package names, which does not include any from \texttt{pkgs}.

See Also

\texttt{package_dependencies()} to get the regular ("forward") dependencies of a package.

Examples

\begin{verbatim}
## there are few dependencies in a vanilla R installation:
## lattice may not be installed
dependsOnPkgs("lattice")
\end{verbatim}
encoded_text_to_latex  Translate non-ASCII Text to \LaTeX\ Escapes

Description

Translate non-ASCII characters in text to \LaTeX\ escape sequences.

Usage

\begin{verbatim}
encoded_text_to_latex(x, 
    encoding = c("latin1", "latin2", "latin9", 
                "UTF-8", "utf8"))
\end{verbatim}

Arguments

- **x**: a character vector.
- **encoding**: the encoding to be assumed. "latin9" is officially ISO-8859-15 or Latin-9, but known as latin9 to \LaTeX\’s inputenc package.

Details

Non-ASCII characters in \(x\) are replaced by an appropriate \LaTeX\ escape sequence, or ‘?’ if there is no appropriate sequence.

Even if there is an appropriate sequence, it may not be supported by the font in use. Hyphen is mapped to ‘\-’.

Value

A character vector of the same length as \(x\).

See Also

iconv

Examples

\begin{verbatim}
x <- "fa\xE7ile"
encoded_text_to_latex(x, "latin1")
\# Not run:
\# create a tex file to show the upper half of 8-bit charsets
x <- rawToChar(as.raw(160:255), multiple = TRUE)
(x <- matrix(x, ncol = 16, byrow = TRUE))
xx <- x
xx[] <- encoded_text_to_latex(x, "latin1")  # or latin2 or latin9
xx <- apply(xx, 1, paste, collapse = "&")
con <- file("test-encoding.tex", "w")
header <- c("\\documentclass{article}",
            \\
            "\\usepackage[T1]{fontenc}",
            "\\usepackage{Rd}",
            "\\begin{document}",
            "\\HeaderA{test}{}{test}"
```r
# and some UTF_8 chars
x <- intToUtf8(as.integer(c(160:383, 0x0192, 0x02C6, 0x02C7, 0x02CA, 0x02D8,
                          0x02D9, 0x02DD, 0x200C, 0x2018, 0x2019, 0x201C,
                          0x201D, 0x2020, 0x2022, 0x2026, 0x20AC)),
             multiple = TRUE)
x <- matrix(x, ncol = 16, byrow = TRUE)
xx[] <- encoded_text_to_latex(x, "UTF-8")
xx <- apply(xx, 1, paste, collapse = "&")
con <- file("test-utf8.tex", "w")
writeLines(header, con)
writeLines(paste(xx, \\", sep = "), con)
writeLines(trailer, con)
close(con)

## End(Not run)
```

---

**fileutils**

*File Utilities*

**Description**

Utilities for listing files, and manipulating file paths.

**Usage**

```r
file_ext(x)
file_path_as_absolute(x)
file_path_sans_ext(x, compression = FALSE)
list_files_with_exts(dir, exts, all.files = FALSE, full.names = TRUE)
list_files_with_type(dir, type, all.files = FALSE, full.names = TRUE, OS_subdirs = .OStype())
```

**Arguments**

- `x` character vector giving file paths.
- `compression` logical: should compression extension `.gz`, `.bz2` or `.xz` be removed first?
- `dir` a character string with the path name to a directory.
- `exts` a character vector of possible file extensions (excluding the leading dot).
- `all.files` a logical. If FALSE (default), only visible files are considered; if TRUE, all files are used.
full.names a logical indicating whether the full paths of the files found are returned (default), or just the file names.

type a character string giving the 'type' of the files to be listed, as characterized by their extensions. Currently, possible values are "code" (R code), "data" (data sets), "demo" (demos), "docs" (R documentation), and "vignette" (vignettes).

OS_subdirs a character vector with the names of OS-specific subdirectories to possibly include in the listing of R code and documentation files. By default, the value of the environment variable R_OSTYPE, or if this is empty, the value of .Platform$OS.type, is used.

Details

file_ext returns the file (name) extensions (excluding the leading dot). (Only purely alphanumeric extensions are recognized.)

file_path_as_absolute turns a possibly relative file path absolute, performing tilde expansion if necessary. This is a wrapper for normalizePath. Currently, x must be a single existing path.

file_path_sans_ext returns the file paths without extensions (and the leading dot). (Only purely alphanumeric extensions are recognized.)

list_files_with_exts returns the paths or names of the files in directory dir with extension matching one of the elements of exts. Note that by default, full paths are returned, and that only visible files are used.

list_files_with_type returns the paths of the files in dir of the given 'type', as determined by the extensions recognized by R. When listing R code and documentation files, files in OS-specific subdirectories are included if present according to the value of OS_subdirs. Note that by default, full paths are returned, and that only visible files are used.

See Also

file.path, file.info, list.files

Examples

dir <- file.path(R.home(), "library", "stats")
list_files_with_exts(file.path(dir, "demo"), "R")
list_files_with_type(file.path(dir, "demo"), "demo") # the same
file_path_sans_ext(list.files(file.path(R.home("modules"))))

find_gs_cmd Find a GhostScript Executable

Description

Find a GhostScript executable in a cross-platform way.

Usage

find_gs_cmd(gs_cmd = "")

Arguments

gs_cmd The name, full or partial path of a GhostScript executable.
Details

The details differ by platform.

On a Unix-alike, the GhostScript executable is usually called gs. The name (and possibly path) of
the command is taken first from argument gs_cmd then from the environment variable R_GSCMD and
default gs. This is then looked for on the system path and the value returned if a match is found.

On Windows, the name of the command is taken from argument gs_cmd then from the environment
variables R_GSCMD and GSC. If neither of those produces a suitable command name, gswin64c and
gswin32c are tried in turn. In all cases the command is looked for on the system PATH.

Note that on Windows (and some other OSes) there are separate GhostScript executables to display
Postscript/PDF files and to manipulate them: this function looks for the latter.

Value

A character string giving the full path to a GhostScript executable if one was found, otherwise an
empty string.

Examples

```r
## Not run:
## Suppose a Solaris system has GhostScript 9.00 on the path and
## 9.07 in /opt/csw/bin. Then one might set
Sys.setenv(R_GSCMD = "/opt/csw/bin/gs")
## End(Not run)
```

getVignetteInfo

Get Information on Installed Vignettes

Description

This function gets information on installed vignettes.

Usage

```r
getVignetteInfo(package = NULL, lib.loc = NULL, all = TRUE)
```

Arguments

- `package` Which package to look in, or NULL for all packages.
- `lib.loc` Which library to look in.
- `all` Whether to search all installed packages, or just attached packages.

Value

A matrix with columns

- **Package** the name of the package
- **Dir** the directory where the package is installed
- **Topic** the name of the vignette
- **File** the base filename of the source of the vignette
Title the title of the vignette
R the tangled R source from the vignette
PDF the PDF or HTML file for display

Note
The last column of the result is named PDF for historical reasons, but it may contain a filename of a PDF or HTML document.

See Also
pkgVignettes is a similar function that can work on an uninstalled package.

Examples
getVignetteInfo("grid")

---

**HTMLheader**

Generate a Standard HTML Header for R Help

**Description**

This function generates the standard HTML header used on R help pages.

**Usage**

```
HTMLheader(title = "R", logo = TRUE, up = NULL,
           top = file.path(Rhome, "doc/html/index.html"),
           Rhome = "",
           css = file.path(Rhome, "doc/html/R.css"),
           headerTitle = paste("R: ", title),
           outputEncoding = "UTF-8")
```

**Arguments**

- **title** The title to display and use in the HTML headers. Should have had any HTML escaping already done.
- **logo** Whether to display the R logo after the title.
- **up** Which page (if any) to link to on the “up” button.
- **top** Which page (if any) to link to on the “top” button.
- **Rhome** A relative path to the R home directory. See the ‘Details’.
- **css** The relative URL for the Cascading Style Sheet.
- **headerTitle** The title used in the headers.
- **outputEncoding** The declared encoding for the whole page.

**Details**

The up and top links should be relative to the current page. The Rhome path default works with dynamic help; for static help, a relative path (e.g., ‘../..’) to it should be used.
Value

A character vector containing the lines of an HTML header which can be used to start a page in the R help system.

Examples

cat(HTMLheader("This is a sample header"), sep="\n")

Description

Compute relative file paths for URLs to other package’s installed HTML documentation.

Usage

findHTMLlinks(pkgDir = "", lib.loc = NULL, level = 0:2)

Arguments

pkgDir the top-level directory of an installed package. The default indicates no package.
lib.loc character vector describing the location of R library trees to scan: the default indicates .libPaths().
level Which level(s) to include.

Details

findHTMLlinks tries to resolve links from one help page to another. It uses in decreasing priority

• The package in pkgDir: this is used when converting HTML help for that package (level 0).
• The base and recommended packages (level 1).
• Other packages found in the library trees specified by lib.loc in the order of the trees and alphabetically within a library tree (level 2).

Value

A named character vector of file paths, relative to the ‘html’ directory of an installed package. So these are of the form ""../.../somepkg/html/sometopic.html"".

Author(s)

Duncan Murdoch, Brian Ripley
### loadRdMacros

**Load User-defined Rd Help System Macros**

#### Description

Loads macros from an `.Rd` file, or from several `.Rd` files contained in a package.

#### Usage

```r
loadRdMacros(file, macros = TRUE)
loadPkgRdMacros(pkgdir, macros = NULL)
```

#### Arguments

- **file**: A file in Rd format containing macro definitions.
- **macros**: optionally, a previous set of macro definitions, in the format expected by the `parse_Rd` macros argument. `loadPkgRdMacros` loads the system Rd macros by default.
- **pkgdir**: The base directory of a source package or an installed package.

#### Details

The Rd files parsed by these functions should contain only macro definitions; a warning will be issued if anything else other than comments or white space is found.

The `macros` argument may be a filename of a base set of macros, or the result of a previous call to `loadRdMacros` or `loadPkgRdMacros` in the same session. These results should be assumed to be valid only within the current session.

The `loadPkgRdMacros` function first looks for an "RdMacros" entry in the package ‘DESCRIPTION’ file. If present, it should contain a comma-separated list of other package names; their macros will be loaded before those of the current package. It will then look in the current package for `.Rd` files in the ‘man/macros’ or ‘help/macros’ subdirectories, and load those.

#### Value

These functions each return an environment containing objects with the names of the newly defined macros from the last file processed. The parent environment will be macros from the previous file, and so on. The first file processed will have `emptyenv()` as its parent.

#### Author(s)

Duncan Murdoch

#### References

See the ‘Writing R Extensions’ manual for the syntax of Rd files, or [https://developer.r-project.org/parseRd.pdf](https://developer.r-project.org/parseRd.pdf) for a technical discussion.

#### See Also

- `parse_Rd`
Examples

```r
f <- tempfile()
writeLines(r"(\newcommand{\Rlogo}{\if{html}{\figure{Rlogo.svg}{options: width=100 alt="R logo"}}\if{latex}{\figure{Rlogo.pdf}{options: width=0.5in}}}\})", f)
m <- loadRdMacros(f)
ls(m)
ls(parent.env(m))
ls(parent.env(parent.env(m)))
parse_Rd(textConnection(r"(\Rlogo)"), fragment = TRUE, macros = m)
```

makevars

User and Site Compilation Variables

Description

Determine the location of the user and site specific ‘Makevars’ files for customizing package compilation.

Usage

makevars_user()
makevars_site()

Details

Package maintainers can use these functions to employ user and site specific compilation settings also for compilations not using R’s mechanisms (in particular, custom compilations in subdirectories of ‘src’), e.g., by adding configure code calling R with cat(tools::makevars_user()) or cat(tools::makevars_site()), and if non-empty passing this with ‘--f’ to custom Make invocations.

Value

A character string with the path to the user or site specific ‘Makevars’ file, or an empty character vector if there is no such file.

See Also

Section ‘Customizing package compilation’ in the ‘R Installation and Administration’ manual.

Examples

makevars_user()
makevars_site()
**make_translations_pkg**  
*Package the Current Translations in the R Sources*

**Description**

A utility for R Core members to prepare a package of updated translations.

**Usage**

```r
make_translations_pkg(srcdir, outDir = ".", append = "-1")
```

**Arguments**

- `srcdir`: The R source directory.
- `outDir`: The directory into which to place the prepared package.
- `append`: The suffix for the package version number, e.g. `3.0.0-1` will be the default in R 3.0.0.

**Details**

This extracts the translations in a current R source distribution and packages them as a source package called `translations` which can be distributed on CRAN and installed by `update.packages`. This allows e.g. the translations shipped in R 3.x.y to be updated to those currently in ‘R-patched’, even by a user without administrative privileges.

The package has a ‘ Depends’ field which restricts it to versions `3.x.*` for a single `x`.

---

**matchConcordance**  
*Concordance between source and target lines.*

**Description**

The Rd parser records locations in `.Rd` files from which components of the file are read. Output generators `Rd2HTML` and `Rd2latex` can output information about these locations as “concordances” between source and output lines.

`matchConcordance` converts from output locations to source locations. The “Rconcordance” method of `as.character` produces strings to embed in output files, and the default method of `as.Rconcordance` converts these back to objects that can be interpreted by `matchConcordance`.

**Usage**

```r
matchConcordance(linenum, concordance)
```

## S3 method for class 'Rconcordance'
```r
as.character(x, targetfile = "", ...)  
as.Rconcordance(x, ...)  
followConcordance(concordance, prevConcordance)
```
**matchConcordance**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>linenum</td>
<td>One or more line numbers being queried.</td>
</tr>
<tr>
<td>concordance</td>
<td>The concordance data for the file containing the lines: an object of class</td>
</tr>
<tr>
<td></td>
<td>&quot;Rconcordance&quot;.</td>
</tr>
<tr>
<td>prevConcordance</td>
<td>A concordance object retrieved from the current file.</td>
</tr>
<tr>
<td>targetfile</td>
<td>The output filename.</td>
</tr>
<tr>
<td>x</td>
<td>The object to convert: for as.character, an &quot;Rconcordance&quot; object; for</td>
</tr>
<tr>
<td></td>
<td>as.concordance, a character vector which contains as.character output,</td>
</tr>
<tr>
<td></td>
<td>typically in comments.</td>
</tr>
<tr>
<td>...</td>
<td>Further arguments passed to other methods.</td>
</tr>
</tbody>
</table>

**Details**

The correspondence between target lines and source lines in Rd file conversion is not one to one. Often a single source line can lead to the generation of multiple output lines, and sometimes more than one source line triggers output on the same output line.

matchConcordance converts from target lines to source lines. This can be used to help in understanding how particular output lines depend on the source, e.g. when an error is found in the output file. When more than one line contributes to the output, the last one will be returned.

The "Rconcordance" method of as.character converts a concordance object to strings suitable for embedding (e.g. in comments) in an output file.

The default method of as.Rconcordance searches for strings matching the pattern of as.character.Rconcordance output, then converts those lines back to a single concordance.

followConcordance is used when a file is transformed more than once. The first transformation records a concordance in the file which is read as prevConcordance. followConcordance chains this with the current concordance, relating the final result to the original source.

There are 3 kinds of objects used to hold concordances.

Objects of class "activeConcordance" are internal to tools; they are used by Rd2HTML and Rd2latex while building the output file and saving links to the source file.

Objects of class "Rconcordance" are visible to users. They are list objects with the following three fields:

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>offset</td>
<td>The number of lines of output before the first one corresponding to this concordance.</td>
</tr>
<tr>
<td>srcLine</td>
<td>For each line of output after the offset, the corresponding input file line number. There may be more lines of output than the length of srcLine, in which case nothing can be inferred about the source of those lines.</td>
</tr>
<tr>
<td>srcFile</td>
<td>A vector of filenames of length 1 or the same length as srcLine giving the source file(s) for each output line.</td>
</tr>
</tbody>
</table>

Concordance strings are produced by the "Rconcordance" method of as.character; they are simply character vectors encoding the concordance data. The default method of the as.concordance generic function converts them to "Rconcordance" objects.

**Value**

matchConcordance returns a character array with one row per input linenum entry and two columns, "srcFile" and "srcLine".
For the "Rconcordance" method of as.character, a character vector used (e.g. in Sweave) to
embed the concordance in a file.

For as.concordance, an "Rconcordance" object, or NULL if no concordance strings are found.

Author(s)

Duncan Murdoch

See Also

Rd2HTML, Rd2latex

---

### md5sum

#### Description

Compute the 32-byte MD5 hashes of one or more files.

#### Usage

md5sum(files)

#### Arguments

files character. The paths of file(s) whose contents are to be hashed.

#### Details

A MD5 ‘hash’ or ‘checksum’ or ‘message digest’ is a 128-bit summary of the file contents repre-
sented by 32 hexadecimal digits. Files with different MD5 sums are different: only very exception-
ally (and usually with the intent to deceive) are those with the same sums different.

On Windows all files are read in binary mode (as the md5sum utilities there do): on other OSes the
files are read in the default mode (almost always text mode where there is more than one).

MD5 sums are used as a check that R packages have been unpacked correctly and not subsequently
accidentally modified.

#### Value

A character vector of the same length as files, with names equal to files (possibly expanded).
The elements will be NA for non-existent or unreadable files, otherwise a 32-character string of
hexadecimal digits.

#### Source

The underlying C code was written by Ulrich Drepper and extracted from a 2001 release of glibc.

#### See Also

checkMD5sums
package_dependencies

Examples

```
as.vector(md5sum(dir(R.home(), pattern = "^COPY", full.names = TRUE)))
```

package_dependencies  Computations on the Dependency Hierarchy of Packages

Description

Find (recursively) dependencies or reverse dependencies of packages.

Usage

```
package_dependencies(packages = NULL, db = NULL, which = "strong",
recursive = FALSE, reverse = FALSE,
verbose = getOption("verbose"))
```

Arguments

- **packages**: a character vector of package names.
- **db**: character matrix as from `available.packages()` (with the default NULL the results of this call) or data frame variants thereof. Alternatively, a package database like the one available from `https://cran.r-project.org/web/packages/packages.rds`.
- **which**: a character vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances", character string "strong" (default) for the first three elements of that vector.
- **recursive**: a logical indicating whether (reverse) dependencies of (reverse) dependencies (and so on) should be included, or a character vector like which indicating the type of (reverse) dependencies to be added recursively.
- **reverse**: logical: if FALSE (default), regular dependencies are calculated, otherwise reverse dependencies.
- **verbose**: logical indicating if output should monitor the package search cycles.

Value

Named list with one element for each package in argument `packages`, each consists of a character vector naming the (recursive) (reverse) dependencies of that package.

For given packages which are not found in the db, NULL entries are returned, as opposed to character(0) entries which indicate no dependencies.

See Also

`dependsOnPkgs`.
package_native_routine_registration_skeleton

Write Skeleton for Adding Native Routine Registration to a Package

Description

Write a skeleton for adding native routine registration to a package.

Usage

package_native_routine_registration_skeleton(dir, con = stdout(),
   align = TRUE, character_only = TRUE, include_declarations = TRUE)

Arguments

dir
   Top-level directory of a package.

con
   Connection on which to write the skeleton: can be specified as a file path.

align
   Logical: should the registration tables be lined up in three columns each?

character_only
   Logical: should only .NAME arguments specified by character strings (and not as names of R objects nor expressions) be extracted?

include_declarations
   Logical: should the output include declarations (also known as ‘prototypes’) for the registered routines?
Details

Registration is described in section ‘Registering native routines’ of ‘Writing R Extensions’. This function produces a skeleton of the C code which needs to be added to enable registration, conventionally as file ‘src/init.c’ or appended to the sole C file of the package.

This function examines the code in the ‘R’ directory of the package for calls to .C, .Fortran, .Call and .External and creates registration information for those it can make sense of. If the number of arguments used cannot be determined it will be recorded as -1: such values should be corrected.

Optionally the skeleton will include declarations for the registered routines: they should be checked against the C/Fortran source code, not least as the number of arguments is taken from the R code. For .Call and .External calls they will often suffice, but for .C and .Fortran calls the void * arguments would ideally be replaced by the actual types. Otherwise declarations need to be included (they may exist earlier in that file if appending to a file, or in a header file which can be included in ‘init.c’).

The default value of character_only is appropriate when working on a package without any existing registration: character_only = FALSE can be used to suggest updates for a package which has been extended since registration. For the default value, if .NAME values are found which are not character strings (e.g. names or expressions) this is noted via a comment in the output.

Packages which used the earlier form of creating R objects for native symbols via additional arguments in a useDynLib directive will probably most easily be updated to use registration with character_only = FALSE.

If an entry point is used with different numbers of arguments in the package’s R code, an entry in the table (and optionally, a declaration) is made for each number, and a comment placed in the output. This needs to be resolved: only .External calls can have a variable number of arguments, which should be declared as -1.

A surprising number of CRAN packages had calls in R code to native routines not included in the package, which will lead to a ‘loading failed’ error during package installation when the registration C code is added.

Calls which do not name a routine such as .Call(...) will be silently ignored.

Value

None: the output is written to the connection con.

Extracting C/C++ prototypes

There are several tools available to extract function declarations from C or C++ code.

For C code one can use cproto (https://invisible-island.net/cproto/cproto.html; Windows executables are available), for example

cproto -I/path/to/R/include -e *.c

ctags (commonly distributed with the OS) covers C and C++, using something like

ctags -x *.c

to list all function usages. (The ‘Exuberant’ version allows a lot more control.)
Extracting Fortran prototypes

gfortran 9.2 and later can extract C prototypes for Fortran subroutines with a special flag:

```
gfortran -c -fc-prototypes-external file.f
```

although ironically not for functions declared bind(C).

Note

This only examines the ‘R’ directory: it will not find e.g. .Call calls used directly in examples, tests etc.

Static code analysis is used to find the .C etc calls: it will find those in parts of the R code ‘commented out’ by inclusion in if(FALSE) {...}. On the other hand, it will fail to find the entry points in constructs like

```
.Call(if(int) "rle_i" else "rle_d", i, force)
```

and does not know the value of variables in calls like

```
.Call (cfun, ...)
.Call(..., PACKAGE="sparseLTSEigen")
```

(but if character_only is false, will extract the first as "cfun"). Calls which have not been fully resolved will be noted via comments in the output file.

Call to entry points in other packages will be ignored if they have an explicit (character string) PACKAGE argument.

See Also

package.skeleton.

Examples

```r
## Not run:
## with a completed splines/DESCRIPTION file,
tools::package_native_routine_registration_skeleton('splines',,,FALSE)
## produces
#include <R.h>
#include <Rinternals.h>
#include <stdlib.h> // for NULL
#include <R_ext/Rdynload.h>

/* FIXME:
Check these declarations against the C/Fortran source code.
*/

/* .Call calls */
extern SEXP spline_basis(SEXP, SEXP, SEXP, SEXP);
extern SEXP spline_value(SEXP, SEXP, SEXP, SEXP, SEXP);

static const R_CallMethodDef CallEntries[] = {
```
parseLatex

Experimental Functions to Work with LaTeX Code

Description

The `parseLatex` function parses LaTeX source, producing a structured object; `deparseLatex` reverses the process. The `latexToUtf8` function takes a LaTeX object, and processes a number of different macros to convert them into the corresponding UTF-8 characters.

Usage

```r
parseLatex(text, filename = deparse1(substitute(text)),
verbose = FALSE,
verbatim = c("verbatim", "verbatim*", "Sinput", "Soutput"))
```

```r
deparseLatex(x, dropBraces = FALSE)
latexToUtf8(x)
```

Arguments

- **text**: A character vector containing LaTeX source code.
- **filename**: A filename to use in syntax error messages.
- **verbose**: If TRUE, print debug error messages.
- **verbatim**: A character vector containing the names of LaTeX environments holding verbatim text.
- **x**: A "LaTeX" object.
- **dropBraces**: Drop unnecessary braces when displaying a "LaTeX" object.

Details

The parser does not recognize all legal LaTeX code, only relatively simple examples. It does not associate arguments with macros, that needs to be done after parsing, with knowledge of the definitions of each macro. The main intention for this function is to process simple LaTeX code used in bibliographic references, not fully general LaTeX documents.

Verbose text is allowed in two forms: the `\verb` macro (with single character delimiters), and environments whose names are listed in the `verbatim` argument.
Value

The `parseLatex()` function returns a recursive object of class "LaTeX". Each of the entries in this object will have a "latex_tag" attribute identifying its syntactic role.

The `deparseLatex()` function returns a single element character vector, possibly containing embedded newlines.

The `latexToUtf8()` function returns a modified version of the "LaTeX" object that was passed to it.

Author(s)

Duncan Murdoch

Examples

```r
latex <- parseLatex("fa\c{c}ile")
deparseLatex(latexToUtf8(latex))
```

### parse_Rd

**Parse an Rd File**

**Description**

This function reads an R documentation (Rd) file and parses it, for processing by other functions.

**Usage**

```r
parse_Rd(file, srcfile = NULL, encoding = "unknown",
          verbose = FALSE, fragment = FALSE, warningCalls = TRUE,
          macros = file.path(R.home("share"), "Rd", "macros", "system.Rd"),
          permissive = FALSE)
```

```r
## S3 method for class 'Rd'
print(x, deparse = FALSE, ...)
## S3 method for class 'Rd'
as.character(x, deparse = FALSE, ...)
```

**Arguments**

- **file**: A filename or text-mode connection. At present filenames work best.
- **srcfile**: `NULL`, or a "srcfile" object. See the 'Details' section.
- **encoding**: Encoding to be assumed for input strings.
- **verbose**: Logical indicating whether detailed parsing information should be printed.
- **fragment**: Logical indicating whether file represents a complete Rd file, or a fragment.
- **warningCalls**: Logical: should parser warnings include the call?
- **macros**: Filename or environment from which to load additional macros, or a logical value. See the Details below.
- **permissive**: Logical indicating that unrecognized macros should be treated as text with no warning.
- **x**: An object of class Rd.
- **deparse**: If TRUE, attempt to reinstate the escape characters so that the resulting characters will parse to the same object.
- **...**: Further arguments to be passed to or from other methods.
Details

This function parses ‘Rd’ files according to the specification given in https://developer.r-project.org/parseRd.pdf.

It generates a warning for each parse error and attempts to continue parsing. In order to continue, it is generally necessary to drop some parts of the file, so such warnings should not be ignored.

Files without a marked encoding are by default assumed to be in the native encoding. An alternate default can be set using the encoding argument. All text in files is translated to the UTF-8 encoding in the parsed object.

As from R version 3.2.0, User-defined macros may be given in a separate file using ‘\newcommand’ or ‘\renewcommand’. An environment may also be given: it would be produced by loadRdMacros, loadPkgRdMacros, or by a previous call to parse_Rd. If a logical value is given, only the default built-in macros will be used; FALSE indicates that no "macros" attribute will be returned with the result.

The permissive argument allows text to be parsed that is not completely in Rd format. Typically it would be LaTeX code, used in an Rd fragment, e.g. in a bibentry. With permissive = TRUE, this will be passed through as plain text. Since parse_Rd doesn’t know how many arguments belong in LaTeX macros, it will guess based on the presence of braces after the macro; this is not infallible.

Value

parse_Rd returns an object of class "Rd". The internal format of this object is subject to change. The as.character() and print() methods defined for the class return character vectors and print them, respectively.

Unless macros = FALSE, the object will have an attribute named "macros", which is an environment containing the macros defined in file, in a format that can be used for further parse_Rd calls in the same session. It is not guaranteed to work if saved to a file and reloaded in a different session.

Author(s)

Duncan Murdoch

References

https://developer.r-project.org/parseRd.pdf

See Also

Rd2HTML for the converters that use the output of parse_Rd().

---

pskill

Kill a Process

Description

pskill sends a signal to a process, usually to terminate it.
Usage

```r
pskill(pid, signal = SIGTERM)
```

Signals

- SIGHUP
- SIGINT
- SIGQUIT
- SIGKILL
- SIGTERM
- SIGSTOP
- SIGTSTP
- SIGCHLD
- SIGUSR1
- SIGUSR2

Arguments

- `pid` positive integers: one or more process IDs as returned by `Sys.getpid`.
- `signal` integer, most often one of the symbolic constants.

Details

Signals are a C99 concept, but only a small number are required to be supported (of those listed, only SIGINT and SIGTERM). They are much more widely used on POSIX operating systems (which should define all of those listed here), which also support a `kill` system call to send a signal to a process, most often to terminate it. Function `pskill` provides a wrapper: it silently ignores invalid values of its arguments, including zero or negative pids.

In normal use on a Unix-alike, Ctrl-C sends SIGINT, Ctrl-\ sends SIGQUIT and Ctrl-Z sends SIGTSTP: that and SIGSTOP suspend a process which can be resumed by SIGCONT.

The signals are small integers, but the actual numeric values are not standardized (and most do differ between OSes). The `SIG*` objects contain the appropriate integer values for the current platform (or `NA_INTEGER` if the signal is not defined).

Only SIGINT and SIGTERM will be defined on Windows, and `pskill` will always use the Windows system call `TerminateProcess`.

Value

A logical vector of the same length as `pid`, TRUE (for success) or FALSE, invisibly.

See Also

Package `parallel` has several means to launch child processes which record the process IDs.

`psnice`

Examples

```r
## Not run:
pskill(c(237, 245), SIGKILL)
```

## End(Not run)
Get or set the 'niceness' of the current process, or one or more other processes.

Usage

\[ \text{psnice}(\text{pid} = \text{Sys.getpid()}, \text{value} = \text{NA}\_\text{integer}_-) \]

Arguments

- **pid**: positive integers: the process IDs of one of more processes: defaults to the R session process.
- **value**: The niceness to be set, or NA for an enquiry.

Details

POSIX operating systems have a concept of process priorities, usually from 0 to 39 (or 40) with 20 being a normal priority and (somewhat confusingly) larger numeric values denoting lower priority. To add to the confusion, there is a 'niceness' value, the amount by which the priority numerically exceeds 20 (which can be negative). Processes with high niceness will receive less CPU time than those with normal priority. On some OSes, processes with niceness +19 are only run when the system would otherwise be idle.

On many OSes utilities such as top report the priority and not the niceness. Niceness is used by the utility '/usr/bin/renice': '/usr/bin/nice' (and /usr/bin/renice -n) specifies an increment in niceness.

Only privileged users (usually super-users) can lower the niceness.

Windows has a slightly different concept of 'priority classes'. We have mapped the idle priority to niceness 19, 'below normal' to 15, normal to 0, 'above normal' to -5 and 'realtime' to -10. Unlike Unix-alikes, a non-privileged user can increase the priority class on Windows (but using 'realtime' is inadvisable).

Value

An integer vector of previous niceness values, NA if unknown for any reason.

See Also

Various functions in package parallel create child processes whose priority may need to be changed. pskill.
** QC Checks for R Code and/or Documentation **

**Description**

Functions for performing various quality control (QC) checks on R code and documentation, notably on R packages.

**Usage**

```r
checkDocFiles (package, dir, lib.loc = NULL, chkInternal = FALSE)
checkDocStyle (package, dir, lib.loc = NULL)
checkReplaceFuns(package, dir, lib.loc = NULL)
checkS3methods (package, dir, lib.loc = NULL)
checkRdContents (package, dir, lib.loc = NULL, chkInternal = FALSE)
```

**Arguments**

- `package` a character string naming an installed package.
- `dir` a character string specifying the path to a package’s root source (or *installed in some cases*) directory. This should contain the subdirectories ‘R’ (for R code) and ‘man’ with R documentation sources (in Rd format). Only used if `package` is not given.
- `lib.loc` a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. The specified library trees are used to search for `package`.
- `chkInternal` logical indicating if Rd files marked with keyword `internal` should be checked as well.

**Details**

- `checkDocFiles` checks, for all Rd files in a package, whether all arguments shown in the usage sections of the Rd file are documented in its arguments section. It also reports duplicated entries in the arguments section, and ‘over-documented’ arguments which are given in the arguments section but not in the usage.
- `checkDocStyle` investigates how (S3) methods are shown in the usages of the Rd files in a package. It reports the methods shown by their full name rather than using the Rd `\method` markup for indicating S3 methods. Earlier versions of R also reported about methods shown along with their generic, which typically caused problems for the documentation of the primary argument in the generic and its methods. With `\method` now being expanded in a way that class information is preserved, joint documentation is no longer necessarily a problem. (The corresponding information is still contained in the object returned by `checkDocStyle`.)
- `checkReplaceFuns` checks whether replacement functions or S3/S4 replacement methods in the package R code have their final argument named `value`.
- `checkS3methods` checks whether all S3 methods defined in the package R code have all arguments of the corresponding generic, with positional arguments of the generics in the same positions for...
the method. As an exception, the first argument of a formula method may be called formula even if this is not the name used by the generic. The rules when ... is involved are subtle: see the source code. Functions recognized as S3 generics are those with a call to `UseMethod` in their body, internal S3 generics (see `InternalMethods`), and S3 group generics (see `Math`). Possible dispatch under a different name is not taken into account. The generics are sought first in the given package, then (if given an installed package) in the package imports, and finally the namespace environment for the base package.

`checkRdContents()` checks Rd content, e.g., whether arguments of functions in the usage section have non empty descriptions.

`nonS3methods(package)` returns a character vector with the names of the functions in package which ‘look’ like S3 methods, but are not. Using `package = NULL` returns all known examples.

`langElt`s is a character vector of names of “language elements” of R. These are implemented as “very primitive” functions (no argument list; `print()`ing as .Primitive("<name>")).

If using an installed package, the checks needing access to all R objects of the package will load the package (unless it is the base package), after possibly detaching an already loaded version of the package.

**Value**

The functions return objects of class the same as the respective function names containing the information about problems detected. There are `print` methods for nicely displaying the information contained in such objects.

---

### Rcmd

**R CMD Interface**

**Description**

Invoke R CMD tools from within R.

**Usage**

```r
Rcmd(args, ...)
```

**Arguments**

- `args` a character vector of arguments to R CMD.
- `...` arguments to be passed to `system2`.

**Details**

Provides a portable convenience interface to the R CMD mechanism by invoking the corresponding system commands (using the version of R currently used) via `system2`.

**Value**

See section “Value” in `system2`. 
Rd2HTML

Rd Converters

Description

These functions take the output of `parse_Rd()`, an Rd object, and produce a help page from it. As they are mainly intended for internal use, their interfaces are subject to change.

Usage

```r
Rd2HTML(Rd, out = "", package = "", defines = .Platform$OS.type,
          Links = NULL, Links2 = NULL,
          stages = "render", outputEncoding = "UTF-8",
          dynamic = FALSE, no_links = FALSE, fragment = FALSE,
          stylesheet = if (dynamic) "/doc/html/R.css" else "R.css",
          texmath = getOption("help.htmlmath"),
          concordance = FALSE,
          standalone = TRUE,
          Rhtml = FALSE,
          ...)
```

```r
Rd2txt(Rd, out = "", package = "", defines = .Platform$OS.type,
        stages = "render", outputEncoding = "",
        fragment = FALSE, options, ...)
```

```r
Rd2latex(Rd, out = "", defines = .Platform$OS.type,
          stages = "render", outputEncoding = "UTF-8",
          fragment = FALSE, ..., writeEncoding = TRUE,
          concordance = FALSE)
```

```r
Rd2ex(Rd, out = "", defines = .Platform$OS.type,
       stages = "render", outputEncoding = "UTF-8",
       commentDontrun = TRUE, commentDonttest = FALSE, ...)
```

Arguments

- **Rd**: a filename or Rd object to use as input.
- **out**: a filename or connection object to which to write the output. The default `out = ""` is equivalent to `out = stdout()`.
- **package**: the package to list in the output.
- **defines**: string(s) to use in `#ifdef` tests.
- **stages**: at which stage ("build", "install", or "render") should \Sexpr macros be executed? See the notes below.
- **outputEncoding**: see the ‘Encodings’ section below.
- **dynamic**: logical: set links for render-time resolution by dynamic help system.
- **no_links**: logical: suppress hyperlinks to other help topics. Used by `R CMD Rdconv`.
- **fragment**: logical: should fragments of Rd files be accepted? See the notes below.
- **stylesheet**: character: a URL for a stylesheet to be used in the header of the HTML output page.
texmath character: controls how mathematics in \texttt{eqn} and \texttt{deqn} commands are typeset in HTML output. Useful values are "katex" (default) and "mathjax" to use \LaTeX{} or MathJax respectively, otherwise basic substitutions are used. May be ignored under certain circumstances, e.g., if the help page already uses macros from the \texttt{mathjaxr} package.

concordance Whether concordance data should be embedded in the output file and attached to the return value.

standalone logical: whether the output is intended to be a standalone HTML file. If FALSE, the header and footer are omitted, so that the output can be combined with other fragments.

Rhtml logical: whether the output is intended to be a Rhtml file that can be processed using \texttt{knitr}. If TRUE, the examples section is wrapped inside a \texttt{rcode} block.

Links, Links2 NULL or a named (by topics) character vector of links, as returned by \texttt{findHTMLlinks}.

options An optional named list of options to pass to \texttt{Rd2txt_options}.

... additional parameters to pass to \texttt{parse_Rd} when Rd is a filename.

writeEncoding should \texttt{inputencoding} lines be written in the file for non-ASCII encodings?

commentDontrun should \texttt{dontrun} sections be commented out?

commentDonttest should \texttt{donttest} sections be commented out?

Details

These functions convert help documents: \texttt{Rd2HTML} produces HTML, \texttt{Rd2txt} produces plain text, \texttt{Rd2latex} produces \LaTeX{}. \texttt{Rd2ex} extracts the examples in the format used by \texttt{example} and \texttt{R} utilities.

Each of the functions accepts a filename for an Rd file, and will use \texttt{parse_Rd} to parse it before applying the conversions or checks.

The difference between arguments \texttt{Link} and \texttt{Link2} is that links are looked in them in turn, so lazy-evaluation can be used to only do a second-level search for links if required.

Before R 3.6.0, the default for \texttt{Rd2latex} was \texttt{outputEncoding = "ASCII"}, including using the second option of \texttt{\enc} markup, because \texttt{\LaTeX} versions did not provide enough coverage of UTF-8 glyphs for a long time.

\texttt{Rd2txt} will format text paragraphs to a width determined by \texttt{width}, with appropriate margins. The default is to be close to the rendering in versions of R < 2.10.0.

\texttt{Rd2txt} will use directional quotes (see \texttt{sQuote}) if option "useFancyQuotes" is true (usually the default, see \texttt{sQuote}) and the current encoding is UTF-8.

Various aspects of formatting by \texttt{Rd2txt} are controlled by the options argument, documented with the \texttt{Rd2txt_options} function. Changes made using options are temporary, those made with \texttt{Rd2txt_options} are persistent.

When \texttt{fragment} = TRUE, the Rd file will be rendered with no processing of \texttt{\Sexpr} elements or conditional defines using \texttt{#ifdef} or \texttt{#ifndef}. Normally a fragment represents text within a section, but if the first element of the fragment is a section macro, the whole fragment will be rendered as a series of sections, without the usual sorting.
Value

These functions are executed mainly for the side effect of writing the converted help page. Their value is the name of the output file (invisibly). For Rd2latex, the output name is given an attribute "latexEncoding" giving the encoding of the file in a form suitable for use with the LaTeX \texttt{inputenc} package.

For Rd2HTML and Rd2latex with concordance = TRUE, a "concordance" attribute is added, containing an \texttt{Rconcordance} object.

Encodings

Rd files are normally intended to be rendered on a wide variety of systems, so care must be taken in the encoding of non-ASCII characters. In general, any such encoding should be declared using the ‘encoding’ section for there to be any hope of correct rendering.

For output, the outputEncoding argument will be used: outputEncoding = "" will choose the native encoding for the current system.

If the text cannot be converted to the outputEncoding, byte substitution will be used (see \texttt{iconv}): Rd2latex and Rd2ex give a warning.

Note

The \texttt{\Sexpr{}} macro includes \texttt{R} code that will be executed at one of three times: build time (when a package’s source code is built into a tarball), install time (when the package is installed or built into a binary package), and render time (when the man page is converted to a readable format).

For example, this man page was:

1. built on 2023-11-22 at 04:34:38,
2. installed on 2023-11-22 at 04:34:38, and
3. rendered on 2023-11-22 at 04:41:06.

Author(s)

Duncan Murdoch, Brian Ripley

References

https://developer.r-project.org/parseRd.pdf

See Also

\texttt{parse_Rd, checkRd, findHTMLlinks, Rd2txt_options, matchConcordance}.

Examples

```r
## Not run:
## Simulate install and rendering of this page in HTML and text format:

Rd <- file.path("src/library/tools/man/Rd2HTML.Rd")
outfile <- tempfile(fileext = ".html")
browseURL(Rd2HTML(Rd, outfile, package = "tools", stages = c("install", "render")))
```
Rd2txt_options

outfile <- tempfile(fileext = "\.txt")
file.show(Rd2txt(Rd, outfile, package = "tools",
   stages = c("install", "render")))

checkRd(Rd) # A stricter test than Rd2HTML uses

## End(Not run)

Rd2txt_options

Set Formatting Options for Text Help

Description

This function sets various options for displaying text help.

Usage

Rd2txt_options(...)

Arguments

... A list containing named options, or options passed as individual named arguments. See below for currently defined ones.

Details

This function persistently sets various formatting options for the Rd2txt function which is used in displaying text format help. Currently defined options are:

width (default 80): The width of the output page.

minIndent (default 10): The minimum indent to use in a list.

extraIndent (default 4): The extra indent to use in each level of nested lists.

sectionIndent (default 5): The indent level for a section.

sectionExtra (default 2): The extra indentation for each nested section level.

itemBullet (default "\* ", with the asterisk replaced by a Unicode bullet in UTF-8 and most Windows locales): The symbol to use as a bullet in itemized lists.

c enumFormat : A function to format item numbers in enumerated lists.

showURLs (default FALSE): Whether to show URLs when expanding \href tags.

code_quote (default TRUE): Whether to render \code and similar with single quotes.

underline_titles (default TRUE): Whether to render section titles with underlines (via backspacing).

Value

If called with no arguments, returns all option settings in a list. Otherwise, it changes the named settings and invisibly returns their previous values.

Author(s)

Duncan Murdoch
See Also

Rd2txt

Examples

# The itemBullet is locale-specific
saveOpts <- Rd2txt_options()
saveOpts
Rd2txt_options(minIndent = 4)
Rd2txt_options()
Rd2txt_options(saveOpts)
Rd2txt_options()

Rdiff

### Difference R Output Files

Description

Given two R output files, compute differences ignoring headers, footers and some other differences.

Usage

Rdiff(from, to, useDiff = FALSE, forEx = FALSE,
nullPointers = TRUE, Log = FALSE)

Arguments

from, to     filepaths to be compared
useDiff     should diff be used to compare results? Overridden to false if the command is
            not available.
forEx       logical: extra pruning for ‘-Ex.Rout’ files to exclude the header.
nullPointers logical: should the displayed addresses of pointers be set to 0x00000000 before
                 comparison?
Log          logical: should the returned value include a log of differences found?

Details

The R startup banner and any timing information from R CMD BATCH are removed from both files, together with lines about loading packages. UTF-8 fancy quotes (see sQuote) and on Windows, Windows’ so-called ‘smart quotes’, are mapped to a simple quote. Addresses of environments, compiled bytecode and other exotic types expressed as hex addresses (e.g., <environment: 0x12345678>) are mapped to 0x00000000. The files are then compared line-by-line. If there are the same number of lines and useDiff is false, a simple diff -b -like display of differences is printed (which ignores trailing spaces and differences in numbers of consecutive spaces), otherwise diff -bw is called on the edited files. (This tries to ignore all differences in whitespace: note that flag ‘-w’ is not required by POSIX but is supported by GNU, Solaris and FreeBSD versions – macOS uses an old GNU version.)

There is limited support for comparing PDF files produced by pdf(compress = FALSE), mainly for use in make check – this requires a diff command and useDiff = TRUE.

Mainly for use in examples and tests, text from marker ‘> ## IGNORE_RDIFF_BEGIN’ up to (but not including) ‘> ## IGNORE_RDIFF_END’ is ignored.
Value

If `Log` is true, a list with components `status` (see below) and `out`, a character vector of descriptions of differences, possibly of zero length.

Otherwise, a status indicator (invisibly), `0L` if and only if no differences were found.

See Also

The shell script run as `R CMD Rdifff`, which uses `useDiff = TRUE`.
RdTextFilter

Select Text in an Rd File

Description

This function blanks out all non-text in an Rd file, for spell checking or other uses.

Usage

RdTextFilter(ifile, encoding = "unknown", keepSpacing = TRUE, drop = character(), keep = character(), macros = file.path(R.home("share"), "Rd", "macros", "system.Rd"))

Arguments

ifile An input file specified as a filename or connection, or an "Rd" object from parse_Rd.
encoding An encoding name to pass to parse_Rd.
keepSpacing Whether to try to leave the text in the same lines and columns as in the original file.
drop Additional sections of the Rd to drop.
keep Sections of the Rd file to keep.
macros Macro definitions to assume when parsing. See parse_Rd.

Details

This function parses the Rd file, then walks through it, element by element. Items with tag "TEXT" are kept in the same position as they appeared in the original file, while other parts of the file are replaced with blanks, so a spell checker such as aspell can check only the text and report the position in the original file. (If keepSpacing is FALSE, blank filling will not occur, and text will not be output in its original location.)

By default, the tags \S3method, \S4method, \command, \docType, \email, \encoding, \file, \keyword, \link, \linkS4class, \method, \pkg, and \var are skipped. Additional tags can be skipped by listing them in the drop argument; listing tags in the keep argument will stop them from being skipped. It is also possible to keep any of the c("R CODE", "COMMENT", "VERB") tags, which correspond to R-like code, comments, and verbatim text respectively, or to drop "TEXT".

Value

A character vector which if written to a file, one element per line, would duplicate the text elements of the original Rd file.

Note

The filter attempts to merge text elements into single words when markup in the Rd file is used to highlight just the start of a word.

Author(s)

Duncan Murdoch
See Also

`aspell`, for which this is an acceptable filter.

Rd-utils

Rd Utilities

Description

Utilities for computing on the information in Rd objects.

Usage

Rd_db(package, dir, lib.loc = NULL, stages = "build")

Arguments

package a character string naming an installed package.
dir a character string specifying the path to a package’s root source directory. This should contain the subdirectory ‘man’ with R documentation sources (in Rd format). Only used if package is not given.
lib.loc a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.
stages if dir is specified and the database is being built from source, which stages of `\Sexpr` processing should be processed?

Details

Rd_db builds a simple database of all Rd objects in a package, as a list of the results of running `parse_Rd` on the Rd source files in the package and processing platform conditionals and some `\Sexpr` macros.

See Also

`parse_Rd`

Examples

```r
## Build the Rd db for the (installed) base package.
db <- Rd_db("base")

## Keyword metadata per Rd object.
keywords <- lapply(db, tools:::Rd_get_metadata, "keyword")
## Tabulate the keyword entries.
kw_table <- sort(table(unlist(keywords)))
## The 5 most frequent ones:
rev(kw_table)[1:5]

## The "most informative" ones:
kw_table[kw_table == 1]

## Concept metadata per Rd file.
concepts <- lapply(db, tools:::Rd_get_metadata, "concept")
```
## How many files already have \concept metadata?

```r
sum(sapply(concepts, length) > 0)
```

## How many concept entries altogether?

```r
length(unlist(concepts))
```

---

### read.00Index

**Read 00Index-style Files**

**Description**

Read item/description information from `00Index`-like files. Such files are description lists rendered in tabular form, and currently used for the `INDEX` and `demo/00Index` files of add-on packages.

**Usage**

```r
read.00Index(file)
```

**Arguments**

- `file` the name of a file to read data values from. If the specified file is "", then input is taken from the keyboard (in this case input can be terminated by a blank line). Alternatively, `file` can be a connection, which will be opened if necessary, and if so closed at the end of the function call.

**Value**

A character matrix with 2 columns named "Item" and "Description" which hold the items and descriptions.

**See Also**

- `formatDL` for the inverse operation of creating a 00Index-style file from items and their descriptions.

---

### showNonASCII

**Pick Out Non-ASCII Characters**

**Description**

This function prints elements of a character vector which contain non-ASCII bytes, printing such bytes as a escape like `\<fc>`.

**Usage**

```r
showNonASCII(x)
```

```r
showNonASCIIfile(file)
```
Arguments

- **x**: a character vector.
- **file**: path to a file.

Details

This was originally written to help detect non-portable text in files in packages.

It prints all element of \( x \) which contain non-ASCII characters, preceded by the element number and with non-ASCII bytes highlighted via \texttt{iconv(sub = "byte")}.

However, this rendering depends on \texttt{iconv(to = "ASCII")} failing to convert, and macOS 14 no longer does so reliably so for example permille (‘\u2030’) is rendered as 0/00.

Value

The elements of \( x \) containing non-ASCII characters will be returned invisibly.

Examples

```r
out <- c(
  "fa\xE7ile test of showNonASCII():",
  "\\details{",
  "  This is a good line",
  "  This has an \xc3mlaut in it",
  "  OK again",
  "}
)
f <- tempfile()
cat(out, file = f, sep = 

## IGNORE_RDIFF_BEGIN
showNonASCIIfile(f)
## IGNORE_RDIFF_END
.unlink(f)
```

Description

This function starts the internal help server, so that HTML help pages are rendered when requested.

Usage

```r
startDynamicHelp(start = TRUE)
```

Arguments

- **start**: logical: whether to start or shut down the dynamic help system. If \texttt{NA}, the server is started if not already running.
Details

This function starts the internal HTTP server, which runs on the loopback interface (127.0.0.1). If options("help.ports") is set to a vector of non-zero integer values, startDynamicHelp will try those ports in order; otherwise, it tries up to 10 random ports to find one not in use. It can be disabled by setting the environment variable R_DISABLE_HTTPD to a non-empty value or options("help.ports") to 0.

startDynamicHelp is called by functions that need to use the server, so would rarely be called directly by a user.

Note that options(help_type = "html") must be set to actually make use of HTML help, although it might be the default for an R installation.

If the server cannot be started or is disabled, help.start will be unavailable and requests for HTML help will give text help (with a warning).

The browser in use does need to be able to connect to the loopback interface: occasionally it is set to use a proxy for HTTP on all interfaces, which will not work – the solution is to add an exception for 127.0.0.1.

Value

The chosen port number is returned invisibly (which will be 0 if the server has been stopped).

See Also

help.start and help(help_type = "html") will attempt to start the HTTP server if required. Rd2HTML is used to render the package help pages.

SweaveTeXFilter

Strip R Code out of Sweave File

Description

This function blanks out code chunks and Noweb markup in an Sweave input file, for spell checking or other uses.

Usage

SweaveTeXFilter(ifile, encoding = "unknown")

Arguments

ifile Input file or connection.

encoding Text encoding to pass to readLines.

Details

This function blanks out all Noweb markup and code chunks from an Sweave input file, leaving behind the LaTeX source, so that a LaTeX-aware spelling checker can check it and report errors in their original locations.
**Value**

A character vector which if written to a file, one element per line, would duplicate the text elements of the original Sweave input file.

**Author(s)**

Duncan Murdoch

**See Also**

`aspell`, for which this is used with `filter = "Sweave"`.

---

### testInstalledPackage  
**Test Installed Packages**

**Description**

These functions allow an installed package to be tested, or all base and recommended packages.

**Usage**

```r
testInstalledPackage(pkg, lib.loc = NULL, outDir = ",.",
  types = c("examples", "tests", "vignettes"),
  srcdir = NULL, Ropts = "", ...)  
testInstalledPackages(outDir = ",.", errorsAreFatal = TRUE,
  scope = c("both", "base", "recommended"),
  types = c("examples", "tests", "vignettes"),
  srcdir = NULL, Ropts = "", ...)  
testInstalledBasic(scope = c("basic", "devel", "both", "internet"))
```

**Arguments**

- `pkg` name of an installed package.
- `lib.loc` library path(s) in which to look for the package. See `library`.
- `outDir` the directory into which to write the output files: this should already exist.
- `types` type(s) of tests to be done.
- `errorsAreFatal` logical: should testing terminate at the first error?
- `srcdir` Optional directory to look for `.save` files.
- `Ropts` Additional options such as `"-d valgrind"` to be passed to `R CMD BATCH` when running examples or tests.
- `...` additional arguments use when preparing the files to be run, e.g. `commentDontrun` and `commentDonttest`.
- `scope` Which set(s) should be tested? Can be abbreviated.
Details

These tests depend on having the package example files installed (which is the default). If package-specific tests are found in a 'tests' directory they can be tested: these are not installed by default, but will be if R CMD INSTALL --install-tests was used. Finally, the R code in any vignettes can be extracted and tested.

Package tests are run in a 'pkg-tests' subdirectory of 'outdir', and leave their output there.

testInstalledBasic runs the basic tests, if installed. This should be run with LC_COLLATE=C set: the function tries to set this by it may not work on all OSes. For non-English locales it may be desirable to set environment variables LANGUAGE to 'en' and LC_TIME to 'C' to reduce the number of differences from reference results.

Except on Windows, if the environment variable TEST_MC_CORES is set to an integer greater than one, testInstalledPackages will run the package tests in parallel using its value as the maximum number of parallel processes.

The package-specific tests for the base and recommended packages are not normally installed, but make install-tests is provided to do so (as well as the basic tests).

Value

Invisibly 0L for success, 1L for failure.

---

texi2dvi

Compile LaTeX Files

Description

Run latex/pdflatex, makeindex and bibtex until all cross-references are resolved to create a dvi or a PDF file.

Usage

texi2dvi(file, pdf = FALSE, clean = FALSE, quiet = TRUE, 
  texi2dvi = getOption("texi2dvi"), 
  texinputs = NULL, index = TRUE)

texi2pdf(file, clean = FALSE, quiet = TRUE, 
  texi2dvi = getOption("texi2dvi"), 
  texinputs = NULL, index = TRUE)

Arguments

file character string. Name of the LaTeX source file.
pdf logical. If TRUE, a PDF file is produced instead of the default dvi file (texi2dvi command line option '--pdf').
clean logical. If TRUE, all auxiliary files created during the conversion are removed.
quiet logical. No output unless an error occurs.
texi2dvi character string (or NULL). Script or program used to compile a TeX file to dvi or PDF. The default (selected by "" or "texi2dvi" or NULL) is to look for a program or script named texi2dvi on the path and otherwise emulate the script with system2 calls (which can be selected by the value "emulation"). See also 'Details'.
texi2dvi

texinputs
NULL or a character vector of paths to add to the LaTeX and bibtex input search
paths.

index
logical: should indices be prepared?

Details
texi2pdf is a wrapper for the common case of texi2dvi(pdf = TRUE).

Despite the name, this is used in R to compile LaTeX files, specifically those generated from
vignettes and by the Rd2pdf script (used for package reference manuals). It ensures that the
'R_HOME/share/texmf' directory is in the TEXINPUTS path, so R style files such as 'Sweave.sty'
and 'Rd.sty' will be found. The TeX search path used is first the existing TEXINPUTS setting (or the
current directory if unset), then elements of argument texinputs, then 'R_HOME/share/texmf'
and finally the default path. Analogous changes are made to BIBINPUTS and BSTINPUTS settings.

The default option for texi2dv1 is set from environment variable R_TEXI2DVICMD, and the default
for that is set from environment variable TEXI2DVI or if that is unset, from a value chosen when
R is configured.

A shell script texi2dv1 is part of GNU’s texinfo. Several issues have been seen with released
versions, so if yours does not work correctly try R_TEXI2DVICMD=emulation.

Occasionally indices contain special characters which cause indexing to fail (particularly when us-
ing the ‘hyperref’ LaTeX package) even on valid input. The argument index = FALSE is provided
to allow package manuals to be made when this happens: it uses emulation.

Value
Invisible NULL. Used for the side effect of creating a dvi or PDF file in the current working directory
(and maybe other files, especially if clean = FALSE).

Note
There are various versions of the texi2dv1 script on Unix-alikes and quite a number of bugs have
been seen, some of which this R wrapper works around.

One that was present with texi2dv1 version 4.8 (as supplied by macOS) is that it will not work
correctly for paths which contain spaces, nor if the absolute path to a file would contain spaces.

The three possible approaches all have their quirks. For example the Unix-alike texi2dv1 script
removes ancillary files that already exist but the other two approaches do not (and may get confused
by such files).

Where supported (texi2dv1 5.0 and later; texify.exe from MiKTeX), option
'--max-iterations=20' is used to avoid infinite retries.

The emulation mode supports quiet = TRUE from R 3.2.3 only. Currently clean = TRUE only cleans
up in this mode if the conversion was successful—this gives users a chance to examine log files in
the event of error.

All the approaches should respect the values of environment variables LATEX, PDFTEX, MAKINDEX
and BIBTEX for the full paths to the corresponding commands.

Author(s)
Originally Achim Zeileis but largely rewritten by R-core.
toHTML

Display an Object in HTML

Description

This generic function generates a complete HTML page from an object.

Usage

toHTML(x, ...)

## S3 method for class 'packageIQR'
toHTML(x, ...)

## S3 method for class 'news_db'
toHTML(x, ...)

Arguments

x
An object to display.

... Optional parameters for methods; the "packageIQR" and "news_db" methods pass these to HTMLheader.

Value

A character vector to display the object x. The "packageIQR" method is designed to display lists in the R help system.

See Also

HTMLheader

Examples

cat(toHTML(demo(package = "base")), sep = "\n")

tools-deprecated

Deprecated Objects in Package tools

Description

(Currently none)

The functions or variables listed here are provided for compatibility with older versions of R only, and may be defunct as soon as of the next release.

See Also

Deprecated, Defunct
toRd

Generic Function to Convert Object to a Fragment of Rd Code

Description

Methods for this function render their associated classes as a fragment of Rd code, which can then be rendered into text, HTML, or LaTeX.

Usage

toRd(obj, ...)

## S3 method for class 'bibentry'
toRd(obj, style = NULL, ...)

Arguments

- **obj**: The object to be rendered.
- **style**: The style to be used in converting a bibentry object.
- **...**: Additional arguments used by methods.

Details

See bibstyle for a discussion of styles. The default style = NULL value gives the default style.

Value

Returns a character vector containing a fragment of Rd code that could be parsed and rendered. The default method converts obj to mode character, then escapes any Rd markup within it. The bibentry method converts an object of that class to markup appropriate for use in a bibliography.

toTitleCase

Convert Titles to Title Case

Description

Convert a character vector to title case, especially package titles.

Usage

toTitleCase(text)

Arguments

- **text**: a character vector.
Details

This is intended for English text only.

No definition of 'title case' is universally accepted: all agree that 'principal' words are capitalized and common words like 'for' are not, but not which words fall into each category.

Generally words in all capitals are left alone: this implementation knows about conventional mixed-case words such as 'LaTeX' and 'OpenBUGS' and a few technical terms which are not usually capitalized such as 'jar' and 'xls'. However, unknown technical terms will be capitalized unless they are single words enclosed in single quotes: names of packages and libraries should be quoted in titles.

Value

A character vector of the same length as text, without names.

undoc

Find Undocumented Objects

Description

Finds the objects in a package which are undocumented, in the sense that they are visible to the user (or data objects or S4 classes provided by the package), but no documentation entry exists.

Usage

undoc(package, dir, lib.loc = NULL)

Arguments

package a character string naming an installed package.
dir a character string specifying the path to a package's root source directory. This must contain the subdirectory 'man' with R documentation sources (in Rd format), and at least one of the 'R' or 'data' subdirectories with R code or data objects, respectively.
lib.loc a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.

Details

This function is useful for package maintainers mostly. In principle, all user-level R objects should be documented.

The base package is special as it contains the primitives and these do not have definitions available at code level. We provide equivalent closures in environments .ArgsEnv and .GenericArgsEnv in the base package that are used for various purposes: undoc("base") checks that all the primitives that are not language constructs are prototyped in those environments and no others are.

Value

An object of class "undoc" which is a list of character vectors containing the names of the undocumented objects split according to documentation type.

There is a print method for nicely displaying the information contained in such objects.
update_PACKAGES

See Also
codoc, QC

Examples

undoc("tools") # Undocumented objects in 'tools'

Description

Update an existing repository by reading the PACKAGES file, retaining entries which are still valid, removing entries which are no longer valid, and only processing built package tarballs which do not match existing entries.

update_PACKAGES can be much faster than write_PACKAGES for small-moderate changes to large repository indexes, particularly in non-strict mode (see Details).

Usage

update_PACKAGES(dir = ".", fields = NULL, type = c("source","mac.binary","win.binary"), verbose.level = as.integer(dryrun), latestOnly = TRUE, addFiles = FALSE, rds_compress = "xz", strict = TRUE, dryrun = FALSE)

Arguments

dir See write_PACKAGES
fields See write_PACKAGES
type See write_PACKAGES
verbose.level (0, 1, 2) What level of informative messages which should be displayed throughout the process. Defaults to 0 if dryrun is FALSE (the default) and 1 otherwise. See details for more information.
latestOnly See write_PACKAGES
addFiles See write_PACKAGES
rds_compress See write_PACKAGES
strict logical. Should 'strict mode' be used when checking existing PACKAGES entries. See details. Defaults to TRUE.
dryrun logical. Should the updates to existing PACKAGES files be computed but NOT applied. Defaults to FALSE.

Details

Throughout this section, package tarball is defined to mean any archive file in dir whose name can be interpreted as <package>_<version>.<ext> - with <ext> the appropriate extension for built packages of type type - (or that is pointed to by the File field of an existing PACKAGES entry). Novel package tarballs are those which do not match an existing PACKAGES file entry.

update_PACKAGES calls directly down to write_PACKAGES with a warning (and thus all package tarballs will be processed), if any of the following conditions hold:
• type is win.binary and strict is TRUE (no MD5 checksums are included in win.binary PACKAGES files)
• No PACKAGES file exists under dir
• A PACKAGES file exists under dir but is empty
• fields is not NULL and one or more specified fields are not present in the existing PACKAGES file

update_PACKAGES avoids (re)processing package tarballs in cases where a PACKAGES file entry already exists and appears to remain valid. The logic for detecting still-valid entries is as follows:

Any package tarball which was last modified more recently than the existing PACKAGES file is considered novel; existing PACKAGES entries appearing to correspond to such tarballs are always considered stale and replaced by newly generated ones. Similarly, all PACKAGES entries that do not correspond to any package tarball found in dir are considered invalid and are excluded from the resulting updated PACKAGES files.

When strict is TRUE, PACKAGES entries that match a package tarball (by package name and version) are confirmed via MD5 checksum; only those that pass are retained as valid. All novel package tarballs are fully processed by the standard machinery underlying write_PACKAGES and the resulting entries are added. Finally, if latestOnly is TRUE, package-version pruning is performed across the entries.

When strict is FALSE, package tarballs are assumed to encode correct metadata in their filenames. PACKAGES entries which appear to match a package tarball are retained as valid (No MD5 checksum testing occurs). If latestOnly is TRUE, package-version pruning is performed across the full set of retained entries and novel package tarballs before the processing of the novel tarballs, at significant computational and time savings in some situations. After the optional pruning, any relevant novel package tarballs are processed via the standard machinery and added to the set of retained entries.

In both cases, after the above process concludes, entries are sorted alphabetically by the string concatenation of Package and Version. This should match the entry order write_PACKAGES outputs.

The fields within the entries are ordered as follows: canonical fields - i.e., those appearing as columns when available.packages is called on a CRAN mirror - appear first in their canonical order, followed by any non-canonical fields.

After entry and field reordering, the final database of PACKAGES entries is written to all three PACKAGES files, overwriting the existing versions.

When verbose.level is 0, no extra messages are displayed to the user. When it is 1, detailed information about what is happening is conveyed via messages, but underlying machinery from write_PACKAGES is called with verbose = FALSE. Behavior when verbose.level is 2 is identical to verbose.level 1 with the exception that underlying machinery from write_PACKAGE is invoked with verbose = TRUE, which will individually list every processed tarball.

Note

While both strict and non-strict modes can offer speedups when updating small percentages of large repositories, non-strict mode is much faster and is recommended in situations where the assumption it makes about tarballs’ filenames encoding accurate information is safe.

Note

Users should expect significantly smaller speedups over write_PACKAGES in the type == "win.binary" case on at least some operating systems. This is due to write_PACKAGES being significantly faster in this context, rather than update_PACKAGES being slower.
update_pkg_po

Author(s)

Gabriel Becker (adapted from previous, related work by him in the switchr package which is copyright Genentech, Inc.)

See Also

write_PACKAGES

Examples

## Not run:
write_PACKAGES("c:/myFolder/myRepository") # on Windows
update_PACKAGES("c:/myFolder/myRepository") # on Windows
write_PACKAGES("/pub/RWin/bin/windows/contrib/2.9",
type = "win.binary") # on Linux
update_PACKAGES("/pub/RWin/bin/windows/contrib/2.9",
type = "win.binary") # on Linux

## End(Not run)

update_pkg_po  Prepare Translations for a Package

Description

Prepare the ‘po’ directory of a package and compile and install the translations.

Usage

update_pkg_po(pkgdir, pkg = NULL, version = NULL, mergeOpts = "", copyright, bugs)

Arguments

pkgdir  The path to the package directory.

pkg  The package name: if NULL it is read from the package’s ‘DESCRIPTION’ file.

version  The package version: if NULL it is read from the package’s ‘DESCRIPTION’ file.

mergeOpts  a string, by default empty, of options to msgmerge in addition to "--update". Since R 4.2.0, "--no-wrap" is used when called from file.path(R.home("po"), "Makefile").

copyright, bugs  optional character strings for the ‘Copyright’ and ‘Report-Msgid-Bugs-To’ details in the template files.

Details

This performs a series of steps to prepare or update messages in the package.

- If the package sources do not already have a ‘po’ directory, one is created.
- xgettext2pot is called to create/update a file ‘po/R-pkgname.pot’ containing the translatable messages in the package.
• All existing files in directory `po` with names `R-lang.po` are updated from `R-pkgname.pot`, `checkPoFile` is called on the updated file, and if there are no problems the file is compiled and installed under `inst/po`.

• In a UTF-8 locale, a ‘translation’ `R-en@quot.po` is created with UTF-8 directional quotes, compiled and installed under `inst/po`.

• The remaining steps are done only if file `po/pkgname.pot` already exists. The `src/*.c,cc,cpp,m,mm` files in the package are examined to create a file `po/pkgname.pot` containing the translatable messages in the C/C++ files. If there is a `src/windows` directory, files within it are also examined.

• All existing files in directory `po` with names `lang.po` are updated from `pkgname.pot`, `checkPoFile` is called on the updated file, and if there are no problems the file is compiled and installed under `inst/po`.

• In a UTF-8 locale, a ‘translation’ `en@quot.po` is created with UTF-8 directional quotes, compiled and installed under `inst/po`.

Note that C/C++ messages are not automatically prepared for translation as they need to be explicitly marked for translation in the source files. Once that has been done, create an empty file `po/pkgname.pot` in the package sources and run this function again.

pkg = "base" is special (and for use by R developers only): the C files are not in the package directory but in the main sources.

### System requirements

This function requires the following tools from the GNU gettext-tools: `xgettext`, `msgmerge`, `msgfmt`, `msginit` and `msgconv`. These are part of most Linux distributions and easily compiled from the sources on Unix-alikes (including macOS). Pre-compiled versions for Windows are available in [https://www.stats.ox.ac.uk/pub/Rtools/goodies/gettext-tools.zip](https://www.stats.ox.ac.uk/pub/Rtools/goodies/gettext-tools.zip).

It will probably not work correctly for `en@quot` translations except in a UTF-8 locale, so these are skipped elsewhere.

#### See Also

`xgettext2pot`.

---

**userdir**

**R User Directories**

**Description**

Directories for storing R-related user-specific data, configuration and cache files.

**Usage**

```r
R_user_dir(package, which = c("data", "config", "cache"))
```

**Arguments**

- `package` a character string giving the name of an R package
- `which` a character string indicating the kind of file(s) of interest. Can be abbreviated.
Details

For desktop environments using X Windows, the freedesktop.org project (formerly X Desktop Group, XDG) developed the XDG Base Directory Specification (https://specifications.freedesktop.org/basedir-spec) for standardizing the location where certain files should be placed. CRAN package `rappdirs` provides these general locations with appropriate values for all platforms for which R is available.

`R_user_dir` specializes the general mechanism to R package specific locations for user files, by providing package specific subdirectories inside a ‘R’ subdirectory inside the “base” directories appropriate for user-specific data, configuration and cache files (see the examples), with the intent that packages will not interfere if they work within their respective subdirectories.

The locations of these base directories can be customized via the specific environment variables `R_USER_DATA_DIR`, `R_USER_CONFIG_DIR` and `R_USER_CACHE_DIR`. If these are not set, the general XDG-style environment variables `XDG_DATA_HOME`, `XDG_CONFIG_HOME` and `XDG_CACHE_HOME` are used if set, and otherwise, defaults appropriate for the R platform in use are employed.

Examples

```r
## IGNORE_RDIFF_BEGIN
R_user_dir("FOO", "cache")
## Create one, platform agnostically, must work if <normal>:
(Rdb <- R_user_dir("base"))
if(noD <- !dir.exists(Rdb)) # should work user specifically:
  dir.create(Rdb, recursive=TRUE)
stopifnot(dir.exists(Rdb)) # "everywhere"
dir(Rdb) # typically empty
if(noD) unlink(Rdb) # cleaning up
list.files(R_user_dir("grid"), full.names = TRUE)
## IGNORE_RDIFF_END
```

vignetteEngine

Set or Get a Vignette Processing Engine

Description

Vignettes are normally processed by Sweave, but package writers may choose to use a different engine (e.g., one provided by the knitr, noweb or R.rsp packages). This function is used by those packages to register their engines, and internally by R to retrieve them.

Usage

```r
vignetteEngine(name, weave, tangle, pattern = NULL,
              package = NULL, aspell = list())
```

Arguments

- `name` the name of the engine.
- `weave` a function to convert vignette source files to PDF/HTML or intermediate LaTeX output.
- `tangle` a function to convert vignette source files to R code.
pattern a regular expression pattern for the filenames handled by this engine, or NULL for the default pattern.

package the package registering the engine. By default, this is the package calling vignetteEngine.

aspell a list with element names filter and/or control giving the respective arguments to be used when spell checking the text in the vignette source file with aspell.

Details

If weave is missing, vignetteEngine will return the currently registered engine matching name and package.

If weave is NULL, the specified engine will be deleted.

Other settings define a new engine. The weave and tangle functions must be defined with argument lists compatible with function(file, ...). Currently the ... arguments may include logical argument quiet and character argument encoding; others may be added in future. These are described in the documentation for Sweave and Stangle.

The weave and tangle functions should return the filename of the output file that has been produced. Currently the weave function, when operating on a file named ‘<name><pattern>’ must produce a file named ‘<name>.[.](tex|pdf|html)’. The ‘.tex’ files will be processed by pdflatex to produce ‘.pdf’ output for display to the user; the others will be displayed as produced. The tangle function must produce a file named ‘<name>.[.][rRsS]’ containing the executable R code from the vignette. The tangle function may support a split = TRUE argument, and then it should produce files named ‘<name>.*[.][rRsS]’.

The pattern argument gives a regular expression to match the extensions of files which are to be processed as vignette input files. If set to NULL, the default pattern “[.]([RrSs](nw|tex))$” is used.

Value

If the engine is being deleted, NULL. Otherwise a list containing components

name The name of the engine
package The name of its package
pattern The pattern for vignette input files
weave The weave function
tangle The tangle function

Author(s)

Duncan Murdoch and Henrik Bengtsson.

See Also

Sweave and the ‘Writing R Extensions’ manual.

Examples

str(vignetteEngine("Sweave"))
vignetteInfo

**Basic Information about a Vignette**

**Description**

Extract metadata from a vignette source file.

**Usage**

vignetteInfo(file)

**Arguments**

- **file**
  - file name of the vignette.

**Value**

A list with the following character components:

- **file**
  - the basename of the file.
- **title**
  - the vignette title from ‘\VignetteIndexEntry’, possibly an empty string.
- **depends**
  - a vector of package dependencies from ‘\VignetteDepends’, possibly of length 0.
- **keywords**
  - a vector of keywords from ‘\VignetteKeyword’, possibly of length 0.
- **engine**
  - the vignetteEngine, such as "utils::Sweave" or "knitr::knitr".

**See Also**

package_dependencies for recursive dependencies.

**Examples**

```r
gridEx <- system.file("doc", "grid.Rnw", package = "grid")
vi <- vignetteInfo(gridEx)
str(vi)
```

---

write_PACKAGES

**Generate PACKAGES Files**

**Description**

Generate ‘PACKAGES’, ‘PACKAGES.gz’ and ‘PACKAGES.rds’ files for a repository of source or Mac/Windows binary packages.

**Usage**

```r
write_PACKAGES(dir = ".", fields = NULL, 
              type = c("source", "mac.binary", "win.binary"), 
              verbose = FALSE, unpacked = FALSE, subdirs = FALSE, 
              latestOnly = TRUE, addFiles = FALSE, rds_compress = "xz", 
              validate = FALSE)
```
**write_PACKAGES**

### Arguments

**dir**
Character vector describing the location of the repository (directory including source or binary packages) to generate the 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files from and write them to.

**fields**
a character vector giving the fields to be used in the 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files in addition to the default ones, or NULL (default).

The default corresponds to the fields needed by `available.packages`:
"Package", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "OS_type", "License" and "Archs", and those fields will always be included, plus the file name in field "File" if addFile = TRUE and the path to the subdirectory in field "Path" if subdirectories are used.

**type**
Type of packages: currently source `.tar.{gz,bz2,xz}` archives, and macOS or Windows binary (`.tgz` or `.zip`, respectively) packages are supported. Defaults to "win.binary" on Windows and to "source" otherwise.

**verbose**
logical. Should packages be listed as they are processed?

**unpacked**
a logical indicating whether the package contents are available in unpacked form or not (default).

**subdirs**
either logical (to indicate if subdirectories should be included, recursively) or a character vector of names of subdirectories to include (which are not recursed).

**latestOnly**
logical: if multiple versions of a package are available should only the latest version be included?

**addFiles**
logical: should the filenames be included as field 'File' in the 'PACKAGES' file.

**rds_compress**
The type of compression to be used for 'PACKAGES.rds': see `saveRDS`. The default is the one found to give maximal compression, and is as used on CRAN.

**validate**
a logical indicating whether 'DESCRIPTION' files should be validated, and the corresponding packages skipped in case this finds problems.

### Details

write_PACKAGES scans the named directory for R packages, extracts information from each package’s 'DESCRIPTION' file, and writes this information into the 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files, where the first two represent the information in DCF format, and the third serializes it via `saveRDS`.

Including non-latest versions of packages is only useful if they have less constraining version requirements, so for example latestOnly = FALSE could be used for a source repository when `foo_1.0` depends on `R >= 2.15.0` but `foo_0.9` is available which depends on `R >= 2.11.0`.

Support for repositories with subdirectories and hence for subdirs != FALSE depends on recording a "Path" field in the 'PACKAGES' files.

Support for more general file names (e.g., other types of compression) via a "File" field in the 'PACKAGES' files can be used by `download.packages`. If the file names are not of the standard form, use addFiles = TRUE.

**type = "win.binary"** uses `unz` connections to read all 'DESCRIPTION' files contained in the (zipped) binary packages for Windows in the given directory dir, and builds files 'PACKAGES', 'PACKAGES.gz' and 'PACKAGES.rds' files from this information.

For a remote repository there is a tradeoff between download speed and time spent by `available.packages` processing the downloaded file(s). For large repositories it is likely to be beneficial to use rds_compress = "xz".
Value

Invisibly returns the number of packages described in the resulting ‘PACKAGES’, ‘PACKAGES.gz’ and ‘PACKAGES.rds’ files. If 0, no packages were found and no files were written.

Note

Processing ‘.tar.gz’ archives to extract the ‘DESCRIPTION’ files is quite slow.
This function can be useful on other OSes to prepare a repository to be accessed by Windows machines, so type = "win.binary" should work on all OSes.

Author(s)

Uwe Ligges and R-core.

See Also

See read.dcf and write.dcf for reading ‘DESCRIPTION’ files and writing the ‘PACKAGES’ and ‘PACKAGES.gz’ files. See update_PACKAGES for efficiently updating existing ‘PACKAGES’ and ‘PACKAGES.gz’ files.

Examples

```r
## Not run:
write_PACKAGES("c:/myFolder/myRepository") # on Windows
write_PACKAGES("/pub/RWin/bin/windows/contrib/2.9",
              type = "win.binary") # on Linux

## End(Not run)
```

xgettext

Extract Translatable Messages from R Files in a Package

Description

For each file in the ‘R’ directory (including system-specific subdirectories) of a source package, extract the unique arguments passed to these “message generating” calls:

for *xgettext()*: to *stop.warning*, *message*, *packageStartupMessage*, *gettext* and *gettextf*,
for *xngettext()*: to *ngettext*.
*xgettext2pot()* calls both *xgettext()* and then *xngettext()*.

Usage

```r
xgettext(dir, verbose = FALSE, asCall = TRUE)

xngettext(dir, verbose = FALSE)

xgettext2pot(dir, potFile, name = "R", version, bugs)
```
Arguments

- **dir**: the directory of a source package, i.e., with a `.R` sub directory.
- **verbose**: logical: should each file be listed as it is processed?
- **asCall**: logical: if TRUE each argument is converted to string and returned whole, otherwise the string literals within each argument are extracted (recursively). See Examples.
- **potFile**: name of po template file to be produced. Defaults to `R-pkgname.pot` where *pkgname* is the basename of ‘*dir*’.
- **name, version, bugs**: as recorded in the template file: version defaults the version number of the currently running R, and bugs to "bugs.r-project.org".

Details

Leading and trailing white space (space, tab and linefeed (aka newline, i.e., \n)) is removed for all the calls extracted by `xgettext()`, see ‘Description’ above, as it is by the internal code that passes strings for translation.

We look to see if the matched functions were called with domain = NA. If so, when asCall is true, the whole call is omitted. Note that a call might contain a nested call to gettext (or warning, etc.) whose strings would be visible if asCall is false.

`xgettext2pot` calls `xgettext` and then `xngettext`, and writes a PO template file (to *potFile*) for use with the GNU Gettext tools. This ensures that the strings for simple translation are unique in the file (as GNU Gettext requires), but does not do so for `ngettext` calls (and the rules are not stated in the Gettext manual, but `msgfmt` complains if there is duplication between the sets.).

If applied to the base package, this also looks in the `.R` files in `R_HOME/share/R`.

Value

For `xgettext`, a list of objects of class "xgettext" (which has a print method), one per source file that contains potentially translatable strings.

For `xngettext`, a list of objects of class "xngettext", which are themselves lists of length-2 character vectors.

See Also

- `update_pkg_po()` which calls `xgettext2pot()`.

Examples

```r
## Not run: ## in a source-directory build (not typical!) of R;
## otherwise, download and unpack the R sources, and replace
## R.home() by "<my_path_to_source_R>"
##
xgettext(file.path(R.home(), "src", "library", "splines"))

## End(Not run)

## Create source package-like <tmp>/R/foo.R and get text from it:
tmpPkg <- tempdir()
tmpRDir <- file.path(tmpPkg, "R")
dir.create(tmpRDir, showWarnings = FALSE)
fnChar <- paste(sep = "\n",
```
"foo <- function(x) {
  # messages unduplicated (not so for ngettext)
  if (x < -1) stop('too small')
  if (x < -.5) stop('too small')
  if (x < 0) {
    warning('',
      'sqrt(x) is', sqrt(as.complex(x)), '',
      'which may be too small''
    )
  }
  # calls with domain=NA are skipped
  if (x == 0) cat(gettext('x is 0!', domain=NA))
  # gettext strings may be ignored due to 'outer' domain=NA
  if (x > 10) stop('x is', gettextf('%.2f', x), domain=NA)
  x
}
writeLines(fnChar, con = file.path(tmpRDir, "foo.R"))

## [[1]] : suppressing (tmpfile) name to make example Rdiff-able
\# xgettext(tmpPkg, asCall=TRUE )[[1]] # default; shows ' sqrt(as.complex(x)) '
\# xgettext(tmpPkg, asCall=FALSE)[[1]] # doesn't ; but then ' %.2f '
unlink(tmpRDir, recursive=TRUE)
Chapter 14

The utils package

---

**utils-package**  
*The R Utils Package*

**Description**  
R utility functions

**Details**  
This package contains a collection of utility functions.
For a complete list, use `library(help = "utils")`.

**Author(s)**  
R Core Team and contributors worldwide  
Maintainer: R Core Team `<R-core@r-project.org>`

---

**adist**  
*Approximate String Distances*

**Description**  
Compute the approximate string distance between character vectors. The distance is a generalized Levenshtein (edit) distance, giving the minimal possibly weighted number of insertions, deletions and substitutions needed to transform one string into another.

**Usage**  
```r
adist(x, y = NULL, costs = NULL, counts = FALSE, fixed = TRUE, partial = !fixed, ignore.case = FALSE, useBytes = FALSE)
```
Arguments

- **x**: a character vector. Long vectors are not supported.
- **y**: a character vector, or NULL (default) indicating taking x as y.
- **costs**: a numeric vector or list with names partially matching 'insertions', 'deletions' and 'substitutions' giving the respective costs for computing the Levenshtein distance, or NULL (default) indicating using unit cost for all three possible transformations.
- **counts**: a logical indicating whether to optionally return the transformation counts (numbers of insertions, deletions and substitutions) as the "counts" attribute of the return value.
- **fixed**: a logical. If TRUE (default), the x elements are used as string literals. Otherwise, they are taken as regular expressions and partial = TRUE is implied (corresponding to the approximate string distance used by agrep with fixed = FALSE).
- **partial**: a logical indicating whether the transformed x elements must exactly match the complete y elements, or only substrings of these. The latter corresponds to the approximate string distance used by agrep (by default).
- **ignore.case**: a logical. If TRUE, case is ignored for computing the distances.
- **useBytes**: a logical. If TRUE, distance computations are done byte-by-byte rather than character-by-character.

Details

The (generalized) Levenshtein (or edit) distance between two strings \( s \) and \( t \) is the minimal possibly weighted number of insertions, deletions and substitutions needed to transform \( s \) into \( t \) (so that the transformation exactly matches \( t \)). This distance is computed for partial = FALSE, currently using a dynamic programming algorithm (see, e.g., https://en.wikipedia.org/wiki/Levenshtein_distance) with space and time complexity \( O(mn) \), where \( m \) and \( n \) are the lengths of \( s \) and \( t \), respectively. Additionally computing the transformation sequence and counts is \( O(\max(m,n)) \).

The generalized Levenshtein distance can also be used for approximate (fuzzy) string matching, in which case one finds the substring of \( t \) with minimal distance to the pattern \( s \) (which could be taken as a regular expression, in which case the principle of using the leftmost and longest match applies), see, e.g., https://en.wikipedia.org/wiki/Approximate_string_matching. This distance is computed for partial = TRUE using 'tre' by Ville Laurikari (https://github.com/laurikari/tre) and corresponds to the distance used by agrep. In this case, the given cost values are coerced to integer.

Note that the costs for insertions and deletions can be different, in which case the distance between \( s \) and \( t \) can be different from the distance between \( t \) and \( s \).

Value

A matrix with the approximate string distances of the elements of \( x \) and \( y \), with rows and columns corresponding to \( x \) and \( y \), respectively.

If counts is TRUE, the transformation counts are returned as the "counts" attribute of this matrix, as a 3-dimensional array with dimensions corresponding to the elements of \( x \), the elements of \( y \), and the type of transformation (insertions, deletions and substitutions), respectively. Additionally, if partial = FALSE, the transformation sequences are returned as the "trafos" attribute of the return value, as character strings with elements 'M', 'I', 'D' and 'S' indicating a match, insertion, deletion and substitution, respectively. If partial = TRUE, the offsets (positions of the first and last element)
of the matched substrings are returned as the "offsets" attribute of the return value (with both offsets − 1 in case of no match).

See Also

agrep for approximate string matching (fuzzy matching) using the generalized Levenshtein distance.

Examples

adist("kitten", "sitting")
## To see the transformation counts for the Levenshtein distance:
drop(attr(adist("kitten", "sitting", counts = TRUE), "counts"))
## To see the transformation sequences:
attr(adist(c("kitten", "sitting"), counts = TRUE), "trafos")

## Cf. the examples for agrep:
adist("lasy", "1 lazy 2")
## For a "partial approximate match" (as used for agrep):
adist("lasy", "1 lazy 2", partial = TRUE)

alarm

Alert the User

Description

Gives an audible or visual signal to the user.

Usage

alarm()

Details

alarm() works by sending a "\a" character to the console. On most platforms this will ring a bell, beep, or give some other signal to the user (unless standard output has been redirected).

It attempts to flush the console (see flush.console).

Value

No useful value is returned.

Examples

alarm()
apropos

Find Objects by (Partial) Name

Description

apropos() returns a character vector giving the names of objects in the search list matching (as a regular expression) what.

find() returns where objects of a given name can be found.

Usage

apropos(what, where = FALSE, ignore.case = TRUE, dot_internals = FALSE, mode = "any")

dot_internals = FALSE, mode = "any")

find(what, mode = "any", numeric = FALSE, simple.words = TRUE)

Arguments

what character string. For simple.words = FALSE the name of an object; otherwise a regular expression to match object names against.

where, numeric a logical indicating whether positions in the search list should also be returned

ignore.case logical indicating if the search should be case-insensitive, TRUE by default.

dot_internals logical indicating if the search result should show base internal objects, FALSE by default.

mode character; if not "any", only objects whose mode equals mode are searched.

simple.words logical; if TRUE, the what argument is only searched as a whole word.

Details

If mode != "any" only those objects which are of mode mode are considered.

find is a different user interface for a similar task to apropos. By default (simple.words == TRUE), only whole names are matched. Unlike apropos, matching is always case-sensitive.

Unlike the default behaviour of ls, names which begin with a `.‘ are included, but base ‘internal’ objects are included only when dot_internals is true.

Value

For apropos, a character vector sorted by name. For where = TRUE this has names giving the (numerical) positions on the search path.

For find, either a character vector of environment names or (for numeric = TRUE) a numerical vector of positions on the search path with names the names of the corresponding environments.

Author(s)

Originally, Kurt Hornik and Martin Maechler (May 1997).
aregexec

Approximate String Match Positions

Description

Determine positions of approximate string matches.

Usage

aregexec(pattern, text, max.distance = 0.1, costs = NULL,
     ignore.case = FALSE, fixed = FALSE, useBytes = FALSE)
Arguments

- **pattern**: a non-empty character string or a character string containing a regular expression (for fixed = FALSE) to be matched. Coerced by `as.character` to a string if possible.
- **text**: character vector where matches are sought. Coerced by `as.character` to a character vector if possible.
- **max.distance**: maximum distance allowed for a match. See `agrep`.
- **costs**: cost of transformations. See `agrep`.
- **ignore.case**: a logical. If TRUE, case is ignored for computing the distances.
- **fixed**: If TRUE, the pattern is matched literally (as is). Otherwise (default), it is matched as a regular expression.
- **useBytes**: a logical. If TRUE comparisons are byte-by-byte rather than character-by-character.

Details

`aregexec` provides a different interface to approximate string matching than `agrep` (along the lines of the interfaces to exact string matching provided by `regexec` and `grep`).

Note that by default, `agrep` performs literal matches, whereas `aregexec` performs regular expression matches.

See `agrep` and `adist` for more information about approximate string matching and distances.

Comparisons are byte-by-byte if `pattern` or any element of `text` is marked as "bytes".

Value

A list of the same length as `text`, each element of which is either −1 if there is no match, or a sequence of integers with the starting positions of the match and all substrings corresponding to parenthesized subexpressions of `pattern`, with attribute "match.length" an integer vector giving the lengths of the matches (or −1 for no match).

See Also

`regmatches` for extracting the matched substrings.

Examples

```r
## Cf. the examples for agrep.
x <- c("1 lazy", "1", "1 LAZY")
aregexec("laysy", x, max.distance = 2)
aregexec("(lay)(sy)", x, max.distance = 2)
aregexec("(lay)(sy)", x, max.distance = 2, ignore.case = TRUE)
m <- aregexec("(lay)(sy)", x, max.distance = 2)
regmatches(x, m)
```
Description

This function allows you to tile or cascade windows, or to minimize or restore them (on Windows, i.e. when `.Platform$OS.type == "windows"`). This may include windows not “belonging” to R.

Usage

`arrangeWindows(action, windows, preserve = TRUE, outer = FALSE)`

Arguments

- `action` a character string, the action to perform on the windows. The choices are c("vertical", "horizontal", "cascade", "minimize", "restore") with default "vertical"; see the ‘Details’ for the interpretation. Abbreviations may be used.
- `windows` a list of window handles, by default produced by `getWindowsHandles()`.
- `preserve` If TRUE, when tiling preserve the outer boundary of the collection of windows; otherwise make them as large as will fit.
- `outer` This argument is only used in MDI mode. If TRUE, tile the windows on the system desktop. Otherwise, tile them within the MDI frame.

Details

The actions are as follows:

- "vertical" Tile vertically.
- "horizontal" Tile horizontally.
- "cascade" Cascade the windows.
- "minimize" Minimize all of the windows.
- "restore" Restore all of the windows to normal size (not minimized, not maximized).

The tiling and cascading are done by the standard Windows API functions, but unlike those functions, they will apply to all of the windows in the `windows` list.

By default, `windows` is set to the result of `getWindowsHandles()` (with one exception described below). This will select windows belonging to the current R process. However, if the global environment contains a variable named `.arrangeWindowsDefaults`, it will be used as the argument list instead. See the `getWindowsHandles` man page for a discussion of the optional arguments to that function.

When `action = "restore"` is used with `windows` unspecified, `minimized = TRUE` is added to the argument list of `getWindowsHandles` so that minimized windows will be restored.

In MDI mode, by default tiling and cascading will happen within the R GUI frame. However, if `outer = TRUE`, tiling is done on the system desktop. This will generally not give desirable results if any R child windows are included within `windows`.


This function is called for the side effect of arranging the windows. The list of window handles is returned invisibly.

Note

This is only available on Windows.

Author(s)

Duncan Murdoch

See Also

getWindowsHandles

Examples

## Not run: ## Only available on Windows :
arrangeWindows("v")
# This default is useful only in SDI mode: it will tile any Firefox window
# along with the R windows
.arrangeWindowsDefaults <- list(c("R", "all"), pattern = c("", "Firefox"))
arrangeWindows("v")

## End(Not run)
aspell

Details

askYesNo will accept case-independent partial matches to the prompts. If no response is given the value of default will be returned; if a non-empty string that doesn’t match any of the prompts is entered, an error will be raised.

If a function or single character string naming a function is given for prompts, it will be called as fn(msg = msg, default = default, prompts = prompts, ...). On Windows, the GUI uses the unexported utils:::askYesNoWinDialog function for this purpose.

If strings (or a string such as "Y/N/C") are given as prompts, the choices will be mapped to lowercase for the non-default choices, and left as-is for the default choice.

Value

TRUE for yes, FALSE for no, and NA for cancel.

See Also

readline for more general user input.

Examples

if (interactive())
  askYesNo("Do you want to use askYesNo?")

aspell

Spell Check Interface

Description

Spell check given files via Aspell, Hunspell or Ispell.

Usage

aspell(files, filter, control = list(), encoding = "unknown",
       program = NULL, dictionaries = character())

Arguments

files a character vector with the names of files to be checked.
filter an optional filter for processing the files before spell checking, given as either a function (with formals ifile and encoding), or a character string specifying a built-in filter, or a list with the name of a built-in filter and additional arguments to be passed to it. See Details for available filters. If missing or NULL, no filtering is performed.
control a list or character vector of control options for the spell checker.
encoding the encoding of the files. Recycled as needed.
program a character string giving the name (if on the system path) or full path of the spell check program to be used, or NULL (default). By default, the system path is searched for aspell, hunspell and ispell (in that order), and the first one found is used.
dictionaries a character vector of names or file paths of additional R level dictionaries to use. Elements with no path separator specify R system dictionaries (in subdirectory 'share/dictionaries' of the R home directory). The file extension (currently, only '.rds') can be omitted.

Details

The spell check programs employed must support the so-called Ispell pipe interface activated via command line option `-a`. In addition to the programs, suitable dictionaries need to be available. See http://aspell.net, https://hunspell.github.io/ and https://www.cs.hmc.edu/~geoff/ispell.html, respectively, for obtaining the Aspell, Hunspell and (International) Ispell programs and dictionaries.

On Windows, Aspell is available via MSYS2. One should use a non-Cygwin version, e.g. package mingw-w64-x86_64-aspell. The version built against the Cygwin runtime (package aspell) requires Unix line endings in files and Unix-style paths, which is incompatible with aspell().

The currently available built-in filters are "Rd" (corresponding to RdTextFilter), "Sweave" (corresponding to SweaveTexFilter), "R", "pot", "dcf" and "md".

Filter "R" is for R code and extracts the message string constants in calls to message, warning, stop, packageStartupMessage, gettext, gettextf, and ngettext (the unnamed string constants for the first five, and fmt and msg1/msg2 string constants, respectively, for the latter two).

Filter "pot" is for message string catalog '.pot' files. Both have an argument ignore allowing to give regular expressions for parts of message strings to be ignored for spell checking: e.g., using "[^\t\[\:punct:\]/*'\"]" ignores all text inside single quotes.

Filter "dcf" is for files in Debian Control File format. The fields to keep can be controlled by argument keep (a character vector with the respective field names). By default, 'Title' and 'Description' fields are kept.

Filter "md" is for files in Markdown format ('.md' and '.Rmd' files), and needs packages commonmark and xml2 to be available.

The print method for the objects returned by aspell has an indent argument controlling the indentation of the positions of possibly misspelled words. The default is 2; Emacs users may find it useful to use an indentation of 0 and visit output in grep-mode. It also has a verbose argument: when this is true, suggestions for replacements are shown as well.

It is possible to employ additional R level dictionaries. Currently, these are files with extension '.rds' obtained by serializing character vectors of word lists using saveRDS. If such dictionaries are employed, they are combined into a single word list file which is then used as the spell checker’s personal dictionary (option '-p'): hence, the default personal dictionary is not used in this case.

Value

A data frame inheriting from aspell (which has a useful print method) with the information about possibly misspelled words.

References


See Also

aspell-utils for utilities for spell checking packages.
Examples

## Not run:
## To check all Rd files in a directory, (additionally) skipping the
## \references sections.
files <- Sys.glob("*.Rd")
aspell(files, filter = list("Rd", drop = "\references"))

## To check all Sweave files
files <- Sys.glob(c("*.Rnw", "*.Snw", "*.rnw", "*.snw"))
aspell(files, filter = "Sweave", control = "-t")

## To check all Texinfo files (Aspell only)
files <- Sys.glob("*.texi")
aspell(files, control = "--mode=texinfo")

## End(Not run)

## List the available R system dictionaries.
Sys.glob(file.path(R.home("share"), "dictionaries", "*.rds"))

aspell-utils

Spell Check Utilities

Description

Utilities for spell checking packages via Aspell, Hunspell or Ispell.

Usage

aspell_package_Rd_files(dir, drop = c("\author", "\references"),
control = list(), program = NULL,
dictionaries = character())

aspell_package_vignettes(dir,
control = list(), program = NULL,
dictionaries = character())

aspell_package_R_files(dir, ignore = character(), control = list(),
program = NULL, dictionaries = character())

aspell_package_C_files(dir, ignore = character(), control = list(),
program = NULL, dictionaries = character())

aspell_write_personal_dictionary_file(x, out, language = "en",
program = NULL)

Arguments

dir a character string specifying the path to a package’s root directory.
drop a character vector naming additional Rd sections to drop when selecting text via
RdTextFilter.
control a list or character vector of control options for the spell checker.
a character string giving the name (if on the system path) or full path of the
spell check program to be used, or NULL (default). By default, the system path
is searched for aspell, hunspell and ispell (in that order), and the first one
found is used.

dictionaries
a character vector of names or file paths of additional R level dictionaries to use.
See aspell.

ignore
a character vector with regular expressions to be replaced by blanks when filter-
ing the message strings.

x
a character vector, or the result of a call to aspell().

out
a character string naming the personal dictionary file to write to.

language
a character string indicating a language as used by Aspell.

Details

Functions aspell_package_Rd_files, aspell_package_vignettes,
aspell_package_R_files and aspell_package_C_files perform spell checking on the
Rd files, vignettes, R files, and C-level messages of the package with root directory dir. They
determine the respective files, apply the appropriate filters, and run the spell checker.

See aspell for details on filters.

The C-level message string are obtained from the ‘po/PACKAGE.pot’ message catalog file, with
PACKAGEx the basename of dir. See the section on ‘C-level messages’ in ‘Writing R Extensions’
for more information.

When using Aspell, the vignette checking skips parameters and/or options of commands \Sexpr,
\citep, \code, \pkg, \proglang and \samp. Further commands can be skipped by adding
--add-tex-command options to the control argument. E.g., to skip both option and parameter
of \mycmd, add --add-tex-command='mycmd op'.

Suitable values for control, program, dictionaries, drop and ignore can also be specified using
a package defaults file which should go as ‘defaults.R’ into the ‘.aspell’ subdirectory of dir,
and provides defaults via assignments of suitable named lists, e.g.,

vignettes <- list(control = "--add-tex-command='mycmd op'")

for vignettes (when using Aspell) and similarly assigning to Rd_files, R_files and C_files for
Rd files, R files and C level message defaults.

Maintainers of packages using both English and American spelling will find it convenient to pass
control options ‘--master=en_US’ and ‘--add-extra-dicts=en_GB’ to Aspell and control options
‘-d en_US, en_GB’ to Hunspell (provided that the corresponding dictionaries are installed).

Older versions of R had no support for R level dictionaries, and hence provided the function
aspell_write_personal_dictionary_file to create (spell check) program-specific personal
dictionary files from words to be accepted. The new mechanism is to use R level dictionaries,
i.e., ‘.rds’ files obtained by serializing character vectors of such words using saveRDS. For such
dictionaries specified via the package defaults mechanism, elements with no path separator can be
R system dictionaries or dictionaries in the ‘.aspell’ subdirectory.

See Also

aspell
available.packages  List Available Packages at CRAN-like Repositories

Description

available.packages returns a matrix of details corresponding to packages currently available at one or more repositories. The current list of packages is downloaded over the internet (or copied from a local mirror).

Usage

available.packages(contriburl = contrib.url(repos, type), method, fields = NULL, type = getOption("pkgType"), filters = NULL, repos = getOption("repos"), ignore_repo_cache = FALSE, max_repo_cache_age, quiet = TRUE, ...)

Arguments

contriburl  URL(s) of the ‘contrib’ sections of the repositories. Specify this argument only if your repository mirror is incomplete, e.g., because you mirrored only the ‘contrib’ section.

method  download method, see download.file.

type  character string, indicate which type of packages: see install.packages. If type = "both" this will use the source repository.

fields  a character vector giving the fields to extract from the ‘PACKAGES’ file(s) in addition to the default ones, or NULL (default). Unavailable fields result in NA values.

filters  a character vector or list or NULL (default). See ‘Details’.

repos  character vector, the base URL(s) of the repositories to use.

ignore_repo_cache  logical. If true, the repository cache is never used (see ‘Details’).

max_repo_cache_age  any cached values older than this in seconds will be ignored. See ‘Details’.

quiet  logical, passed to download.file(); change only if you know what you are doing.

...  allow additional arguments to be passed from callers (which might be arguments to future versions of this function). Currently these are all passed to download.file().

Details

The list of packages is either copied from a local mirror (specified by a ‘file://’ URI) or downloaded. If downloaded and ignore_repo_cache is false (the default), the list is cached for the R session in a per-repository file in tempdir() with a name like

repos_http3a%2f%2fcran.r-project.org%2fsrc%2fcontrib_rds
The cached values are renewed when found to be too old, with the age limit controlled via argument `max_repo_cache_age`. This defaults to the current value of the environment variable `RAVAILABLE_PACKAGES_CACHE_CONTROL_MAX_AGE`, or if unset, to 3600 (one hour).

By default, the return value includes only packages whose version and OS requirements are met by the running version of R, and only gives information on the latest versions of packages.

Argument filters can be used to select which of the packages on the repositories are reported. It is called with its default value (NULL) by functions such as install.packages: this value corresponds to `getOption("available_packages_filters")` and to `c("R_version", "OS_type", "subarch", "duplicates")` if that is unset or set to NULL.

The built-in filters are

"R_version" Exclude packages whose R version requirements are not met.

"OS_type" Exclude packages whose OS requirement is incompatible with this version of R: that is exclude Windows-only packages on a Unix-alike platform and vice versa.

"subarch" For binary packages, exclude those with compiled code that is not available for the current sub-architecture, e.g. exclude packages only compiled for 32-bit Windows on a 64-bit Windows R.

"duplicates" Only report the latest version where more than one version is available, and only report the first-named repository (in contriburl) with the latest version if that is in more than one repository.

"license/FOSS" Include only packages for which installation can proceed solely based on packages which can be verified as Free or Open Source Software (FOSS, e.g., https://en.wikipedia.org/wiki/FOSS) employing the available license specifications. Thus both the package and any packages that it depends on to load need to be known to be FOSS.

Note that this does depend on the repository supplying license information.

"license/restricts_use" Include only packages for which installation can proceed solely based on packages which are known not to restrict use.

"CRAN" Use CRAN versions in preference to versions from other repositories (even if these have a higher version number). This needs to be applied before the default "duplicates" filter, so cannot be used with add = TRUE.

If all the filters are from this set, then they can be specified as a character vector; otherwise filters should be a list with elements which are character strings, user-defined functions or add = TRUE (see below).

User-defined filters are functions which take a single argument, a matrix of the form returned by `available.packages`, and return a matrix consisting of a subset of the rows of the argument.

The special ‘filter’ add = TRUE appends the other elements of the filter list to the default filters.

**Value**

A matrix with one row per package, row names the package names and column names including "Package", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "File" and "Repository". Additional columns can be specified using the fields argument.

Where provided by the repository, fields "OS_type", "License", "License_is_FOSS", "License_restricts_use", "Arches", "MD5sum" and "NeedsCompilation" are reported for use by the filters and package management tools, including `install.packages`. 
BATCH

### Description

Run R non-interactively with input from `infile` and send output (stdout/stderr) to another file.

### Usage

```
R CMD BATCH [options] infile [outfile]
```

### Arguments

- `infile`: the name of a file with R code to be executed.
- `options`: a list of R command line options, e.g., for setting the amount of memory available and controlling the load/save process. If `infile` starts with a `--`, use `--` as the final option. The default options are `--restore --save --no-readline`. (Without `--no-readline` on Windows.)
- `outfile`: the name of a file to which to write output. If not given, the name used is that of `infile`, with a possible `.R` extension stripped, and `.Rout` appended.

---

**See Also**

`install.packages, download.packages, contrib.url`

The `R Installation and Administration` manual for how to set up a repository.

**Examples**

```r
## Not run:
## Count package licenses
db <- available.packages(filters = "duplicates")
table(db[,"License"])

## Use custom filter function to only keep recommended packages
## which do not require compilation
available.packages(filters = list(
  add = TRUE,
  function (db) db[db[,"Priority"] %in% "recommended" &
  db[,"NeedsCompilation"] == "no", ]
))

## Restrict install.packages() (etc) to known-to-be-FOSS packages
options(available_packages_filters =
  c("R.version", "OS_type", "subarch", "duplicates", "license/FOSS"))
## or
options(available_packages_filters = list(add = TRUE, "license/FOSS"))

## Give priority to released versions on CRAN, rather than development
## versions on R-Forge etc.
options(available_packages_filters =
  c("R_version", "OS_type", "subarch", "CRAN", "duplicates"))

## End(Not run)
```
Details

Use `R CMD BATCH --help` to be reminded of the usage.

By default, the input commands are printed along with the output. To suppress this behavior, add `options(echo = FALSE)` at the beginning of `infile`, or use option `--no-echo`.

The `infile` can have end of line marked by LF or CR (but not just CR), and files with an incomplete last line (missing end of line (EOL) mark) are processed correctly.

A final expression `proc.time()` will be executed after the input script unless the latter calls `q(runLast = FALSE)` or is aborted. This can be suppressed by the option `--no-timing`.

Additional options can be set by the environment variable `R_BATCH_OPTIONS`: these come after the default options (see the description of the options argument) and before any options given on the command line.

Note

On Unix-alikes only: Unlike Splus BATCH, this does not run the R process in the background. In most shells,

```bash
R CMD BATCH [options] infile [outfile] &
```

will do so.

bibentry

Bibliography Entries

Description

Functionality for representing and manipulating bibliographic information in enhanced BibTeX style.

Usage

```r
bibentry(bibttype, textVersion = NULL, header = NULL, footer = NULL,
    key = NULL, ..., other = list(),
    mheader = NULL, mfooter = NULL)
```

```r
## S3 method for class 'bibentry'
print(x, style = "text", .bibstyle,
    bibtex = length(x) <= getOption("citation.bibtex.max", 1),
    ...)
```

```r
## S3 method for class 'bibentry'
format(x, style = "text", .bibstyle = NULL,
    bibtex = length(x) <= 1,
    citMsg = missing(bibtex),
    sort = FALSE, macros = NULL, ...)
```

```r
## S3 method for class 'bibentry'
sort(x, decreasing = FALSE, .bibstyle = NULL, drop = FALSE, ...)
```
Arguments

- `bibtype` a character string with a BibTeX entry type. See **Entry Types** for details.
- `textVersion` a character string with a text representation of the reference to optionally be employed for printing. It is recommended to leave this unspecified if `format(x, style = "text")` works correctly. Only if special LaTeX macros (e.g., math formatting) or special characters (e.g., with accents) are necessary, a `textVersion` should be provided.
- `header` a character string with optional header text.
- `footer` a character string with optional footer text.
- `key` a character string giving the citation key for the entry.
- `...` for `bibentry`: arguments of the form `tag=value` giving the fields of the entry, with `tag` and `value` the name and value of the field, respectively. Arguments with empty values are dropped. Field names are case-insensitive. See **Entry Fields** for details.
- `other` a list of arguments as in `...` (useful in particular for fields named the same as formals of `bibentry`).
- `mheader` a character string with optional “outer” header text.
- `mfooter` a character string with optional “outer” footer text.
- `x` an object inheriting from class "bibentry".
- `style` an optional character string specifying the print style. If present, must be a unique abbreviation (with case ignored) of the available styles, see **Details**.
- `decreasing` logical, passed to `order` indicating the sort direction.
- `bibstyle` a character string naming a bibliography style, see `bibstyle`.
- `bibtex` logical indicating if BibTeX code should be given additionally; currently applies only to `style = "citation"`. The default for the `print()` method depends on the number of (bib) entries and `getOption("citation.bibtex.max")` (which itself is 1 by default). For example, to see no bibtex at all, you can change the default by `options(citation.bibtex.max = 0)`.
- `citMsg` logical indicating if a “message” should be added (to the footer) about how to get BibTeX code when `bibtex` is false and `style = "citation"`.
- `sort` logical indicating if `bibentries` should be sorted, using `bibstyle(.bibstyle)$sortKeys(x)`.
- `macros` a character string or an object with already loaded Rd macros, see **Details**.
drop logical used as x[ ..., drop=drop] inside the sort() method.

object an object inheriting from class "bibentry".

escape a logical indicating whether non-ASCII characters should be translated to LaTeX escape sequences.

Details

The bibentry objects created by bibentry can represent an arbitrary positive number of references. One can use c() to combine bibentry objects, and hence in particular build a multiple reference object from single reference ones. Alternatively, one can use bibentry to directly create a multiple reference object by "vectorizing" the given arguments, i.e., use character vectors instead of character strings.

The print method for bibentry objects is based on a corresponding format method and provides a choice between seven different styles: plain text (style "text"), BibTeX ("bibtex"), a mixture of plain text and BibTeX as traditionally used for citations ("citation"), HTML ("html"), \LaTeX ("latex"), R code ("R"), and a simple copy of the textVersion elements (style "textVersion").

The "text", "html" and "latex" styles make use of the .bibstyle argument: a style defined by the \bibstyle function for rendering the bibentry into (intermediate) Rd format. The Rd format uses markup commands documented in the ‘Rd format’ section of the ‘Writing R Extensions’ manual, e.g. \textbf{bold}. In addition, one can use the macros argument to provide additional (otherwise unknown, presumably \LaTeX-style) Rd macros, either by giving the path to a file with Rd macros to be loaded via loadRdMacros, or an object with macros already loaded. Note that the "latex" result may contain commands from the \LaTeX style file ‘\Rd.sty’ shipped with R; put \usepackage{Rd} in the preamble of a \LaTeX document to make these available when compiling, e.g. with texi2pdf.

When printing bibentry objects in citation style, a header/footer for each item can be displayed as well as a mheader/mfooter for the whole vector of references.

For formatting as R code, a choice between giving a character vector with one \bibentry() call for each bibentry (as commonly used in ‘CITATION’ files), or a character string with one collapsed call, obtained by combining the individual calls with c() if there is more than one bibentry. This can be controlled by passing the argument collapse=FALSE (default) or TRUE, respectively, to the format() method. (Printing in R style always collapses to a single call.)

It is possible to subscript bibentry objects by their keys (which are used for character subscripts if the names are NULL).

There is also a toBibtex method for direct conversion to BibTeX.

As of R 4.3.0, there is also a transform method which allows to directly use the current fields, see the examples.

Value

\bibentry produces an object of class "bibentry".

Entry Types

\bibentry creates "bibentry" objects, which are modeled after BibTeX entries. The entry should be a valid BibTeX entry type, e.g.,

**Article**: An article from a journal or magazine.

**Book**: A book with an explicit publisher.

**InBook**: A part of a book, which may be a chapter (or section or whatever) and/or a range of pages.

**InCollection**: A part of a book having its own title.
**InProceedings**: An article in a conference proceedings.

**Manual**: Technical documentation like a software manual.


**Misc**: Use this type when nothing else fits.

**PhdThesis**: A PhD thesis.

**Proceedings**: The proceedings of a conference.

**TechReport**: A report published by a school or other institution, usually numbered within a series.

**Unpublished**: A document having an author and title, but not formally published.

**Entry Fields**

The ... argument of bibentry can be any number of BibTeX fields, including

- **address**: The address of the publisher or other type of institution.
- **author**: The name(s) of the author(s), either as a person object, or as a character string which as.person correctly coerces to such.
- **booktitle**: Title of a book, part of which is being cited.
- **chapter**: A chapter (or section or whatever) number.
- **editor**: Name(s) of editor(s), same format as author.
- **institution**: The publishing institution of a technical report.
- **journal**: A journal name.
- **note**: Any additional information that can help the reader. The first word should be capitalized.
- **number**: The number of a journal, magazine, technical report, or of a work in a series.
- **pages**: One or more page numbers or range of numbers.
- **publisher**: The publisher’s name.
- **school**: The name of the school where a thesis was written.
- **series**: The name of a series or set of books.
- **title**: The work’s title.
- **url**: A URL for the reference. (If the URL is an expanded DOI, we recommend to use the ‘doi’ field with the unexpanded DOI instead.)
- **volume**: The volume of a journal or multi-volume book.
- **year**: The year of publication.

**See Also**

- person
Examples

```r
## R reference
rref <- bibentry(
  bibtype = "Manual",
  title = "R: A Language and Environment for Statistical Computing",
  author = person("R Core Team"),
  organization = "R Foundation for Statistical Computing",
  address = "Vienna, Austria",
  year = 2014,
  url = "https://www.R-project.org/"
)

## Different printing styles
print(rref)
print(rref, style = "bibtex")
print(rref, style = "citation")
print(rref, style = "html")
print(rref, style = "latex")
print(rref, style = "R")

## References for boot package and associated book
bref <- c(
  bibentry(
    bibtype = "Manual",
    title = "boot: Bootstrap R (S-PLUS) Functions",
    author = c(
      person("Angelo", "Canty", role = "aut", comment = "S original"),
      person(c("Brian", "D."), "Ripley", role = c("aut", "trl", "cre"),
        comment = "R port, author of parallel support",
        email = "ripley@stats.ox.ac.uk")
    ),
    year = "2012",
    note = "R package version 1.3-4",
    url = "https://CRAN.R-project.org/package=boot",
    key = "boot-package"
  ),
  bibentry(
    bibtype = "Book",
    title = "Bootstrap Methods and Their Applications",
    author = as.person("Anthony C. Davison [aut], David V. Hinkley [aut]"),
    year = "1997",
    publisher = "Cambridge University Press",
    address = "Cambridge",
    isbn = "0-521-57391-2",
    url = "http://statwww.epfl.ch/davison/BMA/",
    key = "boot-book"
  )
)

## Combining and subsetting
c(rref, bref)
bref[2]
bref["boot-book"]

## Extracting fields
```
browseEnv

browseEnv

bref$author
bref[1]$author

## Field names are case-insensitive
rref$Year
rref$Year <- R.version$year
stopifnot(identical(rref$year, R.version$year))

## Convert to BibTeX
toBibtex(bref)

## Transform
transform(rref, address = paste0(address, ", Europe"))

## BibTeX reminder message (in case of >= 2 refs):
print(bref, style = "citation")

## Format in R style
## One bibentry() call for each bibentry:
writeLines(paste(format(bref, "R"), collapse = "\n\n"))
## One collapsed call:
writeLines(format(bref, "R", collapse = TRUE))

browseEnv

Browse Objects in Environment

Description

The browseEnv function opens a browser with list of objects currently in sys.frame() environment.

Usage

browseEnv(envir = .GlobalEnv, pattern,
excludepatt = "^last\.\\"\.\warning",
html = .Platform$GUI != "AQUA",
expanded = TRUE, properties = NULL,
main = NULL, debugMe = FALSE)

Arguments

envir an environment the objects of which are to be browsed.
pattern a regular expression for object subselection is passed to the internal ls() call.
excludepatt a regular expression for dropping objects with matching names.
html is used to display the workspace on a HTML page in your favorite browser. The default except when running from R.app on macOS.
expanded whether to show one level of recursion. It can be useful to switch it to FALSE if your workspace is large. This option is ignored if html is set to FALSE.
properties a named list of global properties (of the objects chosen) to be showed in the browser; when NULL (as per default), user, date, and machine information is used.
browseURL

main a title string to be used in the browser; when NULL (as per default) a title is constructed.
debugeMe logical switch; if true, some diagnostic output is produced.

Details

Very experimental code: displays a static HTML page on all platforms except R.app on macOS.
Only allows one level of recursion into object structures.
It can be generalized. See sources for details. Most probably, this should rather work through using the tkWidget package (from https://www.bioconductor.org).

See Also

str, ls.

Examples

if(interactive()) {
  ## create some interesting objects:
ofa <- ordered(4:1)
ex1 <- expression(1+ 0:9)
ex3 <- expression(u, v, 1+ 0:9)
example(factor, echo = FALSE)
example(table, echo = FALSE)
example(ftable, echo = FALSE)
example(lm, echo = FALSE, ask = FALSE)
example(str, echo = FALSE)

  ## and browse them:
browseEnv()

  ## a (simple) function's environment:
  af12 <- approxfun(1:2, 1:2, method = "const")
browseEnv(envir = environment(af12))
}
Arguments

url a non-empty character string giving the URL to be loaded. Some platforms also accept file paths.

browser a non-empty character string giving the name of the program to be used as the HTML browser. It should be in the PATH, or a full path specified. Alternatively, an R function to be called to invoke the browser. Under Windows NULL is also allowed (and is the default), and implies that the file association mechanism will be used.

encodeIfNeeded Should the URL be encoded by URLencode before passing to the browser? This is not needed (and might be harmful) if the browser program/function itself does encoding, and can be harmful for 'file:///' URLs on some systems and for 'http:///' URLs passed to some CGI applications. Fortunately, most URLs do not need encoding.

Details

On Unix-alikes: The default browser is set by option "browser", in turn set by the environment variable R_BROWSER which is by default set in file ‘$R_HOME/etc/Renviron’ to a choice made manually or automatically when R was configured. (See Startup for where to override that default value.) To suppress showing URLs altogether, use the value "false". On many platforms it is best to set option "browser" to a generic program/script and let that invoke the user’s choice of browser. For example, on macOS use open and on many other Unix-alikes use xdg-open.

If browser supports remote control and R knows how to perform it, the URL is opened in any already-running browser or a new one if necessary. This mechanism currently is available for browsers which support the "-remote openURL(...)") interface (which includes Mozilla and Opera), Galeon, KDE konqueror (via kfmclient) and the GNOME interface to Mozilla. (Firefox has dropped support, but defaults to using an already-running browser.) Note that the type of browser is determined from its name, so this mechanism will only be used if the browser is installed under its canonical name.

Because "-remote" will use any browser displaying on the X server (whatever machine it is running on), the remote control mechanism is only used if DISPLAY points to the local host. This may not allow displaying more than one URL at a time from a remote host. It is the caller’s responsibility to encode url if necessary (see URLencode).

To suppress showing URLs altogether, set browser = "false".

The behaviour for arguments url which are not URLs is platform-dependent. Some platforms accept absolute file paths; fewer accept relative file paths.

On Windows: The default browser is set by option "browser", in turn set by the environment variable R_BROWSER if that is set, otherwise to NULL. To suppress showing URLs altogether, use the value "false".

Some browsers have required : be replaced by \ in file paths: others do not accept that. All seem to accept \ as a path separator even though the RFC1738 standard requires /.

To suppress showing URLs altogether, set browser = "false".

URL schemes

Which URL schemes are accepted is platform-specific: expect 'http:///', ‘https://’ and ‘ftp://’ to work, but ‘mailto:’ may or may not (and if it does may not use the user’s preferred email client). However, modern browsers are unlikely to handle ‘ftp://’.

For the ‘file://’ scheme the format accepted (if any) can depend on both browser and OS.
Examples

```r
## Not run:
## for KDE users who want to open files in a new tab
options(browser = "kfmclient newTab")

browseURL("https://www.r-project.org")

## On Windows-only, something like
browseURL("file://d:/R/R-2.5.1/doc/html/index.html",
          browser = "C:/Program Files/Mozilla Firefox/firefox.exe")

## End(Not run)
```

browseVignettes

List Vignettes in an HTML Browser

Description

List available vignettes in an HTML browser with links to PDF, LaTeX/noweb source, and (tangled) R code (if available).

Usage

```r
browseVignettes(package = NULL, lib.loc = NULL, all = TRUE)
```

## S3 method for class 'browseVignettes'
print(x, ...)

Arguments

- `package`: a character vector with the names of packages to search through, or NULL in which "all" packages (as defined by argument `all`) are searched.
- `lib.loc`: a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known.
- `all`: logical; if TRUE search all available packages in the library trees specified by `lib.loc`, and if FALSE, search only attached packages.
- `x`: Object of class browseVignettes.
- `...`: Further arguments, ignored by the `print` method.

Details

Function `browseVignettes` returns an object of the same class; the print method displays it as an HTML page in a browser (using `browseURL`).

See Also

`browseURL`, `vignette`
**Examples**

```r
## List vignettes from all *attached* packages
browseVignettes(all = FALSE)

## List vignettes from a specific package
browseVignettes("grid")
```

---

**Description**

Invokes an editor or email program to write a bug report or opens a web page for bug submission. Some standard information on the current version and configuration of R are included automatically.

**Usage**

```r
bug.report(subject = "", address, 
            file = "R.bug.report", package = NULL, lib.loc = NULL, 
            ...)```

**Arguments**

- `subject` Subject of the email.
- `address` Recipient’s email address, where applicable: for package bug reports sent by email this defaults to the address of the package maintainer (the first if more than one is listed).
- `file` filename to use (if needed) for setting up the email.
- `package` Optional character vector naming a single package which is the subject of the bug report.
- `lib.loc` A character vector describing the location of R library trees in which to search for the package, or NULL. The default value of NULL corresponds to all libraries currently known.
- `...` additional named arguments such as `method` and `ccaddress` to pass to `create.post`.

**Details**

If `package` is NULL or a base package, this opens the R bugs tracker at [https://bugs.r-project.org/](https://bugs.r-project.org/).

If `package` is specified, it is assumed that the bug report is about that package, and parts of its ‘DESCRIPTION’ file are added to the standard information. If the package has a non-empty `BugReports` field in the ‘DESCRIPTION’ file specifying the URL of a webpage, that URL will be opened using `browseURL`, otherwise an email directed to the package maintainer will be generated using `create.post`. If there is any other form of `BugReports` field or a `Contact` field, this is examined as it may provide a preferred email address.

**Value**

Nothing useful.
When is there a bug?

If \( R \) executes an illegal instruction, or dies with an operating system error message that indicates a problem in the program (as opposed to something like "disk full"), then it is certainly a bug.

Taking forever to complete a command can be a bug, but you must make certain that it was really \( R \)'s fault. Some commands simply take a long time. If the input was such that you KNOW it should have been processed quickly, report a bug. If you don’t know whether the command should take a long time, find out by looking in the manual or by asking for assistance.

If a command you are familiar with causes an \( R \) error message in a case where its usual definition ought to be reasonable, it is probably a bug. If a command does the wrong thing, that is a bug. But be sure you know for certain what it ought to have done. If you aren’t familiar with the command, or don’t know for certain how the command is supposed to work, then it might actually be working right. Rather than jumping to conclusions, show the problem to someone who knows for certain.

Finally, a command’s intended definition may not be best for statistical analysis. This is a very important sort of problem, but it is also a matter of judgement. Also, it is easy to come to such a conclusion out of ignorance of some of the existing features. It is probably best not to complain about such a problem until you have checked the documentation in the usual ways, feel confident that you understand it, and know for certain that what you want is not available. The mailing list \( r-devel@r-project.org \) is a better place for discussions of this sort than the bug list.

If you are not sure what the command is supposed to do after a careful reading of the manual this indicates a bug in the manual. The manual’s job is to make everything clear. It is just as important to report documentation bugs as program bugs.

If the online argument list of a function disagrees with the manual, one of them must be wrong, so report the bug.

How to report a bug

When you decide that there is a bug, it is important to report it and to report it in a way which is useful. What is most useful is an exact description of what commands you type, from when you start \( R \) until the problem happens. Always include the version of \( R \), machine, and operating system that you are using; type \( \text{version} \) in \( R \) to print this. To help us keep track of which bugs have been fixed and which are still open please send a separate report for each bug.

The most important principle in reporting a bug is to report FACTS, not hypotheses or categorizations. It is always easier to report the facts, but people seem to prefer to strain to posit explanations and report them instead. If the explanations are based on guesses about how \( R \) is implemented, they will be useless; we will have to try to figure out what the facts must have been to lead to such speculations. Sometimes this is impossible. But in any case, it is unnecessary work for us.

For example, suppose that on a data set which you know to be quite large the command \( \text{data.frame}(x, y, z, \text{monday}, \text{tuesday}) \) never returns. Do not report that \( \text{data.frame()} \) fails for large data sets. Perhaps it fails when a variable name is a day of the week. If this is so then when we got your report we would try out the \( \text{data.frame()} \) command on a large data set, probably with no day of the week variable name, and not see any problem. There is no way in the world that we could guess that we should try a day of the week variable name.

Or perhaps the command fails because the last command you used was a `[ method that had a bug causing \( R \)'s internal data structures to be corrupted and making the \( \text{data.frame()} \) command fail from then on. This is why we need to know what other commands you have typed (or read from your startup file).

It is very useful to try and find simple examples that produce apparently the same bug, and somewhat useful to find simple examples that might be expected to produce the bug but actually do not. If you want to debug the problem and find exactly what caused it, that is wonderful. You should still report the facts as well as any explanations or solutions.
Invoking R with the ‘--vanilla’ option may help in isolating a bug. This ensures that the site profile and saved data files are not read.

A bug report can be generated using the function bug.report(). For reports on R this will open the Web page at https://bugs.r-project.org/: for a contributed package it will open the package’s bug tracker Web page or help you compose an email to the maintainer.

Bug reports on contributed packages should not be sent to the R bug tracker: rather make use of the package argument.

**Author(s)**

This help page is adapted from the Emacs manual and the R FAQ

**See Also**

help.request which you possibly should try before bug.report.
create.post, which handles emailing reports.
The R FAQ, also sessionInfo() from which you may add to the bug report.

---

**Description**

Evaluates its arguments with the output being returned as a character string or sent to a file. Related to sink similarly to how with is related to attach.

**Usage**

capture.output(..., file = NULL, append = FALSE, type = c("output", "message"), split = FALSE)

**Arguments**

... expressive to be evaluated.

file A file name or a connection, or NULL to return the output as a character vector. If the connection is not open, it will be opened initially and closed on exit.

append logical. If file a file name or unopened connection, append or overwrite?

type, split are passed to sink(), see there.

**Details**

It works via sink(<file connection>) and hence the R code in dots must *not* interfere with the connection (e.g., by calling closeAllConnections()).

An attempt is made to write output as far as possible to file if there is an error in evaluating the expressions, but for file = NULL all output will be lost.

Messages sent to stderr() (including those from message, warning and stop) are captured by type = "message". Note that this can be “unsafe” and should only be used with care.
changedFiles

Detect which Files Have Changed

Description

fileSnapshot takes a snapshot of a selection of files, recording summary information about each. changedFiles compares two snapshots, or compares one snapshot to the current state of the file system. The snapshots need not be the same directory; this could be used to compare two directories.

Usage

fileSnapshot(path = ".", file.info = TRUE, timestamp = NULL, md5sum = FALSE, digest = NULL, full.names = length(path) > 1, ...) changedFiles(before, after, path = before$path, timestamp = before$timestamp, check.file.info = c("size", "isdir", "mode", "mtime"), md5sum = before$md5sum, digest = before$digest, full.names = before$full.names, ...) ## S3 method for class 'fileSnapshot'
print(x, verbose = FALSE, ...) ## S3 method for class 'changedFiles'
print(x, verbose = FALSE, ...)
changedFiles

Arguments

- **path**: character vector; the path(s) to record.
- **file.info**: logical; whether to record file.info values for each file.
- **timestamp**: character string or NULL; the name of a file to write at the time the snapshot is taken. This gives a quick test for modification, but may be unreliable; see the Details.
- **md5sum**: logical; whether MD5 summaries of each file should be taken as part of the snapshot.
- **digest**: a function or NULL; a function with header function(filename) which will take a vector of filenames and produce a vector of values of the same length, or a matrix with that number of rows.
- **full.names**: logical; whether full names (as in list.files) should be recorded. Must be TRUE if length(path) > 1.
- **...**: additional parameters to pass to list.files to control the set of files in the snapshots.
- **before, after**: objects produced by fileSnapshot; two snapshots to compare. If after is missing, a new snapshot of the current file system will be produced for comparison, using arguments recorded in before as defaults.
- **check.file.info**: character vector; which columns from file.info should be compared.
- **x**: the object to print.
- **verbose**: logical; whether to list all data when printing.

Details

The fileSnapshot function uses list.files to obtain a list of files, and depending on the file.info, md5sum, and digest arguments, records information about each file.

The changedFiles function compares two snapshots.

If the timestamp argument to fileSnapshot is length 1, a file with that name is created. If it is length 1 in changedFiles, the file.test function is used to compare the age of all files common to both before and after to it. This test may be unreliable: it compares the current modification time of the after files to the timestamp; that may not be the same as the modification time when the after snapshot was taken. It may also give incorrect results if the clock on the file system holding the timestamp differs from the one holding the snapshot files.

If the check.file.info argument contains a non-empty character vector, the indicated columns from the result of a call to file.info will be compared.

If md5sum is TRUE, fileSnapshot will call the tools::md5sum function to record the 32 byte MD5 checksum for each file, and changedFiles will compare the values. The digest argument allows users to provide their own digest function.

Value

fileSnapshot returns an object of class "fileSnapshot". This is a list containing the fields

- **info**: a data frame whose rownames are the filenames, and whose columns contain the requested snapshot data
- **path**: the normalized path from the call
timestamp, file.info, md5sum, digest, full.names
    a record of the other arguments from the call
args
    other arguments passed via ... to list.files.

changedFiles produces an object of class "changedFiles". This is a list containing
added, deleted, changed, unchanged
    character vectors of filenames from the before and after snapshots, with obvious
    meanings
changes
    a logical matrix with a row for each common file, and a column for each com-
    parison test. TRUE indicates a change in that test.

print methods are defined for each of these types. The print method for "fileSnapshot" objects
displays the arguments used to produce them, while the one for "changedFiles" displays the
added, deleted and changed fields if non-empty, and a submatrix of the changes matrix containing
all of the TRUE values.

Author(s)

Duncan Murdoch, using suggestions from Karl Millar and others.

See Also

file.info, file_test, md5sum.

Examples

# Create some files in a temporary directory
dir <- tempfile()
dir.create(dir)
writeBin(1L, file.path(dir, "file1"))
writeBin(2L, file.path(dir, "file2"))
dir.create(file.path(dir, "dir"))

# Take a snapshot
snapshot <- fileSnapshot(dir, timestamp = tempfile("timestamp"), md5sum=TRUE)

# Change one of the files.
writeBin(3L:4L, file.path(dir, "file2"))

# Display the detected changes. We may or may not see mtime change...
changedFiles(snapshot)
changedFiles(snapshot)$changes

---

classChar  Character Classification

Description

An interface to the (C99) wide character classification functions in use.

Usage

classChar(x, class)
charClass

Arguments

x Either a UTF-8-encoded length-1 character vector or an integer vector of Unicode points (or a vector coercible to integer).

class A character string, one of those given in the ‘Details’ section.

Details

The classification into character classes is platform-dependent. The classes are determined by internal tables on Windows and (optionally but by default) on macOS and AIX.

The character classes are interpreted as follows:

"alnum" Alphabetic or numeric.
"alpha" Alphabetic.
"blank" Space or tab.
"cntrl" Control characters.
"digit" Digits 0-9.
"graph" Graphical characters (printable characters except whitespace).
"lower" Lower-case alphabetic.
"print" Printable characters.
"punct" Punctuation characters. Some platforms treat all non-alphanumeric graphical characters as punctuation.
"space" Whitespace, including tabs, form and line feeds and carriage returns. Some OSes include non-breaking spaces, some exclude them.
"upper" Upper-case alphabetic.
"xdigit" Hexadecimal character, one of 0-9A-Fa-f.

Alphabetic characters contain all lower- and upper-case ones and some others (for example, those in ‘title case’).

Whether a character is printable is used to decide whether to escape it when printing – see the help for print.default.

If x is a character string it should either be ASCII or declared as UTF-8 – see Encoding.

charClass was added in R 4.1.0. A less direct way to examine character classes which also worked in earlier versions is to use something like grep("[:print:]", intToUtf8(x)) – however, the regular-expression code might not use the same classification functions as printing and on macOS used not to.

Value

A logical vector of the length the number of characters or integers in x.

Note

Non-ASCII digits are excluded by the C99 standard from the class "digit": most platforms will have them as alphabetic.

It is an assumption that the system’s wide character classification functions are coded in Unicode points, but this is known to be true for all recent platforms.

The classification may depend on the locale even on one platform.
Character classes are used in regular expressions.

The OS's man pages for iswctype and wctype.

Examples

```r
x <- c(48:70, 32, 0xa0) # Last is non-breaking space
cl <- c("alnum", "alpha", "blank", "digit", "graph", "punct", "upper", "xdigit")
X <- lapply(cl, function(y) charClass(x,y)); names(X) <- cl
X <- as.data.frame(X); row.names(X) <- sQuote(intToUtf8(x, multiple = TRUE))
X

charClass("ABC123", "alpha")
## Some accented capital Greek characters
(x <- "\u0386\u0388\u0389")
charClass(x, "upper")
## How many printable characters are there? (Around 280,000 in Unicode 13.)
## There are 2^21-1 possible Unicode points (most not yet assigned).
pr <- charClass(1:0x1fffff, "print")
table(pr)
```

```
choose.dir

Choose a Folder Interactively on MS Windows

Description

Use a Windows shell folder widget to choose a folder interactively.

Usage

choose.dir(default = "", caption = "Select folder")

Arguments

default which folder to show initially.
caption the caption on the selection dialog.

Details

This brings up the Windows shell folder selection widget. With the default default = "", 'My Computer' (or similar) is initially selected.

To workaround a bug, on Vista and later only folders under 'Computer' are accessible via the widget.

Value

A length-one character vector, character NA if 'Cancel' was selected.

Note

This is only available on Windows.
choose.files

See Also

choose.files (on Windows) and file.choose (on all platforms).

Examples

if (interactive() && .Platform$OS.type == "windows")
  choose.dir(getwd(), "Choose a suitable folder")

choose.files

Choose a List of Files Interactively on MS Windows

Description

Use a Windows file dialog to choose a list of zero or more files interactively.

Usage

choose.files(default = ", caption = "Select files",
  multi = TRUE, filters = Filters,
  index = nrow(Filters))

Filters

Arguments

default which filename to show initially
caption the caption on the file selection dialog
multi whether to allow multiple files to be selected
filters a matrix of filename filters (see Details)
index which row of filters to use by default

Details

Unlike file.choose, choose.files will always attempt to return a character vector giving a list of files. If the user cancels the dialog, then zero files are returned, whereas file.choose would signal an error. choose.dir chooses a directory.

Windows file dialog boxes include a list of ‘filters’, which allow the file selection to be limited to files of specific types. The filters argument to choose.files allows the list of filters to be set. It should be an n by 2 character matrix. The first column gives, for each filter, the description the user will see, while the second column gives the mask(s) to select those files. If more than one mask is used, separate them by semicolons, with no spaces. The index argument chooses which filter will be used initially.

Filters is a matrix giving the descriptions and masks for the file types that R knows about. Print it to see typical formats for filter specifications. The examples below show how particular filters may be selected.

If you would like to display files in a particular directory, give a fully qualified file mask (e.g., "c:\\*.*") in the default argument. If a directory is not given, the dialog will start in the current directory the first time, and remember the last directory used on subsequent invocations.

There is a buffer limit on the total length of the selected filenames: it is large but this function is not intended to select thousands of files, when the limit might be reached.
chooseBioCmirror

Value

A character vector giving zero or more file paths.

Note

This is only available on Windows.

See Also

file.choose, choose.dir,
Sys.glob or list.files to select multiple files by pattern.

Examples

if (interactive() && .Platform$OS.type == "windows")
choose.files(filters = Filters[c("zip", "All"),])

chooseBioCmirror  Select a Bioconductor Mirror

Description

Interact with the user to choose a Bioconductor mirror.

Usage

chooseBioCmirror(graphics = getOption("menu.graphics"), ind = NULL,
local.only = FALSE)

Arguments

graphics Logical. If true, use a graphical list: on Windows or the macOS GUI use a list box, and on a Unix-alike use a Tk widget if package tcltk and an X server are available. Otherwise use a text menu.

ind Optional numeric value giving which entry to select.

local.only Logical, try to get most recent list from the Bioconductor master or use file on local disk only.

Details

This sets the option "BioC_mirror": it is used before a call to setRepositories. The out-of-the-box default for that option is NULL, which currently corresponds to the mirror https://bioconductor.org.

The 'Bioconductor (World-wide)' 'mirror' is a network of mirrors providing reliable world-wide access; other mirrors may provide faster access on a geographically local scale. ind chooses a row in ‘R_HOME/doc/BioC_mirrors.csv’, by number.

Value

None: this function is invoked for its side effect of updating options("BioC_mirror").
chooseCRANmirror

**Description**
Interact with the user to choose a CRAN mirror.

**Usage**
```r
chooseCRANmirror(graphics = getOption("menu.graphics"), ind = NULL, local.only = FALSE)
getCRANmirrors(all = FALSE, local.only = FALSE)
```

**Arguments**
- `graphics`: Logical. If true, use a graphical list: on Windows or the macOS GUI use a list box, and on a Unix-alike use a Tk widget if package `tcltk` and an X server are available. Otherwise use a text menu.
- `ind`: Optional numeric value giving which entry to select.
- `all`: Logical, get all known mirrors or only the ones flagged as OK.
- `local.only`: Logical, try to get most recent list from the CRAN master or use file on local disk only.

**Details**
A list of mirrors is stored in file 'R_HOME/doc/CRAN_mirrors.csv', but first an on-line list of current mirrors is consulted, and the file copy used only if the on-line list is inaccessible.

`chooseCRANmirror` is called by a Windows GUI menu item and by `contrib.url` if it finds the initial dummy value of `options("repos")`.

HTTPS mirrors with mirroring over ssh will be offered in preference to other mirrors (which are listed in a sub-menu).

`ind` chooses a row in the list of current mirrors, by number. It is best used with `local.only = TRUE` and row numbers in 'R_HOME/doc/CRAN_mirrors.csv'.

**Value**
None for `chooseCRANmirror()`, this function is invoked for its side effect of updating `options("repos")`.
`getCRANmirrors()` returns a data frame with mirror information.

**See Also**
- `setRepositories`, `chooseCRANmirror`, `findCRANmirror`, `chooseBioCmirror`, `contrib.url`.
citation

Citing R and R Packages in Publications

Description

How to cite R and R packages in publications.

Usage

citation(package = "base", lib.loc = NULL, auto = NULL)
readCitationFile(file, meta = NULL)
citHeader(...)  
citFooter(...)  

Arguments

package  a character string with the name of a single package. An error occurs if more than one package name is given.
lib.loc  a character vector with path names of R libraries, or the directory containing the source for package, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
auto  a logical indicating whether the default citation auto-generated from the package ‘DESCRIPTION’ metadata should be used or not, or NULL (default), indicating that a ‘CITATION’ file is used if it exists, or an object of class “packageDescription” with package metadata (see below).
file  a file name.
meta  a list of package metadata as obtained by packageDescription, or NULL (the default).
...  character strings (which will be pasted).

Details

The R core development team and the very active community of package authors have invested a lot of time and effort in creating R as it is today. Please give credit where credit is due and cite R and R packages when you use them for data analysis.

Execute function citation() for information on how to cite the base R system in publications. If the name of a non-base package is given, the function either returns the information contained in the ‘CITATION’ file of the package (using readCitationFile with meta equal to packageDescription(package, lib.loc)) or auto-generates citation information from the ‘DESCRIPTION’ file.

Packages can use an ‘Authors@R’ field in their ‘DESCRIPTION’ to provide (R code giving) a person object with a refined, machine-readable description of the package “authors” (in particular specifying their precise roles). Only those with an author role will be included in the auto-generated citation.

If the object returned by citation() contains only one reference, the associated print method shows both a text version and a BibTeX entry for it. If a package has more than one reference then only the text versions are shown. This threshold is controlled by
The `CITATION` file of an R package should be placed in the `inst` subdirectory of the package source. The file is an R source file and may contain arbitrary R commands including conditionals and computations. Function `readCitationFile()` is used by `citation()` to extract the information in `CITATION` files. The file is `source()`ed by the R parser in a temporary environment and all resulting bibliographic objects (specifically, inheriting from "bibentry") are collected. These are typically produced by one or more `bibentry()` calls, optionally preceded by a `citHeader()` and followed by a `citFooter()` call. One can include an auto-generated package citation in the `CITATION` file via `citation(auto = meta)`.

`readCitationFile` makes use of the Encoding element (if any) of `meta` to determine the encoding of the file.

**Value**

An object of class "citation", inheriting from class "bibentry"; see there, notably for the `print` and `format` methods.

`citHeader` and `citFooter` return an empty "bibentry" storing “outer” header/footer text for the package citation.

**See Also**

`bibentry`

**Examples**

```r
## the basic R reference
citation()

## extract the BibTeX entry from the return value
x <- citation()
toBibtex(x)

## references for a package
citation("lattice")
citation("lattice", auto = TRUE)  # request the Manual-type reference
citation("foreign")

## a CITATION file with more than one bibentry:
file.show(system.file("CITATION", package="mgcv"))
cm <- citation("mgcv")
cm # header, text references, plus "reminder" about getting BibTeX
print(cm, bibtex = TRUE)  # each showing its bibtex code

## a CITATION file including citation(auto = meta)
file.show(system.file("CITATION", package="nlme"))
citation("nlme")
```
cite (Cite a Bibliography Entry)

Description
Cite a bibentry object in text. The cite() function uses the cite() function from the default bibstyle if present, or citeNatbib() if not. citeNatbib() uses a style similar to that used by the LaTeX package natbib.

Usage
cite(keys, bib, ...) citeNatbib(keys, bib, textual = FALSE, before = NULL, after = NULL, mode = c("authoryear", "numbers", "super"), abbreviate = TRUE, longnamesfirst = TRUE, bibpunct = c("(" , ")", ";", "a", ",", ","), previous)

Arguments
keys A character vector of keys of entries to cite. May contain multiple keys in a single entry, separated by commas.
bib A "bibentry" object containing the list of documents in which to find the keys.
... Additional arguments to pass to the cite() function for the default style.
textual Produce a “textual” style of citation, i.e. what \citet would produce in LaTeX.
before Optional text to display before the citation.
after Optional text to display after the citation.
mode The “mode” of citation.
abbreviate Whether to abbreviate long author lists.
longnamesfirst If abbreviate == TRUE, whether to leave the first citation long.
bibpunct A vector of punctuation to use in the citation, as used in natbib. See the Details section.
previous A list of keys that have been previously cited, to be used when abbreviate == TRUE and longnamesfirst == TRUE

Details
Argument names are chosen based on the documentation for the LaTeX natbib package. See that documentation for the interpretation of the bibpunct entries.

The entries in bibpunct are as follows:
1. The left delimiter.
2. The right delimiter.
3. The separator between references within a citation.
4. An indicator of the “mode”: "n" for numbers, "s" for superscripts, anything else for author-year.
5. Punctuation to go between the author and year.
6. Punctuation to go between years when authorship is suppressed.

Note that if mode is specified, it overrides the mode specification in bibpunct[4]. Partial matching is used for mode.

The defaults for citeNatbib have been chosen to match the JSS style, and by default these are used in cite. See bibstyle for how to set a different default style.

Value

A single element character string is returned, containing the citation.

Author(s)

Duncan Murdoch

Examples

```r
## R reference
rref <- bibentry(
  bibtype = "Manual",
  title = "R: A Language and Environment for Statistical Computing",
  author = person("R Core Team"),
  organization = "R Foundation for Statistical Computing",
  address = "Vienna, Austria",
  year = 2013,
  url = "https://www.R-project.org/",
  key = "R"
)

## References for boot package and associated book
bref <- c(
  bibentry(
    bibtype = "Manual",
    title = "boot: Bootstrap R (S-PLUS) Functions",
    author = c(
      person("Angelo", "Canty", role = "aut",
              comment = "S original"),
      person(c("Brian", "D."), "Ripley", role = c("aut", "trl", "cre"),
              comment = "R port, author of parallel support",
              email = "ripley@stats.ox.ac.uk")
    ),
    year = "2012",
    note = "R package version 1.3-4",
    url = "https://CRAN.R-project.org/package=boot",
    key = "boot-package"
  ),
  bibentry(
    bibtype = "Book",
    title = "Bootstrap Methods and Their Applications",
    author = as.person("Anthony C. Davison [aut], David V. Hinkley [aut]"),
    year = "1997",
    publisher = "Cambridge University Press",
    address = "Cambridge",
    isbn = "0-521-57391-2",
    url = "http://statwww.epfl.ch/davison/BMA/",
    key = "boot-book"
  )
)```

citEntry

Bibliography Entries (Older Interface)

Description

Old interface providing functionality for specifying bibliographic information in enhanced BibTeX style. Since R 2.14.0 this has been superseded by bibentry.

Usage

citEntry(entry, textVersion = NULL, header = NULL, footer = NULL, ...)

Arguments

entry a character string with a BibTeX entry type. See section Entry Types in bibentry for details.
textVersion a character string with a text representation of the reference to optionally be employed for printing.
header a character string with optional header text.
footer a character string with optional footer text.
... for citEntry, arguments of the form tag=value giving the fields of the entry, with tag and value the name and value of the field, respectively. See section Entry Fields in bibentry for details.

Value

citEntry produces an object of class "bibentry".

See Also

citation for more information about citing R and R packages and 'CITATION' files; bibentry for the newer functionality for representing and manipulating bibliographic information.
Description

Transfer text between a character vector and the Windows clipboard in MS Windows (only).

Usage

```r
getClipboardFormats(numeric = FALSE)
readClipboard(format = 13, raw = FALSE)
writeClipboard(str, format = 13)
```

Arguments

- `numeric`: logical: should the result be in human-readable form (the default) or raw numbers?
- `format`: an integer giving the desired format.
- `raw`: should the value be returned as a raw vector rather than as a character vector?
- `str`: a character vector or a raw vector.

Details

The Windows clipboard offers data in a number of formats: see e.g. [https://docs.microsoft.com/en-gb/windows/desktop/dataxchg/clipboard-formats](https://docs.microsoft.com/en-gb/windows/desktop/dataxchg/clipboard-formats).

The standard formats include

- **CF_TEXT** 1: Text in the machine’s locale
- **CF_BITMAP** 2: Metafile picture
- **CF_SYLK** 4: Symbolic link
- **CF_DIF** 5: Data Interchange Format
- **CF_TIFF** 6: Tagged-Image File Format
- **CF_OEMTEXT** 7: Text in the OEM codepage
- **CF_DIB** 8: Device-Independent Bitmap
- **CF_PALETTE** 9
- **CF_PENDATA** 10
- **CF_RIFF** 11: Audio data
- **CF_WAVE** 12: Audio data
- **CF_UNICODETEXT** 13: Text in Unicode (UCS-2)
- **CF_ENHMETAFILE** 14: Enhanced metafile
- **CF_HDROP** 15: Drag-and-drop data
- **CF_LOCALE** 16: Locale for the text on the clipboard
- **CF_MAX** 17: Shell-oriented formats

Applications normally make data available in one or more of these and possibly additional private formats. Use `raw = TRUE` to read binary formats, `raw = FALSE` (the default) for text formats. The current codepage is used to convert text to Unicode text, and information on that is contained in the **CF_LOCALE** format. (Take care if you are running R in a different locale from Windows. It is
The `writeClipboard` function will write a character vector as text or Unicode text with standard CR-LF line terminators. It will copy a raw vector directly to the clipboard without any changes. It is recommended to use Unicode text (the default) instead of text to avoid interoperability problems. (Note that R 4.2 and newer on recent systems uses UTF-8 as the native encoding but the machine’s locale uses a different encoding.)

**Value**

For `getClipboardFormats`, a character or integer vector of available formats, in numeric order. If non-human-readable character representation is known, the number is returned.

For `readClipboard`, a character vector by default, a raw vector if `raw` is `TRUE`, or `NULL`, if the format is unavailable.

For `writeClipboard` an invisible logical indicating success or failure.

**Note**

This is only available on Windows.

**See Also**

`file` which can be used to set up a connection to a clipboard.

---

**close.socket**

**Close a Socket**

**Description**

Closes the socket and frees the space in the file descriptor table. The port may not be freed immediately.

**Usage**

`close.socket(socket, ...)`

**Arguments**

- `socket` a socket object
- `...` further arguments passed to or from other methods.

**Value**

logical indicating success or failure

**Author(s)**

Thomas Lumley
See Also

make.socket, read.socket

Compiling in support for sockets was optional prior to R 3.3.0: see capabilities("sockets") to see if it is available.

combn

Generate All Combinations of \( n \) Elements, Taken \( m \) at a Time

Description

Generate all combinations of the elements of \( x \) taken \( m \) at a time. If \( x \) is a positive integer, returns all combinations of the elements of \( \text{seq}(x) \) taken \( m \) at a time. If argument \( \text{FUN} \) is not \( \text{NULL} \), applies a function given by the argument to each point. If simplify is \( \text{FALSE} \), returns a list; otherwise returns an \text{array}, typically a \text{matrix} ... are passed unchanged to the \text{FUN} function, if specified.

Usage

\[
\text{combn}(x, m, \text{FUN} = \text{NULL}, \text{simplify} = \text{TRUE}, ...) 
\]

Arguments

\begin{itemize}
  \item \( x \) vector source for combinations, or integer \( n \) for \( x \leftarrow \text{seq}\_\text{len}(n) \).
  \item \( m \) number of elements to choose.
  \item \( \text{FUN} \) function to be applied to each combination; default \( \text{NULL} \) means the identity, i.e., to return the combination (vector of length \( m \)).
  \item \( \text{simplify} \) logical indicating if the result should be simplified to an \text{array} (typically a \text{matrix}); if \( \text{FALSE} \), the function returns a \text{list}. Note that when \( \text{simplify} = \text{TRUE} \) as by default, the dimension of the result is simply determined from \( \text{FUN}(1\text{st combination}) \) (for efficiency reasons). This will badly fail if \( \text{FUN}(u) \) is not of constant length.
  \item \( ... \) optionally, further arguments to \( \text{FUN} \).
\end{itemize}

Details

Factors \( x \) are accepted.

Value

A \text{list} or \text{array}, see the \text{simplify} argument above. In the latter case, the identity \( \text{dim}(\text{combn}(n, m)) = c(m, \text{choose}(n, m)) \) holds.

Author(s)

Scott Chasalow wrote the original in 1994 for S; R package \text{combinat} and documentation by Vince Carey <stvjc@channing.harvard.edu>; small changes by the R core team, notably to return an array in all cases of \( \text{simplify} = \text{TRUE} \), e.g., for \text{combn}(5,5).

References

compareVersion

Compare Two Package Version Numbers

Description

Compare two package version numbers to see which is later.

Usage

compareVersion(a, b)

Arguments

a, b

Character strings representing package version numbers.

Details

R package version numbers are of the form x.y-z for integers x, y and z, with components after x optionally missing (in which case the version number is older than those with the components present).

Value

0 if the numbers are equal, -1 if b is later and 1 if a is later (analogous to the C function strcmp).

See Also

package_version, library, packageStatus.
Examples

```r
compareVersion("1.0", "1.0-1")
compareVersion("7.2-0", "7.1-12")
```

**Description**

Compile given source files so that they can subsequently be collected into a shared object using `R CMD SHLIB` or an executable program using `R CMD LINK`. Not available on Windows.

**Usage**

```r
R CMD COMPILE [options] srcfiles
```

**Arguments**

- **srcfiles**: A list of the names of source files to be compiled. Currently, C, C++, Objective C, Objective C++ and Fortran are supported; the corresponding files should have the extensions `.c`, `.cc` (or `.cpp`), `.m`, `.mm` (or `.M`), `.f` and `.f90` or `.f95`, respectively.
- **options**: A list of compile-relevant settings, or for obtaining information about usage and version of the utility.

**Details**

`R CMD SHLIB` can both compile and link files into a shared object: since it knows what run-time libraries are needed when passed C++, Fortran and Objective C(++) sources, passing source files to `R CMD SHLIB` is more reliable.

Objective C and Objective C++ support is optional and will work only if the corresponding compilers were available at R configure time: their main usage is on macOS.

Compilation arranges to include the paths to the R public C/C++ headers.

As this compiles code suitable for incorporation into a shared object, it generates PIC code: that might occasionally be undesirable for the main code of an executable program.

This is a make-based facility, so will not compile a source file if a newer corresponding `.o` file is present.

**Note**

Some binary distributions of R have `COMPILE` in a separate bundle, e.g. an `R-devel` RPM.

This is not available on Windows.

**See Also**

`LINK`, `SHLIB`, `dyn.load`; the section on “Customizing compilation under Unix” in “R Administration and Installation” (see the ‘doc/manual’ subdirectory of the R source tree).
contrib.url  

Find Appropriate Paths in CRAN-like Repositories

Description

contrib.url adds the appropriate type-specific path within a repository to each URL in repos.

Usage

contrib.url(repos, type = getOption("pkgType"))

Arguments

repos character vector, the base URL(s) of the repositories to use.
type character string, indicating which type of packages: see install.packages.

Details

If type = "both" this will use the source repository.

Value

A character vector of the same length as repos.

See Also

setRepositories to set options("repos"), the most common value used for argument repos.
available.packages, download.packages, install.packages.
The ‘R Installation and Administration’ manual for how to set up a repository.

count.fields  

Count the Number of Fields per Line

Description

count.fields counts the number of fields, as separated by sep, in each of the lines of file read.

Usage

count.fields(file, sep = "", quote = ":", skip = 0,
blank.lines.skip = TRUE, comment.char = ":")
create.post

Arguments

file a character string naming an ASCII data file, or a connection, which will be opened if necessary, and if so closed at the end of the function call.
sep the field separator character. Values on each line of the file are separated by this character. By default, arbitrary amounts of whitespace can separate fields.
quote the set of quoting characters
skip the number of lines of the data file to skip before beginning to read data.
blank.lines.skip logical: if TRUE blank lines in the input are ignored.
comment.char character: a character vector of length one containing a single character or an empty string.

Details

This used to be used by read.table and can still be useful in discovering problems in reading a file by that function.
For the handling of comments, see scan.
Consistent with scan, count.fields allows quoted strings to contain newline characters. In such a case the starting line will have the field count recorded as NA, and the ending line will include the count of all fields from the beginning of the record.

Value

A vector with the numbers of fields found.

See Also

read.table

Examples

fil <- tempfile()
cat("NAME", "1:John", "2:Paul", file = fil, sep = "\n")
count.fields(fil, sep = ":")
unlink(fil)

count.fields

Ancillary Function for Preparing Emails and Postings

Description

An ancillary function used by bug.report and help.request to prepare emails for submission to package maintainers or to R mailing lists.

Usage

create.post(instructions = character(), description = "post", subject = "", method = getOption("mailer"), address = "the relevant mailing list", ccaddress = getOption("ccaddress", ""), filename = "R.post", info = character())
Arguments

- **instructions**: Character vector of instructions to put at the top of the template email.
- **description**: Character string: a description to be incorporated into messages.
- **subject**: Subject of the email. Optional except for the "mailx" method.
- **method**: Submission method, one of "none", "mailto", "gnudoit", "ess" or (Unix only) "mailx". See ‘Details’.
- **address**: Recipient’s email address, where applicable: for package bug reports sent by email this defaults to the address of the package maintainer (the first if more than one is listed).
- **ccaddress**: Optional email address for copies with the "mailx" and "mailto" methods. Use ccaddress = "" for no copy.
- **filename**: Filename to use for setting up the email (or storing it when method is "none" or sending mail fails).
- **info**: Character vector of information to include in the template email below the ‘please do not edit the information below’ line.

Details

What this does depends on the method. The function first creates a template email body.

- **none**: A file editor (see file.edit) is opened with instructions and the template email. When this returns, the completed email is in file file ready to be read/pasted into an email program.
- **mailto**: This opens the default email program with a template email (including address, Cc: address and subject) for you to edit and send.
  - This works where default mailers are set up (usual on macOS and Windows, and where xdg-open is available and configured on other Unix-alikes: if that fails it tries the browser set by R_BROWSER).
  - This is the ‘factory-fresh’ default method.
- **mailx** (Unix-alikes only): A file editor (see file.edit) is opened with instructions and the template email. When this returns, it is mailed using a Unix command line mail utility such as mailx, to the address (and optionally, the Cc: address) given.
- **gnudoit**: An (X)emacs mail buffer is opened for the email to be edited and sent: this requires the gnudoit program to be available. Currently subject is ignored.
- **ess**: The body of the template email is sent to stdout.

Value

Invisible NULL.

See Also

- bug.report, help.request.
**data**

**Data Sets**

**Description**

Loads specified data sets, or list the available data sets.

**Usage**

```r
data(..., list = character(), package = NULL, lib.loc = NULL,
    verbose = getOption("verbose"), envir = .GlobalEnv,
    overwrite = TRUE)
```

**Arguments**

- `...`    literal character strings or names.
- `list`    a character vector.
- `package` a character vector giving the package(s) to look in for data sets, or NULL. By default, all packages in the search path are used, then the ‘data’ subdirectory (if present) of the current working directory.
- `lib.loc` a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known.
- `verbose` a logical. If TRUE, additional diagnostics are printed.
- `envir`   the environment where the data should be loaded.
- `overwrite` logical: should existing objects of the same name in `envir` be replaced?

**Details**

Currently, four formats of data files are supported:

1. files ending `.R` or `.r` are `source()`d in, with the R working directory changed temporarily to the directory containing the respective file. (`data` ensures that the `utils` package is attached, in case it had been run via `utils:::data`.)
2. files ending `.RData` or `.rda` are `load()`ed.
3. files ending `.tab`, `.txt` or `.TXT` are read using `read.table(..., header = TRUE, as.is=False)`, and hence result in a data frame.
4. files ending `.csv` or `.CSV` are read using `read.table(..., header = TRUE, sep = ";", as.is=False)`, and also result in a data frame.

If more than one matching file name is found, the first on this list is used. (Files with extensions `.txt`, `.tab` or `.csv` can be compressed, with or without further extension `.gz`, `.b2z` or `.xz`.)

The data sets to be loaded can be specified as a set of character strings or names, or as the character vector `list`, or as both.

For each given data set, the first two types (`.R` or `.r`, and `.RData` or `.rda` files) can create several variables in the load environment, which might all be named differently from the data set. The third and fourth types will always result in the creation of a single variable with the same name (without extension) as the data set.
If no data sets are specified, `data` lists the available data sets. For each package, it looks for a data index in the 'Meta' subdirectory or, if this is not found, scans the 'data' subdirectory for data files using `list_files_with_type`. The information about available data sets is returned in an object of class "packageIQR". The structure of this class is experimental. Where the datasets have a different name from the argument that should be used to retrieve them the index will have an entry like `beaver1 (beavers)` which tells us that dataset `beaver1` can be retrieved by the call `data(beavers).

If `lib.loc` and `package` are both `NULL` (the default), the data sets are searched for in all the currently loaded packages then in the ‘data’ directory (if any) of the current working directory.

If `lib.loc = NULL` but `package` is specified as a character vector, the specified package(s) are searched for first amongst loaded packages and then in the default library/ies (see `.libPaths`).

If `lib.loc` is specified (and not `NULL`), packages are searched for in the specified library/ies, even if they are already loaded from another library.

To just look in the ‘data’ directory of the current working directory, set `package = character(0)` (and `lib.loc = NULL`, the default).

**Value**

A character vector of all data sets specified (whether found or not), or information about all available data sets in an object of class "packageIQR" if none were specified.

**Good practice**

There is no requirement for `data(foo)` to create an object named `foo` (nor to create one object), although it much reduces confusion if this convention is followed (and it is enforced if datasets are lazy-loaded).

`data()` was originally intended to allow users to load datasets from packages for use in their examples, and as such it loaded the datasets into the workspace `.GlobalEnv`. This avoided having large datasets in memory when not in use: that need has been almost entirely superseded by lazy-loading of datasets.

The ability to specify a dataset by name (without quotes) is a convenience: in programming the datasets should be specified by character strings (with quotes).

Use of `data` within a function without an `envir` argument has the almost always undesirable side-effect of putting an object in the user’s workspace (and indeed, of replacing any object of that name already there). It would almost always be better to put the object in the current evaluation environment by `data(..., envir = environment())`. However, two alternatives are usually preferable, both described in the ‘Writing R Extensions’ manual.

- For sets of data, set up a package to use lazy-loading of data.
- For objects which are system data, for example lookup tables used in calculations within the function, use a file ‘R/sysdata.rda’ in the package sources or create the objects by R code at package installation time.

A sometimes important distinction is that the second approach places objects in the namespace but the first does not. So if it is important that the function sees `mytable` as an object from the package, it is system data and the second approach should be used. In the unusual case that a package uses a lazy-loaded dataset as a default argument to a function, that needs to be specified by `::`, e.g., `survival::survexp.us`. 


**Warning**

This function creates objects in the `envir` environment (by default the user’s workspace) replacing any which already existed. `data("foo")` can silently create objects other than `foo`: there have been instances in published packages where it created/replaced `.Random.seed` and hence change the seed for the session.

**Note**

One can take advantage of the search order and the fact that a `.R` file will change directory. If raw data are stored in `mydata.txt` then one can set up `mydata.R` to read `mydata.txt` and pre-process it, e.g., using `transform()`. For instance one can convert numeric vectors to factors with the appropriate labels. Thus, the `.R` file can effectively contain a metadata specification for the plaintext formats.

**See Also**

`help` for obtaining documentation on data sets, `save` for creating the second (`.rda`) kind of data, typically the most efficient one.

The ‘Writing R Extensions’ for considerations in preparing the ‘data’ directory of a package.

**Examples**

```r
require(utils)
data() # list all available data sets
try(data(package = "rpart"), silent = TRUE) # list the data sets in the rpart package
data(USArrests, "VADeaths") # load the data sets 'USArrests' and 'VADeaths'
## Not run: ## Alternatively
ds <- c("USArrests", "VADeaths"); data(list = ds)
## End(Not run)
help(USArrests) # give information on data set 'USArrests'
```

---

**dataentry**

*Spreadsheet Interface for Entering Data*

**Description**

A spreadsheet-like editor for entering or editing data.

**Usage**

```r
data.entry(..., Modes = NULL, Names = NULL)
dataentry(data, modes)
de(..., Modes = list(), Names = NULL)
```

**Arguments**

- `...` A list of variables: currently these should be numeric or character vectors or list containing such vectors.
- `Modes` The modes to be used for the variables.
- `Names` The names to be used for the variables.
- `data` A list of numeric and/or character vectors.
- `modes` A list of length up to that of `data` giving the modes of (some of) the variables. `list()` is allowed.
Details

The data entry editor is only available on some platforms and GUIs. Where available it provides a means to visually edit a matrix or a collection of variables (including a data frame) as described in the Notes section.

data.entry has side effects, any changes made in the spreadsheet are reflected in the variables. Function de and the internal functions de.ncols, de.setup and de.restore are designed to help achieve these side effects. If the user passes in a matrix, X say, then the matrix is broken into columns before dataentry is called. Then on return the columns are collected and glued back together and the result assigned to the variable X. If you don’t want this behaviour use dataentry directly.

The primitive function is dataentry. It takes a list of vectors of possibly different lengths and modes (the second argument) and opens a spreadsheet with these variables being the columns. The columns of the dataentry window are returned as vectors in a list when the spreadsheet is closed.

de.ncols counts the number of columns which are supplied as arguments to data.entry. It attempts to count columns in lists, matrices and vectors. de.setup sets things up so that on return the columns can be regrouped and reassigned to the correct name. This is handled by de.restore.

Value

def and dataentry return the edited value of their arguments. data.entry invisibly returns a vector of variable names but its main value is its side effect of assigning new version of those variables in the user’s workspace.

Resources

The data entry window responds to X resources of class R_dataentry. Resources foreground, background and geometry are utilized.

Note

The details of interface to the data grid may differ by platform and GUI. The following description applies to the X11-based implementation under Unix.

You can navigate around the grid using the cursor keys or by clicking with the (left) mouse button on any cell. The active cell is highlighted by thickening the surrounding rectangle. Moving to the right or down will scroll the grid as needed: there is no constraint to the rows or columns currently in use.

There are alternative ways to navigate using the keys. Return and (keypad) Enter and LineFeed all move down. Tab moves right and Shift-Tab move left. Home moves to the top left.

PageDown or Control-F moves down a page, and PageUp or Control-B up by a page. End will show the last used column and the last few rows used (in any column).

Using any other key starts an editing process on the currently selected cell: moving away from that cell enters the edited value whereas Esc cancels the edit and restores the previous value. When the editing process starts the cell is cleared. In numerical columns (the default) only letters making up a valid number (including -.eE) are accepted, and entering an invalid edited value (such as blank) enters NA in that cell. The last entered value can be deleted using the BackSpace or Del(ete) key. Only a limited number of characters (currently 29) can be entered in a cell, and if necessary only the start or end of the string will be displayed, with the omissions indicated by > or <. (The start is shown except when editing.)

Entering a value in a cell further down a column than the last used cell extends the variable and fills the gap (if any) by NAs (not shown on screen).
The column names can only be selected by clicking in them. This gives a popup menu to select
the column type (currently Real (numeric) or Character) or to change the name. Changing the type
converts the current contents of the column (and converting from Character to Real may generate
NAs.) If changing the name is selected the header cell becomes editable (and is cleared). As with all
cells, the value is entered by moving away from the cell by clicking elsewhere or by any of the keys
for moving down (only).

New columns are created by entering values in them (and not by just assigning a new name). The
mode of the column is auto-detected from the first value entered: if this is a valid number it gives a
numeric column. Unused columns are ignored, so adding data in var5 to a three-column grid adds
one extra variable, not two.

The Copy button copies the currently selected cell: paste copies the last copied value to the current
cell, and right-clicking selects a cell and copies in the value. Initially the value is blank, and attempts
to paste a blank value will have no effect.

Control-L will refresh the display, recalculating field widths to fit the current entries.

In the default mode the column widths are chosen to fit the contents of each column, with a de-
fault of 10 characters for empty columns. you can specify fixed column widths by setting option
de.cellwidth to the required fixed width (in characters). (set it to zero to return to variable widths).
The displayed width of any field is limited to 600 pixels (and by the window width).

See Also

\texttt{vi, edit}: edit uses dataentry to edit data frames.

Examples

\begin{verbatim}
# call data entry with variables x and y
## Not run: data.entry(x, y)
\end{verbatim}

\begin{verbatim}
ddebugcall
\end{verbatim}

\begin{verbatim}
  Debug a Call
\end{verbatim}

Description

Set or unset debugging flags based on a call to a function. Takes into account S3/S4 method dispatch
based on the classes of the arguments in the call.

Usage

ddebugcall(call, once = FALSE)
undebugcall(call)

Arguments

call An R expression calling a function. The called function will be debugged. See Details.

once logical; if TRUE, debugging only occurs once, as via debugonce. Defaults to FALSE
Details

dbgcall debugs the non-generic function, S3 method or S4 method that would be called by evaluating call. Thus, the user does not need to specify the signature when debugging methods. Although the call is actually to the generic, it is the method that is debugged, not the generic, except for non-standard S3 generics (see isS3stdGeneric).

Value

dbgcall invisibly returns the debugged call expression.

Note

Non-standard evaluation is used to retrieve the call (via substitute). For this reason, passing a variable containing a call expression, rather than the call expression itself, will not work.

See Also

dbg for the primary debugging interface

Examples

## Not run:
## Evaluate call after setting debugging
##
f <- factor(1:10)
res <- eval(dbgcall(summary(f)))
## End(Not run)

---

dbgger  

Post-Mortem Debugging

Description

Functions to dump the evaluation environments (frames) and to examine dumped frames.

Usage

dump.frames(dumpto = "last.dump", to.file = FALSE,
include.GlobalEnv = FALSE)
dbgger(dump = last.dump)
limitedLabels(value, maxwidth = getOption("width") - 5L)

Arguments

dumpto  a character string. The name of the object or file to dump to.
to.file  logical. Should the dump be to an R object or to a file?
include.GlobalEnv  logical indicating if a copy of the .GlobalEnv environment should be included in addition to the sys.frames(). Will be particularly useful when used in a batch job.
**debugger**

**dump**
- an R dump object created by `dump.frames`.

**value**
- a list of calls to be formatted, e.g., for user menus.

**maxwidth**
- optional length to which to trim the result of `limitedLabels()`; values smaller than 40 or larger than 1000 are winsorized.

**Details**

To use post-mortem debugging, set the option `error` to be a call to `dump.frames`. By default this dumps to an R object `last.dump` in the workspace, but it can be set to dump to a file (a dump of the object produced by a call to `save`). The dumped object contain the call stack, the active environments and the last error message as returned by `geterrmessage`.

When dumping to file, `dumpto` gives the name of the dumped object and the file name has `'.rda'` appended.

A dump object of class "dump.frames" can be examined by calling `debugger`. This will give the error message and a list of environments from which to select repeatedly. When an environment is selected, it is copied and the `browser` called from within the copy. Note that not all the information in the original frame will be available, e.g. promises which have not yet been evaluated and the contents of any `. . .` argument.

If `dump.frames` is installed as the error handler, execution will continue even in non-interactive sessions. See the examples for how to dump and then quit.

`limitedLabels(v)` takes a list of calls whose elements may have a `srcRef` attribute and returns a vector that pastes a formatted version of those attributes onto the formatted version of the elements, all finally `strtrim()`med to `maxwidth`.

**Value**

Invisible NULL.

**Note**

Functions such as `sys.parent` and `environment` applied to closures will not work correctly inside `debugger`.

If the error occurred when computing the default value of a formal argument the debugger will report "recursive default argument reference" when trying to examine that environment.

Of course post-mortem debugging will not work if R is too damaged to produce and save the dump, for example if it has run out of workspace.

**References**


**See Also**

`browser` for the actions available at the Browse prompt.

`options` for setting error options; `recover` is an interactive debugger working similarly to `debugger` but directly after the error occurs.
Examples

```r
## Not run:
options(error = quote(dump.frames("testdump", TRUE)))

f <- function() {
  g <- function() stop("test dump.frames")
  g()
}
f() # will generate a dump on file "testdump.rda"
options(error = NULL)

## possibly in another R session
load("testdump.rda")
debugger(testdump)
Available environments had calls:
1: f()
2: g()
3: stop("test dump.frames")

Enter an environment number, or 0 to exit
Selection: 1
Browsing in the environment with call:
f()
Called from: debugger.look(ind)
Browse[1]> ls()
[1] "g"
Browse[1]> g
function() stop("test dump.frames")
<environment: 759818>
Browse[1]> Available environments had calls:
1: f()
2: g()
3: stop("test dump.frames")

Enter an environment number, or 0 to exit
Selection: 0

## A possible setting for non-interactive sessions
options(error = quote({dump.frames(to.file = TRUE); q(status = 1)}))

## End(Not run)
```

demo

Demonstrations of R Functionality

Description

demo is a user-friendly interface to running some demonstration R scripts. demo() gives the list of available topics.

Usage

demo(topic, package = NULL, lib.loc = NULL,
character.only = FALSE, verbose =getOption("verbose"),
type = c("console", "html"), echo = TRUE,
ask =getOption("demo.ask"),
encoding =getOption("encoding"))

Arguments

- **topic**: the topic which should be demonstrated, given as a `name` or literal character string, or a character string, depending on whether `character.only` is `FALSE` (default) or `TRUE`. If omitted, the list of available topics is displayed.
- **package**: a character vector giving the packages to look into for demos, or `NULL`. By default, all packages in the search path are used.
- **lib.loc**: a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
- **character.only**: logical; if `TRUE`, use `topic` as character string.
- **verbose**: a logical. If `TRUE`, additional diagnostics are printed.
- **type**: character: whether to show output in the console or a browser (using the dynamic help system). The latter is honored only in interactive sessions and if the `knitr` package is installed. Several other arguments are silently ignored in that case, including `lib.loc`.
- **echo**: a logical. If `TRUE`, show the R input when sourcing.
- **ask**: a logical (or "default") indicating if `devAskNewPage(ask = TRUE)` should be called before graphical output happens from the demo code. The value "default" (the factory-fresh default) means to ask if `echo == TRUE` and the graphics device appears to be interactive. This parameter applies both to any currently opened device and to any devices opened by the demo code. If this is evaluated to `TRUE` and the session is interactive, the user is asked to press RETURN to start.
- **encoding**: See `source`. If the package has a declared encoding, that takes preference.

Details

If no topics are given, `demo` lists the available demos. For `type = "console"`, the corresponding information is returned in an object of class "packageIQR".

See Also

- `source` and `devAskNewPage` which are called by demo. `example` to run code in the Examples section of help pages.

Examples

demo() # for attached packages

### All available demos:
demo(package = .packages(all.available = TRUE))

### Display a demo, pausing between pages
demo(lm.glm, package = "stats", ask = TRUE)
## Display it without pausing
demo(lm.glm, package = "stats", ask = FALSE)

## Not run:
ch <- "scoping"
demo(ch, character = TRUE)

## End(Not run)

## Find the location of a demo
system.file("demo", "lm.glm.R", package = "stats")

---

### DLL.version

**DLL Version Information on MS Windows**

#### Description

On MS Windows only, return the version of the package and the version of R used to build the DLL, if available.

#### Usage

`DLL.version(path)`

#### Arguments

- `path` character vector of length one giving the complete path to the DLL.

#### Value

If the DLL does not exist, `NULL`.

A character vector of length two, giving the DLL version and the version of R used to build the DLL. If the information is not available, the corresponding string is empty.

#### Note

This is only available on Windows.

#### Examples

```r
if(.Platform$OS.type == "windows") withAutoprint({
  DLL.version(file.path(R.home("bin"), "R.dll"))
  DLL.version(file.path(R.home(), "library/stats/libs", .Platform$r_arch, "stats.dll"))
})
```
**download.file**

*Download File from the Internet*

**Description**

This function can be used to download a file from the Internet.

**Usage**

```r
download.file(url, destfile, method = "auto", quiet = FALSE, mode = "w",
              cacheOK = TRUE,
              extra = getOption("download.file.extra"),
              headers = NULL, ...)
```

**Arguments**

- `url` a character string (or longer vector for the "libcurl" method) naming the URL of a resource to be downloaded.
- `destfile` a character string (or vector, see the `url` argument) with the file path where the downloaded file is to be saved. Tilde-expansion is performed.
- `method` Method to be used for downloading files. Current download methods are "internal", "libcurl", "wget", "curl" and "wininet" (Windows only), and there is a value "auto": see 'Details' and 'Note'. The method can also be set through the option "download.file.method": see `options()`.
- `quiet` If TRUE, suppress status messages (if any), and the progress bar.
- `mode` character. The mode with which to write the file. Useful values are "w", "wb" (binary), "a" (append) and "ab". Not used for methods "wget" and "curl". See also 'Details', notably about using "wb" for Windows.
- `cacheOK` logical. Is a server-side cached value acceptable?
- `extra` character vector of additional command-line arguments for the "wget" and "curl" methods.
- `headers` named character vector of additional HTTP headers to use in HTTP[S] requests. It is ignored for non-HTTP[S] URLs. The User-Agent header taken from the `HTTPUserAgent` option (see `options`) is automatically used as the first header.
- `...` allow additional arguments to be passed, unused.

**Details**

The function `download.file` can be used to download a single file as described by `url` from the internet and store it in `destfile`.

The `url` must start with a scheme such as `http://`, `https://` or `file://`. Which methods support which schemes varies by R version, but `method = "auto"` will try to find a method which supports the scheme.

For `method = "auto"` (the default) currently the "internal" method is used for `file://` URLs and "libcurl" for all others.
Support for method "libcurl" was optional on Windows prior to R 4.2.0: use 
capabilities("libcurl") to see if it is supported on an earlier version. It uses an external library of that name (https://curl.se/libcurl/) against which R can be compiled.

When method "libcurl" is used, there is support for simultaneous downloads, so url and destfile can be character vectors of the same length greater than one (but the method has to be specified explicitly and not via "auto"). For a single URL and quiet = FALSE a progress bar is shown in interactive use.

Nowadays the "internal" method only supports the ‘file://’ scheme (for which it is the default). On Windows the "wininet" method currently supports ‘file://’ and (but deprecated with a warning) ‘http://’ and ‘https://’ schemes.

For methods "wget" and "curl" a system call is made to the tool given by method, and the respective program must be installed on your system and be in the search path for executables. They will block all other activity on the R process until they complete: this may make a GUI unresponsive.

cacheOK = FALSE is useful for ‘http://’ and ‘https://’ URLs: it will attempt to get a copy directly from the site rather than from an intermediate cache. It is used by available.packages.

The "libcurl" and "wget" methods follow ‘http://’ and ‘https://’ redirections to any scheme they support. (For method "curl" use argument extra = "-L". To disable redirection in wget, use extra = "--max-redirect=0"). The "wininet" method supports some redirections but not all. (For method "libcurl", messages will quote the endpoint of redirections.)

See url for how ‘file://’ URLs are interpreted, especially on Windows. The "internal" and "wininet" methods do not percent-decode, but the "libcurl" and "curl" methods do: method "wget" does not support them.

Most methods do not percent-encode special characters such as spaces in URLs (see URLencode), but it seems the "wininet" method does.

The remaining details apply to the "wininet" and "libcurl" methods only.

The timeout for many parts of the transfer can be set by the option timeout which defaults to 60 seconds. This is often insufficient for downloads of large files (50MB or more) and so should be increased when download.file is used in packages to do so. Note that the user can set the default timeout by the environment variable R_DEFAULT_INTERNET_TIMEOUT in recent versions of R, so to ensure that this is not decreased packages should use something like

   options(timeout = max(300, getOption("timeout")))

(It is unrealistic to require download times of less than 1s/MB.)

The level of detail provided during transfer can be set by the quiet argument and the internet.info option: the details depend on the platform and scheme. For the "libcurl" method values of the option less than 2 give verbose output.

A progress bar tracks the transfer platform-specifically:

**On Windows** If the file length is known, the full width of the bar is the known length. Otherwise the initial width represents 100 Kbytes and is doubled whenever the current width is exceeded. (In non-interactive use this uses a text version. If the file length is known, an equals sign represents 2% of the transfer completed: otherwise a dot represents 10Kb.)

**On a Unix-alike** If the file length is known, an equals sign represents 2% of the transfer completed; otherwise a dot represents 10Kb.

The choice of binary transfer (mode = "wb" or "ab") is important on Windows, since unlike Unix-alikes it does distinguish between text and binary files and for text transfers changes \
line endings to \r\n (aka "CRLF").
On Windows, if mode is not supplied (missing()) and url ends in one of .gz, .bz2, .xz, .tgz, .zip, .jar, .rda, .rds or .RData, mode = "wb" is set so that a binary transfer is done to help unwary users.

Code written to download binary files must use mode = "wb" (or "ab"), but the problems incurred by a text transfer will only be seen on Windows.

Value

An (invisible) integer code, 0 for success and non-zero for failure. For the "wget" and "curl" methods this is the status code returned by the external program. The "internal" method can return 1, but will in most cases throw an error.

What happens to the destination file(s) in the case of error depends on the method and R version. Currently the "internal", "wininet" and "libcurl" methods will remove the file if the URL is unavailable except when mode specifies appending when the file should be unchanged.

Setting Proxies

For the Windows-only method "wininet", the 'Internet Options' of the system are used to choose proxies and so on; these are set in the Control Panel and are those used for system browsers.

For the "libcurl" and "curl" methods, proxies can be set via the environment variables http_proxy or ftp_proxy. See https://curl.se/libcurl/c/libcurl-tutorial.html for further details.

Secure URLs

Methods which access ‘https://’ and (where supported) ‘ftps://’ URLs should try to verify the site certificates. This is usually done using the CA root certificates installed by the OS (although we have seen instances in which these got removed rather than updated). For further information see https://curl.se/docs/sslcerts.html.

On Windows with method = "libcurl", the CA root certificates are provided by the OS when R was linked with libcurl with Schannel enabled, which is the current default in Rtools. This can be verified by checking that libcurlVersion() returns a version string containing "Schannel". If it does not, for verification to be on the environment variable CURL_CA_BUNDLE must be set to a path to a certificate bundle file, usually named 'ca-bundle.crt' or 'curl-ca-bundle.crt'. (This is normally done automatically for a binary installation of R, which installs 'R_HOME/etc/curl-ca-bundle.crt' and sets CURL_CA_BUNDLE to point to it if that environment variable is not already set.) For an updated certificate bundle, see https://curl.se/docs/sslcerts.html. Currently one can download a copy from https://raw.githubusercontent.com/bagder/ca-bundle/master/ca-bundle.crt and set CURL_CA_BUNDLE to the full path to the downloaded file.

On Windows with method = "libcurl", when R was linked with libcurl with Schannel enabled, the connection fails if it cannot be established that the certificate has not been revoked. Some MITM proxies present particularly in corporate environments do not work with this behavior. It can be changed by setting environment variable R_LIBCURL_SSL_REVOKE_BEST_EFFORT to TRUE, with the consequence of reducing security.

Note that the root certificates used by R may or may not be the same as used in a browser, and indeed different browsers may use different certificate bundles (there is typically a build option to choose either their own or the system ones).
download.file

Good practice

Setting the method should be left to the end user. Neither of the `wget` nor `curl` commands is widely available: you can check if one is available via `Sys.which`, and should do so in a package or script.

If you use `download.file` in a package or script, you must check the return value, since it is possible that the download will fail with a non-zero status but not an R error.

The supported methods do change: method `libcurl` was introduced in R 3.2.0 and was optional on Windows until R 4.2.0 – use `capabilities("libcurl")` in a program to see if it is available.

ftp:// URLs

Most modern browsers do not support such URLs, and `https://` ones are much preferred for use in R. `ftps://` URLs have always been rare, and are nowadays even less supported.

It is intended that R will continue to allow such URLs for as long as `libcurl` does, but as they become rarer this is increasingly untested. What 'protocols' the version of `libcurl` being used supports can be seen by calling `libcurlVersion()`.

These URLs are accessed using the FTP protocol which has a number of variants. One distinction is between 'active' and '(extended) passive' modes: which is used is chosen by the client. The "libcurl" method uses passive mode which was almost universally used by browsers before they dropped support altogether.

Note

Files of more than 2GB are supported on 64-bit builds of R; they may be truncated on some 32-bit builds.

Methods "wget" and "curl" are mainly for historical compatibility but provide may provide capabilities not supported by the "libcurl" or "wininet" methods.

Method "wget" can be used with proxy firewalls which require user/password authentication if proper values are stored in the configuration file for `wget`.

`wget` ([https://www.gnu.org/software/wget/](https://www.gnu.org/software/wget/)) is commonly installed on Unix-alikes (but not macOS). Windows binaries are available from MSYS2 and elsewhere.

`curl` ([https://curl.se/](https://curl.se/)) is installed on macOS and increasingly commonly on Unix-alikes. Windows binaries are available at that URL.

See Also

`options` to set the `HTTPUserAgent`, `timeout` and `internet.info` options used by some of the methods.

`url` for a finer-grained way to read data from URLs.

`url.show`, `available.packages`, `download.packages` for applications.

Contributed packages `RCurl` and `curl` provide more comprehensive facilities to download from URLs.
download.packages  Download Packages from CRAN-like Repositories

Description

These functions can be used to automatically compare the version numbers of installed packages with the newest available version on the repositories and update outdated packages on the fly.

Usage

download.packages(pkgs, destdir, available = NULL,
repos = getOption("repos"),
contriburl = contrib.url(repos, type),
method, type = getOption("pkgType"), ...)

Arguments

pkgs character vector of the names of packages whose latest available versions should be downloaded from the repositories.
destdir directory where downloaded packages are to be stored.
available an object as returned by \texttt{available.packages} listing packages available at the repositories, or \texttt{NULL} which makes an internal call to \texttt{available.packages}.
repos character vector, the base URL(s) of the repositories to use, i.e., the URL of the CRAN master such as "https://cran.r-project.org" or its Statlib mirror, "http://lib.stat.cmu.edu/R/CRAN".
contriburl URL(s) of the contrib sections of the repositories. Use this argument only if your repository mirror is incomplete, e.g., because you burned only the ‘contrib’ section on a CD. Overrides argument repos.
method Download method, see \texttt{download.file}.
type character string, indicate which type of packages: see \texttt{install.packages} and ‘Details’.
... additional arguments to be passed to \texttt{download.file} and \texttt{available.packages}.

Details

download.packages takes a list of package names and a destination directory, downloads the newest versions and saves them in destdir. If the list of available packages is not given as argument, it is obtained from repositories. If a repository is local, i.e. the URL starts with “file:”, then the packages are not downloaded but used directly. Both “file:” and “file:///” are allowed as prefixes to a file path. Use the latter only for URLs: see \texttt{url} for their interpretation. (Other forms of ‘file://’ URLs are not supported.)

For download.packages, type = “both” looks at source packages only.

Value

A two-column matrix of names and destination file names of those packages successfully downloaded. If packages are not available or there is a problem with the download, suitable warnings are given.
Invoke a Text Editor

Invoke a text editor on an \texttt{R} object.

Usage

\begin{verbatim}
edit(name, ...) 
## Default S3 method:
edit(name = NULL, file = "", title = NULL, 
      editor = getOption("editor"), ...)

vi(name = NULL, file = "")
emacs(name = NULL, file = "")
pico(name = NULL, file = "")
xemacs(name = NULL, file = "")
xedit(name = NULL, file = "")
\end{verbatim}

Arguments

- \texttt{name} a named object that you want to edit. For the default method, if \texttt{name} is missing then the file specified by \texttt{file} is opened for editing.
- \texttt{file} a string naming the file to write the edited version to.
- \texttt{title} a display name for the object being edited.
- \texttt{editor} usually a character string naming (or giving the path to) the text editor you want to use. On Unix the default is set from the environment variables \texttt{EDITOR} or \texttt{VISUAL} if either is set, otherwise \texttt{vi} is used. On Windows it defaults to "internal", the script editor. On the macOS GUI the argument is ignored and the document editor is always used. \texttt{editor} can also be an \texttt{R} function, in which case it is called with the arguments \texttt{name}, \texttt{file}, and \texttt{title}. Note that such a function will need to independently implement all desired functionality.
- ... further arguments to be passed to or from methods.

Details

\texttt{edit} invokes the text editor specified by \texttt{editor} with the object \texttt{name} to be edited. It is a generic function, currently with a default method and one for data frames and matrices.

\texttt{data.entry} can be used to edit data, and is used by \texttt{edit} to edit matrices and data frames on systems for which \texttt{data.entry} is available.
It is important to realize that edit does not change the object called name. Instead, a copy of name is made and it is that copy which is changed. Should you want the changes to apply to the object name you must assign the result of edit to name. (Try fix if you want to make permanent changes to an object.)

In the form edit(name), edit deparses name into a temporary file and invokes the editor editor on this file. Quitting from the editor causes file to be parsed and that value returned. Should an error occur in parsing, possibly due to incorrect syntax, no value is returned. Calling edit(), with no arguments, will result in the temporary file being reopened for further editing.

Note that deparsing is not perfect, and the object recreated after editing can differ in subtle ways from that deparsed: see dput and .deparseOpts. (The deparse options used are the same as the defaults for dump.) Editing a function will preserve its environment. See edit.data.frame for further changes that can occur when editing a data frame or matrix.

Currently only the internal editor in Windows makes use of the title option; it displays the given name in the window header.

Note

The functions vi, emacs, pico, xemacs, xedit rely on the corresponding editor being available and being on the path. This is system-dependent.

See Also

edit.data.frame, data.entry, fix.

Examples

## Not run:
# use xedit on the function mean and assign the changes
mean <- edit(mean, editor = "xedit")

# use vi on mean and write the result to file mean.out
vi(mean, file = "mean.out")

## End(Not run)
Arguments

name
factor.mode
edit.row.names

A data frame or (numeric, logical or character) matrix.
How to handle factors (as integers or using character levels) in a data frame. Can be abbreviated.
logical. Show the row names (if they exist) be displayed as a separate editable column? It is an error to ask for this on a matrix with NULL row names.

... further arguments passed to or from other methods.

Details

At present, this only works on simple data frames containing numeric, logical or character vectors and factors, and numeric, logical or character matrices. Any other mode of matrix will give an error, and a warning is given when the matrix has a class (which will be discarded).

Data frame columns are coerced on input to character unless numeric (in the sense of is.numeric), logical or factor. A warning is given when classes are discarded. Special characters (tabs, non-printing ASCII, etc.) will be displayed as escape sequences.

Factors columns are represented in the spreadsheet as either numeric vectors (which are more suitable for data entry) or character vectors (better for browsing). After editing, vectors are padded with NA to have the same length and factor attributes are restored. The set of factor levels can not be changed by editing in numeric mode; invalid levels are changed to NA and a warning is issued. If new factor levels are introduced in character mode, they are added at the end of the list of levels in the order in which they encountered.

It is possible to use the data-editor’s facilities to select the mode of columns to swap between numerical and factor columns in a data frame. Changing any column in a numerical matrix to character will cause the result to be coerced to a character matrix. Changing the mode of logical columns is not supported.

For a data frame, the row names will be taken from the original object if edit.row.names = FALSE and the number of rows is unchanged, and from the edited output if edit.row.names = TRUE and there are no duplicates. (If the row.names column is incomplete, it is extended by entries like row223.) In all other cases the row names are replaced by seq(length = nrows).

For a matrix, colnames will be added (of the form col7) if needed. The rownames will be taken from the original object if edit.row.names = FALSE and the number of rows is unchanged (otherwise NULL), and from the edited output if edit.row.names = TRUE. (If the row.names column is incomplete, it is extended by entries like row223.)

Editing a matrix or data frame will lose all attributes apart from the row and column names.

Value

The edited data frame or matrix.

Note

fix(dataframe) works for in-place editing by calling this function.

If the data editor is not available, a dump of the object is presented for editing using the default method of edit.

At present the data editor is limited to 65535 rows.

Author(s)

Peter Dalgaard
### Examples

```r
## Not run:
edit(InsectSprays)
edit(InsectSprays, factor.mode = "numeric")
## End(Not run)
```

### Description

Run all the R code from the Examples part of R’s online help topic topic with possible exceptions dontrun, dontshow, and donttest, see ‘Details’ below.

### Usage

```r
example(topic, package = NULL, lib.loc = NULL,
character.only = FALSE, give.lines = FALSE, local = FALSE,
type = c("console", "html"), echo = TRUE,
verbose = getOption("verbose"),
setRNG = FALSE, ask = getOption("example.ask"),
prompt.prefix = abbreviate(topic, 6),
run.dontrun = FALSE, run.donttest = interactive())
```

### Arguments

- **topic**: name or literal character string: the online help topic the examples of which should be run.
- **package**: a character vector giving the package names to look into for the topic, or NULL (the default), when all packages on the search path are used.
- **lib.loc**: a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
- **character.only**: a logical indicating whether topic can be assumed to be a character string.
- **give.lines**: logical: if true, the lines of the example source code are returned as a character vector.
- **local**: logical: if TRUE evaluate locally, if FALSE evaluate in the workspace.
- **type**: character: whether to show output in the console or a browser (using the dynamic help system). The latter is honored only in interactive sessions and if the knitr package is installed. Several other arguments are silently ignored in that case, including setRNG and lib.loc.
- **echo**: logical: if TRUE, show the R input when sourcing.
- **verbose**: logical; if TRUE, show even more when running example code.
setRNG logical or expression; if not FALSE, the random number generator state is saved, then initialized to a specified state, the example is run and the (saved) state is restored. setRNG = TRUE sets the same state as R CMD check does for running a package's examples. This is currently equivalent to setRNG = (RNGkind("default", "default", "default"); set.seed(1)).

ask logical (or "default") indicating if devAskNewPage(ask = TRUE) should be called before graphical output happens from the example code. The value "default" (the factory-fresh default) means to ask if echo is true and the graphics device appears to be interactive. This parameter applies both to any currently opened device and to any devices opened by the example code.

prompt.prefix character; prefixes the prompt to be used if echo is true (as it is by default).

run.dontrun logical indicating that \dontrun should be ignored.

run.donttest logical indicating that \donttest should be ignored.

Details

If lib.loc is not specified, the packages are searched for amongst those already loaded, then in the libraries given by .libPaths(). If lib.loc is specified, packages are searched for only in the specified libraries, even if they are already loaded from another library. The search stops at the first package found that has help on the topic.

An attempt is made to load the package before running the examples, but this will not replace a package loaded from another location.

If local = TRUE objects are not created in the workspace and so not available for examination after example completes: on the other hand they cannot overwrite objects of the same name in the workspace.

As detailed in the manual Writing R Extensions, the author of the help page can markup parts of the examples for exception rules.

dontrun encloses code that should not be run.

dontshow encloses code that is invisible on help pages, but will be run both by the package checking tools, and the example() function. This was previously testonly, and that form is still accepted.

donttest encloses code that typically should be run, but not during package checking. The default run.donttest = interactive() leads example() use in other help page examples to skip \donttest sections appropriately.

Value

The value of the last evaluated expression, unless give.lines is true, where a character vector is returned.

Author(s)

Martin Maechler and others

See Also

demo
Examples

```r
example(InsectSprays)
## force use of the standard package 'stats':
example("smooth", package = "stats", lib.loc = .Library)

## set RNG *before* example as when R CMD check is run:

r1 <- example(quantile, setRNG = TRUE)
x1 <- rnorm(1)

u <- runif(1)

## identical random numbers
r2 <- example(quantile, setRNG = TRUE)
x2 <- rnorm(1)

stopifnot(identical(r1, r2))
## but x1 and x2 differ since the RNG state from before example()
## differs and is restored!
x1; x2

## Exploring examples code:
## How large are the examples of "lm...()" functions?

lmex <- sapply(apropos("^lm", mode = "function"),
    example, character.only = TRUE, give.lines = TRUE)

lengths(lmex)
```

---

### file.edit

**Edit One or More Files**

**Description**

Edit one or more files in a text editor.

**Usage**

```r
file.edit(..., title = file, editor = getOption("editor"),
    fileEncoding = "")
```

**Arguments**

- `...`: one or more character vectors containing the names of the files to be displayed. These will be tilde-expanded: see `path.expand`.
- `title`: the title to use in the editor; defaults to the filename.
- `editor`: the text editor to be used, usually as a character string naming (or giving the path to) the text editor you want to use. See ‘Details’.
- `fileEncoding`: the encoding to assume for the file: the default is to assume the native encoding. See the ‘Encoding’ section of the help for `file`.

**Details**

The behaviour of this function is very system-dependent. Currently files can be opened only one at a time on Unix; on Windows, the internal editor allows multiple files to be opened, but has a limit of 50 simultaneous edit windows.
The `title` argument is used for the window caption in Windows, and is currently ignored on other platforms.

Any error in re-encoding the files to the native encoding will cause the function to fail.

The default for `editor` is system-dependent. On Windows it defaults to "internal", the script editor, and in the macOS GUI the document editor is used whatever the value of `editor`. On Unix the default is set from the environment variables `EDITOR` or `VISUAL` if either is set, otherwise `vi` is used.

`editor` can also be an R function, in which case it is called with the arguments `name`, `file`, and `title`. Note that such a function will need to independently implement all desired functionality.

On Windows, UTF-8-encoded paths not valid in the current locale can be used.

See Also

`files`, `file.show`, `edit`, `fix`,

Examples

```r
## Not run:
# open two R scripts for editing
calls <- file.edit("script1.R", "script2.R")

## End(Not run)
```

file_test

---

Shell-style Tests on Files

description

Utility for shell-style file tests.

Usage

`file_test(op, x, y)`

Arguments

- `op` a character string specifying the test to be performed. Unary tests (only `x` is used) are 
  "-f" (existence and not being a directory), "-d" (existence and directory), "-L" or "-h" (existence and symbolic link), "-x" (executable as a file or searchable as a directory), "-w" (writable) and "-r" (readable). Binary tests are 
  "-nt" (strictly newer than, using the modification dates) and "-ot" (strictly older than): in both cases the test is false unless both files exist.
- `x`, `y` character vectors giving file paths.

details

‘Existence’ here means being on the file system and accessible by the `stat` system call (or a 64-bit extension) – on a Unix-alike this requires execute permission on all of the directories in the path that leads to the file, but no permissions on the file itself.

For the meaning of "-x" on Windows see `file.access`.

findCRANmirror

See Also

file.exists which only tests for existence (test -e on some systems) but not for not being a directory.

file.path, file.info

Examples

dir <- file.path(R.home(), "library", "stats")
file_test("-d", dir)
file_test("-nt", file.path(dir, "R"), file.path(dir, "demo"))

Examples

```r
Sys.setenv(R_CRAN_WEB = "https://cloud.r-project.org")
c(findCRANmirror("src"), findCRANmirror("web"))
```

**findLineNum**

*Find the Location of a Line of Source Code, or Set a Breakpoint There*

Description

These functions locate objects containing particular lines of source code, using the information saved when the code was parsed with `keep.source = TRUE`.

Usage

```r
findLineNum(srcfile, line, nameonly = TRUE, 
            envir = parent.frame(), lastenv)
```

```r
setBreakpoint(srcfile, line, nameonly = TRUE, 
             envir = parent.frame(), lastenv, verbose = TRUE, 
             tracer, print = FALSE, clear = FALSE, ...)
```

Arguments

- **srcfile**
  - The name of the file containing the source code.

- **line**
  - The line number within the file. See Details for an alternate way to specify this.

- **nameonly**
  - If TRUE (the default), we require only a match to basename(srcfile), not to the full path.

- **envir**
  - Where do we start looking for function objects?

- **lastenv**
  - Where do we stop? See the Details.

- **verbose**
  - Should we print information on where breakpoints were set?

- **tracer**
  - An optional tracer function to pass to trace. By default, a call to browser is inserted.

- **print**
  - The print argument to pass to trace.

- **clear**
  - If TRUE, call untrace rather than trace.

- **...**
  - Additional arguments to pass to trace.

Details

The `findLineNum` function searches through all objects in environment `envir`, its parent, grandparent, etc., all the way back to `lastenv`.

`lastenv` defaults to the global environment if `envir` is not specified, and to the root environment `emptyenv()` if `envir` is specified. (The first default tends to be quite fast, and will usually find all user code other than S4 methods; the second one is quite slow, as it will typically search all attached system libraries.)
findLineNum

For convenience, \texttt{envir} may be specified indirectly: if it is not an environment, it will be replaced with \texttt{environment(envir)}.

\texttt{setBreakpoint} is a simple wrapper function for \texttt{trace} and \texttt{untrace}. It will set or clear breakpoints at the locations found by \texttt{findLineNum}.

The \texttt{srcfile} is normally a filename entered as a character string, but it may be a "\texttt{srcfile}" object, or it may include a suffix like "filename.R#nn", in which case the number \texttt{nn} will be used as a default value for \texttt{line}.

As described in the description of the \texttt{where} argument on the man page for \texttt{trace}, the \texttt{R} package system uses a complicated scheme that may include more than one copy of a function in a package. The user will typically see the public one on the search path, while code in the package will see a private one in the package namespace. If you set \texttt{envir} to the environment of a function in the package, by default \texttt{findLineNum} will find both versions, and \texttt{setBreakpoint} will set the breakpoint in both. (This can be controlled using \texttt{lastenv}; e.g., \texttt{envir = environment(foo)}, \texttt{lastenv = globalenv()} will find only the private copy, as the search is stopped before seeing the public copy.)

S version 4 methods are also somewhat tricky to find. They are stored with the generic function, which may be in the \texttt{base} or other package, so it is usually necessary to have \texttt{lastenv = emptyenv()} in order to find them. In some cases transformations are done by \texttt{R} when storing them and \texttt{findLineNum} may not be able to find the original code. Many special cases, e.g. methods on primitive generics, are not yet supported.

\textbf{Value}

\texttt{findLineNum} returns a list of objects containing location information. A \texttt{print} method is defined for them.

\texttt{setBreakpoint} has no useful return value; it is called for the side effect of calling \texttt{trace} or \texttt{untrace}.

\textbf{Author(s)}

Duncan Murdoch

\textbf{See Also}

\texttt{trace}

\textbf{Examples}

```r
## Not run:
# Find what function was defined in the file mysource.R at line 100:
findLineNum("mysource.R#100")

# Set a breakpoint in both copies of that function, assuming one is in the
# same namespace as myfunction and the other is on the search path
setBreakpoint("mysource.R#100", envir = myfunction)

## End(Not run)
```
fix

Fix an Object

Description

fix invokes edit on x and then assigns the new (edited) version of x in the user's workspace.

Usage

fix(x, ...)

Arguments

x  the name of an R object, as a name or a character string.
...
  arguments to pass to editor: see edit.

Details

The name supplied as x need not exist as an R object, in which case a function with no arguments and an empty body is supplied for editing.

Editing an R object may change it in ways other than are obvious: see the comment under edit. See edit.data.frame for changes that can occur when editing a data frame or matrix.

See Also

edit, edit.data.frame

Examples

## Not run:
## Assume 'my.fun' is a user defined function:
 fix(my.fun)
## now my.fun is changed
## Also,
 fix(my.data.frame) # calls up data editor
 fix(my.data.frame, factor.mode="char") # use of ...
## End(Not run)

flush.console

Flush Output to a Console

Description

This does nothing except on console-based versions of R. On the macOS and Windows GUIs, it ensures that the display of output in the console is current, even if output buffering is on.

Usage

flush.console()
Description

Format unordered (itemize) and ordered (enumerate) lists.

Usage

formatUL(x, label = "*", offset = 0,
       width = 0.9 * getOption("width"))
formatOL(x, type = "arabic", offset = 0, start = 1,
       width = 0.9 * getOption("width"))

Arguments

x a character vector of list items.
label a character string used for labelling the items.
offset a non-negative integer giving the offset (indentation) of the list.
width a positive integer giving the target column for wrapping lines in the output.
type a character string specifying the 'type' of the labels in the ordered list. If
"arabic" (default), arabic numerals are used. For "Alph" or "alph", single
upper or lower case letters are employed (in this case, the number of the last
item must not exceed 26). Finally, for "Roman" or "roman", the labels are given
as upper or lower case roman numerals (with the number of the last item max-
imally 3899). type can be given as a unique abbreviation of the above, or as
one of the HTML style tokens "1" (arabic), "A"/"a" (alphabetic), or "I"/"i" (roman), respectively.
start a positive integer specifying the starting number of the first item in an ordered
list.

Value

A character vector with the formatted entries.

See Also

formatDL for formatting description lists.

Examples

## A simpler recipe.
x <- c("Mix dry ingredients thoroughly.",
       "Pour in wet ingredients.",
       "Mix for 10 minutes.",
       "Bake for one hour at 300 degrees."
## Format and output as an unordered list.
writeLines(formatUL(x))
## Format and output as an ordered list.
writeLines(formatOL(x))
## Ordered list using lower case roman numerals.
getAnywhere

Retrieve an R Object, Including from a Namespace

Description

These functions locate all objects with name matching their argument, whether visible on the search path, registered as an S3 method or in a namespace but not exported. `getAnywhere()` returns the objects and `argsAnywhere()` returns the arguments of any objects that are functions.

Usage

```r
getAnywhere(x)
argsAnywhere(x)
```

Arguments

- `x`: a character string or name.

Details

These functions look at all loaded namespaces, whether or not they are associated with a package on the search list.

They do not search literally “anywhere”: for example, local evaluation frames and namespaces that are not loaded will not be searched.

Where functions are found as registered S3 methods, an attempt is made to find which namespace registered them. This may not be correct, especially if namespaces have been unloaded.

Value

For `getAnywhere()` an object of class "getAnywhere". This is a list with components

- `name`: the name searched for
- `objs`: a list of objects found
- `where`: a character vector explaining where the object(s) were found
- `visible`: logical: is the object visible
- `dups`: logical: is the object identical to one earlier in the list.

In computing whether objects are identical, their environments are ignored.

Normally the structure will be hidden by the `print` method. There is a `[` method to extract one or more of the objects found.

For `argsAnywhere()` one or more argument lists as returned by `args`.

See Also

`getS3method` to find the method which would be used: this might not be the one of those returned by `getAnywhere` since it might have come from a namespace which was unloaded or be registered under another name.

`get`, `getFromNamespace`, `args`
Examples

```
getAnywhere("format.dist")
getAnywhere("simpleLoess") # not exported from stats
argsAnywhere(format.dist)
```

---

**getFromNamespace**  
Utility Functions for Developing Namespaces

**Description**

Utility functions to access and replace the non-exported functions in a namespace, for use in developing packages with namespaces.

They should not be used in production code (except perhaps `assignInMyNamespace`, but see the ‘Note’).

**Usage**

```
getFromNamespace(x, ns, pos = -1, envir = as.environment(pos))
assignInNamespace(x, value, ns, pos = -1,
   envir = as.environment(pos))
assignInMyNamespace(x, value)
fixInNamespace(x, ns, pos = -1, envir = as.environment(pos), ...)
```

**Arguments**

- **x**  
  an object name (given as a character string).
- **value**  
  an R object.
- **ns**  
  a namespace, or character string giving the namespace.
- **pos**  
  where to look for the object: see `get`.
- **envir**  
  an alternative way to specify an environment to look in.
- **...**  
  arguments to pass to the editor: see `edit`.

**Details**

`assignInMyNamespace` is intended to be called from functions within a package, and chooses the namespace as the environment of the function calling it.

The namespace can be specified in several ways. Using, for example, `ns = "stats"` is the most direct, but a loaded package can be specified via any of the methods used for `get`: `ns` can also be the environment printed as `<namespace:foo>`.

`getFromNamespace` is similar to (but predates) the `:::` operator: it is more flexible in how the namespace is specified.

`fixInNamespace` invokes `edit` on the object named `x` and assigns the revised object in place of the original object. For compatibility with `fix`, `x` can be unquoted.
Value

getFromNamespace returns the object found (or gives an error).
assignInNamespace, assignInMyNamespace and fixInNamespace are invoked for their side effect of changing the object in the namespace.

Warning

assignInNamespace should not be used in final code, and will in future throw an error if called from a package. Already certain uses are disallowed.

Note

assignInNamespace, assignInMyNamespace and fixInNamespace change the copy in the namespace, but not any copies already exported from the namespace, in particular an object of that name in the package (if already attached) and any copies already imported into other namespaces. They are really intended to be used only for objects which are not exported from the namespace. They do attempt to alter a copy registered as an S3 method if one is found.

They can only be used to change the values of objects in the namespace, not to create new objects.

See Also

get, fix, getS3method

Examples

getFromNamespace("findGeneric", "utils")
## Not run:
fixInNamespace("predict.ppr", "stats")
stats:::predict.ppr
getS3method("predict", "ppr")
## alternatively
fixInNamespace("predict.ppr", pos = 3)
fixInNamespace("predict.ppr", pos = "package:stats")
## End(Not run)

getParseData 

Get Detailed Parse Information from Object

Description

If the "keep.source" option is TRUE, R's parser will attach detailed information on the object it has parsed. These functions retrieve that information.

Usage

getParseData(x, includeText = NA)
getParseText(parseData, id)
getParseData

Arguments

x an expression returned from `parse`, or a function or other object with source reference information

includeText logical; whether to include the text of parsed items in the result

parseData a data frame returned from `getParseData`

id a vector of item identifiers whose text is to be retrieved

Details

In version 3.0.0, the R parser was modified to include code written by Romain Francois in his `parser` package. This constructs a detailed table of information about every token and higher level construct in parsed code. This table is stored in the `srcfile` record associated with source references in the parsed code, and retrieved by the `getParseData` function.

Value

For `getParseData`:

If parse data is not present, `NULL`. Otherwise a data frame is returned, containing the following columns:

- `line1` integer. The line number where the item starts. This is the parsed line number called "parse" in `getSrcLocation`, which ignores `#line` directives.
- `col1` integer. The column number where the item starts. The first character is column 1. This corresponds to "column" in `getSrcLocation`.
- `line2` integer. The line number where the item ends.
- `col2` integer. The column number where the item ends.
- `id` integer. An identifier associated with this item.
- `parent` integer. The `id` of the parent of this item.
- `token` character string. The type of the token.
- `terminal` logical. Whether the token is "terminal", i.e. a leaf in the parse tree.
- `text` character string. If `includeText` is `TRUE`, the text of all tokens; if it is `NA` (the default), the text of terminal tokens. If `includeText == FALSE`, this column is not included. Very long strings (with source of 1000 characters or more) will not be stored; a message giving their length and delimiter will be included instead.

The rownames of the data frame will be equal to the `id` values, and the data frame will have a "srcfile" attribute containing the `srcfile` record which was used. The rows will be ordered by starting position within the source file, with parent items occurring before their children.

For `getParseText`:

A character vector of the same length as `id` containing the associated text items. If they are not included in `parseData`, they will be retrieved from the original file.

Note

There are a number of differences in the results returned by `getParseData` relative to those in the original `parser` code:

- Fewer columns are kept.
- The internal token number is not returned.
• `col1` starts counting at 1, not 0.
• The `id` values are not attached to the elements of the parse tree, they are only retained in the table returned by `getParseData`.
• `#line` directives are identified, but other comment markup (e.g., `roxygen` comments) are not.

Parse data by design explore details of the parser implementation, which are subject to change without notice. Applications computing on the parse data may require updates for each R release.

**Author(s)**

Duncan Murdoch

**References**


**See Also**

`parse`, `srcRef`

**Examples**

```r
defn <- function(x) {
  x + 1  # A comment, kept as part of the source
}
d <- getParseData(fn)
if (!is.null(d)) {
  plus <- which(d$token == "+"")
  sum <- d$parent[plus]
  print(d[as.character(sum),])
  print(getParseText(d, sum))
}
```

---

**getS3method**

Get an S3 Method

**Description**

Get a method for an S3 generic, possibly from a namespace or the generic’s registry.

**Usage**

```r
gETCH3METHOD(f, class, optional = FALSE, envir = parent.frame())
```

**Arguments**

- `f`: a character string giving the name of the generic.
- `class`: a character string giving the name of the class.
- `optional`: logical: should failure to find the generic or a method be allowed?
- `envir`: the `environment` in which the method and its generic are searched first.
S3 methods may be hidden in namespaces, and will not then be found by `get`: this function can retrieve such functions, primarily for debugging purposes.

Further, S3 methods can be registered on the generic when a namespace is loaded, and the registered method will be used if none is visible (using namespace scoping rules).

It is possible that which S3 method will be used may depend on where the generic `f` is called from: `getS3method` returns the method found if `f` were called from the same environment.

The function found, or `NULL` if no function is found and `optional = TRUE`.

The function found, or `NULL` if no function is found and `optional = TRUE`.

See Also

`methods`, `get`, `getAnywhere`

Examples

```r
require(stats)
exists("predict.ppr")  # false
getS3method("predict", "ppr")
```

getWindowsHandle

Get a Windows Handle

Get the Windows handle of a window or of the `R` process in MS Windows.

Usage

`getWindowsHandle(which = "Console")`

Arguments

`which`  
a string (see below), or the number of a graphics device window (which must a `windows` one).

Details

`getWindowsHandle` gets the Windows handle. Possible choices for `which` are:

- "Console"  
The console window handle.
- "Frame"  
The MDI frame window handle.
- "Process"  
The process pseudo-handle.
- A device number  
The window handle of a graphics device

These values are not normally useful to users, but may be used by developers making add-ons to `R`. `NULL` is returned for the Frame handle if not running in MDI mode, for the Console handle when running `Rterm`, for any unrecognized string for which, or for a graphics device with no corresponding window.

Other windows (help browsers, etc.) are not accessible through this function.
Value

An external pointer holding the Windows handle, or NULL.

Note

This is only available on Windows.

See Also

getIdentification, getWindowsHandles

Examples

```r
if(.Platform$OS.type == "windows")
  print( getWindowsHandle() )
```

---

getWindowsHandles  Get handles of Windows in the MS Windows RGui

Description

This function gets the Windows handles of visible top level windows or windows within the R MDI frame (when using the Rgui).

Usage

getWindowsHandles(which = "R", pattern = "", minimized = FALSE)

Arguments

- **which**: A vector of strings "R" or "all" (possibly with repetitions). See the Details section.
- **pattern**: A vector of patterns that the titles of the windows must match.
- **minimized**: A logical vector indicating whether minimized windows should be considered.

Details

This function will search for Windows handles, for passing to external GUIs or to the arrangeWindows function. Each of the arguments may be a vector of values. These will be treated as follows:

- The arguments will all be recycled to the same length.
- The corresponding elements of each argument will be applied in separate searches.
- The final result will be the union of the windows identified in each of the searches.

If an element of `which` is "R", only windows belonging to the current R process will be returned. In MDI mode, those will be the child windows within the R GUI (Rgui) frame. In SDI mode, all windows belonging to the process will be included.

If the element is "all", then top level windows will be returned.

The elements of `pattern` will be used to make a subset of windows whose title text matches (according to `grep`) the pattern.

If `minimized` = FALSE, minimized windows will be ignored.
**glob2rx**

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**Value**

A list of external pointers containing the window handles.

**Note**

This is only available on Windows.

**Author(s)**

Duncan Murdoch

**See Also**

`arrangeWindows`, `getWindowsHandle` (singular).

**Examples**

```r
if(.Platform$OS.type == "windows") withAutoprint({
  getWindowsHandles()
  getWindowsHandles("all")
})
```

---

**glob2rx**

*Change Wildcard or Globbing Pattern into Regular Expression*

**Description**

Change *wildcard* aka *globbing* patterns into the corresponding regular expressions (*regexp*).

**Usage**

`glob2rx(pattern, trim.head = FALSE, trim.tail = TRUE)`

**Arguments**

- `pattern` character vector
- `trim.head` logical specifying if leading `"^.*"` should be trimmed from the result.
- `trim.tail` logical specifying if trailing `".*$"` should be trimmed from the result.

**Details**

This takes a wildcard as used by most shells and returns an equivalent regular expression. `?` is mapped to `.` (match a single character), `*` to `.*` (match any string, including an empty one), and the pattern is anchored (it must start at the beginning and end at the end). Optionally, the resulting regexp is simplified.

Note that now even `(`, `[]` and `{` can be used in `pattern`, but `glob2rx()` may not work correctly with arbitrary characters in `pattern`.

**Value**

A character vector of the same length as the input `pattern` where each wildcard is translated to the corresponding regular expression.
Author(s)

Martin Maechler, Unix/sed based version, 1991; current: 2004

See Also

regexp about regular expression, sub, etc about substitutions using regexprs.

Examples

```r
call('stopifnot(glob2rx("abc.*") == "abc\..",
glob2rx("a?b.*") == "a.b\.",
glob2rx("a?b.*", trim.tail = FALSE) == "a.b\..*$",
glob2rx("\*.doc") == "\*.\\.doc\$",
glob2rx("\*.doc", trim.head = TRUE) == "\\.doc\$",
glob2rx("\*.t*") == "\*.\\.t",
glob2rx("\*.t??") == "\*.\\.t..$",
glob2rx("\*\*") == "\*.\\["
)
```

Usage

globalVariables(names, package, add = TRUE)
suppressForeignCheck(names, package, add = TRUE)

Arguments

names The character vector of object names. If omitted, the current list of global variables declared in the package will be returned, unchanged.
package

The relevant package, usually the character string name of the package but optionally its corresponding namespace environment.

When the call to `globalVariables` or `suppressForeignCheck` comes in the package's source file, the argument is normally omitted, as in the example below.

add

Should the contents of `names` be added to the current global variables or replace it?

Details

The lists of declared global variables and native symbol objects are stored in a metadata object in the package's namespace, assuming the `globalVariables` or `suppressForeignCheck` call(s) occur as top-level calls in the package's source code.

The check command, as implemented in package `tools`, queries the list before checking the R source code in the package for possible problems.

`globalVariables` was introduced in R 2.15.1 and `suppressForeignCheck` was introduced in R 3.1.0 so both should be used conditionally: see the example.

Value

`globalVariables` returns the current list of declared global variables, possibly modified by this call.

`suppressForeignCheck` returns the current list of native symbol objects which are not to be checked.

Note

The global variables list really belongs to a restricted scope (a function or a group of method definitions, for example) rather than the package as a whole. However, implementing finer control would require changes in `check` and/or in `codetools`, so in this version the information is stored at the package level.

Author(s)

John Chambers and Duncan Murdoch

See Also

dontCheck.

Examples

```r
## Not run:
## assume your package has some code that assigns ".obj1" and ".obj2"
## but not in a way that codetools can find.
## In the same source file (to remind you that you did it) add:
if(getRversion() >= "2.15.1") utils::globalVariables(c(".obj1", "obj2"))

## To suppress messages about a run-time calculated native symbol,
## save it to a local variable.

## At top level, put this:
if(getRversion() >= "3.1.0") utils::suppressForeignCheck("localvariable")
```
## Within your function, do the call like this:
localvariable <- if (condition) entry1 else entry2
.Call(localvariable, 1, 2, 3)

## HOWEVER, it is much better practice to write code
## that can be checked thoroughly, e.g.
if(condition) .Call(entry1, 1, 2, 3) else .Call(entry2, 1, 2, 3)

## End(Not run)

hashtab

Description
Create and manipulate mutable hash tables.

Usage
hashtab(type = c("identical", "address"), size)
gethash(h, key, nomatch = NULL)
sethash(h, key, value)
remhash(h, key)
numhash(h)
typhash(h)
maphash(h, FUN)
clrhash(h)
is.hashtab(x)

## S3 method for class 'hashtab'
h[[key, nomatch = NULL, ...]]
## S3 replacement method for class 'hashtab'
h[[key, ...]] <- value
## S3 method for class 'hashtab'
print(x, ...)
## S3 method for class 'hashtab'
format(x, ...)
## S3 method for class 'hashtab'
length(x)
## S3 method for class 'hashtab'
str(object, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>character string specifying the hash table type.</td>
</tr>
<tr>
<td>size</td>
<td>an integer specifying the expected number of entries.</td>
</tr>
<tr>
<td>h, object</td>
<td>a hash table.</td>
</tr>
<tr>
<td>key</td>
<td>an R object to use as a key.</td>
</tr>
<tr>
<td>nomatch</td>
<td>value to return if key does not match.</td>
</tr>
<tr>
<td>value</td>
<td>new value to associate with key.</td>
</tr>
<tr>
<td>FUN</td>
<td>a function of two arguments, the key and the value, to call for each entry.</td>
</tr>
<tr>
<td>x</td>
<td>object to be tested, printed, or formatted.</td>
</tr>
<tr>
<td>...</td>
<td>additional arguments.</td>
</tr>
</tbody>
</table>
Details

Hash tables are a data structure for efficiently associating keys with values. Hash tables are similar to environments, but keys can be arbitrary objects. Like environments, and unlike named lists and most other objects in R, hash tables are mutable, i.e., they are not copied when modified and assignment means just giving a new name to the same object.

New hash tables are created by hashtab. Two variants are available: keys can be considered to match if they are identical() (type = "identical", the default), or if their addresses in memory are equal (type = "address"). The default “identical” type is almost always the right choice. The size argument provides a hint for setting the initial hash table size. The hash table will grow if necessary, but specifying an expected size can be more efficient.

getchash returns the value associated with key. If key is not present in the table, then the value of nomatch is returned.

sethash adds a new key/value association or changes the current value for an existing key. remhash removes the entry for key, if there is one.

maphash calls FUN for each entry in the hash table with two arguments, the entry key and the entry value. The order in which the entries are processed is not predictable. The consequence of FUN adding entries to the table or deleting entries from the table is also not predictable, except that removing the entry currently being processed will have the desired effect.

clrhash removes all entries from the hash table.

Value

hashtab returns a new hash table of the specified type.

getchash returns the value associated with key, or nomatch if there is no such value.

sethash returns value invisibly.

remhash invisibly returns TRUE if an entry for key was found and removed, and FALSE if no entry was found.

numhash returns the current number of entries in the table.

typhash returns a character string specifying the type of the hash table, one of "identical" or "address".

maphash and clrhash return NULL invisibly.

Notes

The interface design is based loosely on hash table support in Common Lisp.

The hash function and equality test used for "identical" hash tables are the same as the ones used internally by duplicated and unique, with two exceptions:

- Closure environments are not ignored when comparing closures. This corresponds to calling identical() with ignore.environment = FALSE, which is the default for identical().
- External pointer objects are compared as reference objects, corresponding to calling identical() with extptr.as.ref = TRUE. This ensures that hash tables with keys containing external pointers behave reasonably when serialized and unserialized.

As an experimental feature, the element operator [[] can also be used get or set hash table entries, and length can be used to obtain the number of entries. It is not yet clear whether this is a good idea.
Examples

## Create a new empty hash table.

```r
h1 <- hashtab()

h1
```

## Add some key/value pairs.

```r
sethash(h1, NULL, 1)
sethash(h1, .GlobalEnv, 2)
for (i in seq_along(LETTERS)) sethash(h1, LETTERS[i], i)
```

## Look up values for some keys.

```r
gethash(h1, NULL)
gethash(h1, .GlobalEnv)
gethash(h1, "Q")
```

## Remove an entry.

```r
(remhash(h1, NULL))
gethash(h1, NULL)
(remhash(h1, "XYZ"))
```

## Using the element operator.

```r
h1[["ABC"]]
h1[["ABC", nomatch = 77]]
h1[["ABC"]]
<"DEF"
h1[["ABC"]]
```

## Integers and real numbers that are equal are considered different
## (not identical) as keys:

```r
identical(3, 3L)
sethash(h1, 3L, "DEF")
gethash(h1, 3L)
gethash(h1, 3)
```

## Two variables can refer to the same hash table.

```r
h2 <- h1
identical(h1, h2)
```

## set in one, see in the "other" <=> really one object with 2 names

```r
sethash(h2, NULL, 77)
gethash(h1, NULL)
str(h1)
```

## An example of using maphash(): get all hashkeys of a hash table:

```r
hashkeys <- function(h) {
  val <- vector("list", numhash(h))
  idx <- 0
  maphash(h, function(k, v) { idx <<- idx + 1
    val[idx] <<- list(k )})
  val
}
```

```r
# IGNORE_RDIFF_BEGIN

kList <- hashkeys(h1)
str(kList) # the *order* is "arbitrary" & cannot be "known"
# IGNORE_RDIFF_END
```
hasName

Check for Name

Description

hasName is a convenient way to test for one or more names in an R object.

Usage

hasName(x, name)

Arguments

x

Any object.

name

One or more character values to look for.

Details

hasName(x, name) is defined to be equivalent to name %in% names(x), though it will evaluate slightly more quickly. It is intended to replace the common idiom !is.null(x$name). The latter can be unreliable due to partial name matching; see the example below.

Value

A logical vector of the same length as name containing TRUE if the corresponding entry is in names(x).

See Also

%in%, exists

Examples

x <- list(abc = 1, def = 2)
!is.null(x$abc) # correct
!is.null(x$a)  # this is the wrong test!
hasName(x, "abc")
hasName(x, "a")

head

Return the First or Last Parts of an Object

Description

Returns the first or last parts of a vector, matrix, table, data frame or function. Since head() and tail() are generic functions, they may also have been extended to other classes.
Usage

head(x, ...)  
## Default S3 method:
head(x, n = 6L, ...)

## S3 method for class 'matrix'
head(x, n = 6L, ...) # is exported as head.matrix()
## NB: The methods for 'data.frame' and 'array' are identical to the 'matrix' one

## S3 method for class 'ftable'
head(x, n = 6L, ...)

## S3 method for class 'function'
head(x, n = 6L, ...)

tail(x, ...)
## Default S3 method:
tail(x, n = 6L, keepnums = FALSE, addrownums, ...)
## S3 method for class 'matrix'
tail(x, n = 6L, keepnums = TRUE, addrownums, ...) # exported as tail.matrix()
## NB: The methods for 'data.frame', 'array', and 'table'
## are identical to the 'matrix' one

## S3 method for class 'ftable'
tail(x, n = 6L, keepnums = FALSE, addrownums, ...)

## S3 method for class 'function'
tail(x, n = 6L, ...)

Arguments

x
an object
n
an integer vector of length up to \text{dim}(x) (or 1, for non-dimensioned objects). A
logical is silently coerced to integer. Values specify the indices to be selected
in the corresponding dimension (or along the length) of the object. A
positive value of \text{n[i]} includes the first/last \text{n[i]} indices in that dimension, while a
negative value excludes the last/first \text{abs(n[i])}, including all remaining indices.
\text{NA} or non-specified values (when \text{length(n) < length(dim(x))}) select all indices
in that dimension. Must contain at least one non-missing value.

keepnums
in each dimension, if no names in that dimension are present, create them using
the indices included in that dimension. Ignored if \text{dim(x)} is NULL or its length
1.

addrownums
deprecated - keepnums should be used instead. Taken as the value of keepnums
if it is explicitly set when keepnums is not.

... arguments to be passed to or from other methods.

Details

For vector/array based objects, head() (tail()) returns a subset of the same dimensionality as x,
usually of the same class. For historical reasons, by default they select the first (last) 6 indices in
the first dimension ("rows") or along the length of a non-dimensioned vector, and the full extent (all
indices) in any remaining dimensions. head.matrix() and tail.matrix() are exported.
The default and array/matrix methods for head() and tail() are quite general. They will work as is for any class which has a dim() method, a length() method (only required if dim() returns NULL), and a [ method (that accepts the drop argument and can subset in all dimensions in the dimensioned case).

For functions, the lines of the deparsed function are returned as character strings.

When x is an array/matrix of dimensionality two and more, tail() will add dimnames similar to how they would appear in a full printing of x for all dimensions k where n[k] is specified and non-missing and dimnames(x)[[k]] (or dimnames(x) itself) is NULL. Specifically, the form of the added dimnames will vary for different dimensions as follows:

k=1 (rows): "[n,]" (right justified with whitespace padding)

k=2 (columns): "[ ,n]" (with no whitespace padding)

k>2 (higher dims): "n", i.e., the indices as character values

Setting keepnums = FALSE suppresses this behaviour.

As data.frame subsetting (‘indexing’) keeps attributes, so do the head() and tail() methods for data frames.

Value

An object (usually) like x but generally smaller. Hence, for arrays, the result corresponds to x[.., drop=FALSE]. For ftable objects x, a transformed format(x).

Note

For array inputs the output of tail when keepnums is TRUE, any dimnames vectors added for dimensions >2 are the original numeric indices in that dimension as character vectors. This means that, e.g., for 3-dimensional array arr, tail(arr, c(2,2,-1))[ , , 2] and tail(arr, c(2,2,-1))[ , , "2"] may both be valid but have completely different meanings.

Author(s)

Patrick Burns, improved and corrected by R-Core. Negative argument added by Vincent Goulet. Multi-dimension support added by Gabriel Becker.

Examples

head(letters)
head(letters, n = -6L)

head(freeny.x, n = 10L)
head(freeny.y)

head(iris3)
head(iris3, c(6L, 2L))
head(iris3, c(6L, -1L, 2L))

tail(letters)
tail(letters, n = -6L)

tail(freeny.x)
## the bottom-right "corner" :
tail(freeny.x, n = c(4, 2))
tail(freeny.y)
tail(iris3)
tail(iris3, c(6L, 2L))
tail(iris3, c(6L, -1L, 2L))

## iris with dimnames stripped
a3d <- iris3 ; dimnames(a3d) <- NULL
tail(a3d, c(6, -1, 2)) # keepnums = TRUE is default here!
tail(a3d, c(6, -1, 2), keepnums = FALSE)

## data frame w/ a (non-standard) attribute:
treeS <- structure(trees, foo = "bar")
(n <- nrow(treeS))
stopifnot(exprs = { # attribute is kept
  identical(htS <- head(treeS), treeS[1:6, ])
  identical(attr(htS, "foo"), "bar")
  identical(t1S <- tail(treeS), treeS[(n-5):n, ])
  ## BUT if I use "useAttrib(.)", this is *not* ok, when n is of length 2:
  ## --- because [i,j]-indexing of data frames *also* drops "other" attributes ..
  identical(tail(treeS, 3:2), treeS[(n-2):n, 2:3] )
})
tail(library) # last lines of function

head(stats::ftable(Titanic))

## 1d-array (with named dim):
a1 <- array(1:7, 7); names(dim(a1)) <- "O2"
stopifnot(exprs = {
  identical( tail(a1, 10), a1)
  identical( head(a1, 10), a1)
  identical( head(a1, 1), a1[1 , drop=FALSE] ) # was a1[1] in R <= 3.6.x
  identical( tail(a1, 2), a1[6:7] )
  identical( tail(a1, 1), a1[7 , drop=FALSE] ) # was a1[7] in R <= 3.6.x
})

---

### help

**Documentation**

**Description**

help is the primary interface to the help systems.

**Usage**

```r
help(topic, package = NULL, lib.loc = NULL,
     verbose = getOption("verbose"),
     try.all.packages = getOption("help.try.all.packages"),
     help_type = getOption("help_type"))
```

**Arguments**

- `topic` usually, a name or character string specifying the topic for which help is sought. A character string (enclosed in explicit single or double quotes) is always taken as naming a topic.
If the value of `topic` is a length-one character vector the topic is taken to be the value of the only element. Otherwise `topic` must be a name or a reserved word (if syntactically valid) or character string.

See ‘Details’ for what happens if this is omitted.

`package` a name or character vector giving the packages to look into for documentation, or `NULL`. By default, all packages whose namespaces are loaded are used. To avoid a name being deparsed use e.g. `pkg_ref` (see the examples).

`lib.loc` a character vector of directory names of R libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries. This is not used for HTML help (see ‘Details’).

`verbose` logical; if `TRUE`, the file name is reported.

`try.all.packages` logical; see Note.

`help_type` character string: the type of help required. Possible values are “text”, “html” and “pdf”. Case is ignored, and partial matching is allowed.

### Details

The following types of help are available:

- Plain text help
- HTML help pages with hyperlinks to other topics, shown in a browser by `browseURL`.

(On Unix-alikes, where possible an existing browser window is re-used: the macOS GUI uses its own browser window.)

If for some reason HTML help is unavailable (see `startDynamicHelp`), plain text help will be used instead.

- For help only, typeset as PDF – see the section on ‘Offline help’.

**On Unix-alikes**: The ‘factory-fresh’ default is text help except from the macOS GUI, which uses HTML help displayed in its own browser window.

**On Windows**: The default for the type of help is selected when R is installed – the ‘factory-fresh’ default is HTML help.

The rendering of text help will use directional quotes in suitable locales (UTF-8 and single-byte Windows locales); sometimes the fonts used do not support these quotes so this can be turned off by setting `options(useFancyQuotes = FALSE)`.

`topic` is not optional: if it is omitted R will give

- If a package is specified, (text or, in interactive use only, HTML) information on the package, including hints/links to suitable help topics.
- If `lib.loc` only is specified, a (text) list of available packages.
- Help on `help` itself if none of the first three arguments is specified.

Some topics need to be quoted (by backticks) or given as a character string. These include those which cannot syntactically appear on their own such as unary and binary operators, function and control-flow reserved words (including if, else for, in, repeat, while, break and next). The other reserved words can be used as if they were names, for example `TRUE`, `NA` and `Inf`.

If multiple help files matching `topic` are found, in interactive use a menu is presented for the user to choose one; in batch use the first on the search path is used. (For HTML help the menu will be
an HTML page, otherwise a graphical menu if possible if `getOption("menu.graphics")` is true, the default.)

Note that HTML help does not make use of `.lib.loc`: it will always look first in the loaded packages and then along `.libPaths()`.

### Offline help

Typeset documentation is produced by running the LaTeX version of the help page through `pdflatex`: this will produce a PDF file.

The appearance of the output can be customized through a file `Rhelp.cfg` somewhere in your LaTeX search path: this will be input as a LaTeX style file after `Rd.sty`. Some `environment` variables are consulted, notably `R_PAPERSIZE` (via `getOption("papersize")`) and `R_RD4PDF` (see ‘Making manuals’ in the ‘R Installation and Administration’ manual).

If there is a function `offline_help_helper` in the workspace or further down the search path it is used to do the typesetting, otherwise the function of that name in the `utils` namespace (to which the first paragraph applies). It should accept at least two arguments, the name of the LaTeX file to be typeset and the type (which is nowadays ignored). It accepts a third argument, `texinputs`, which will give the graphics path when the help document contains figures, and will otherwise not be supplied.

### Note

Unless `.lib.loc` is specified explicitly, the loaded packages are searched before those in the specified libraries. This ensures that if a library is loaded from a library not in the known library trees, then the help from the loaded library is used. If `.lib.loc` is specified explicitly, the loaded packages are not searched.

If this search fails and argument `try.all.packages` is TRUE and neither packages nor `.lib.loc` is specified, then all the packages in the known library trees are searched for help on topic and a list of (any) packages where help may be found is displayed (with hyperlinks for help_type = "html"). **NB:** searching all packages can be slow, especially the first time (caching of files by the OS can expedite subsequent searches dramatically).

### References


### See Also

? for shortcuts to help topics.

`help.search()` or ?? for finding help pages on a vague topic; `help.start()` which opens the HTML version of the R help pages; `library()` for listing available packages and the help objects they contain; `data()` for listing available data sets; `methods()`.

Use `prompt()` to get a prototype for writing help pages of your own package.

### Examples

```
help()
help(help)              # the same
help(lapply)
```
help("for")  # or ?"for", but quotes/backticks are needed

try({# requires working TeX installation:
    help(dgamma, help_type = "pdf")
    ## -> nicely formatted pdf -- including math formula -- for help(dgamma):
    system2(getOption("pdfviewer"), "dgamma.pdf", wait = FALSE)
})

help(package = "splines")  # get help even when package is not loaded

topi <- "women"
help(topi)

try(help("bs", try.all.packages = FALSE))  # reports not found (an error)
help("bs", try.all.packages = TRUE)  # reports can be found
    # in package 'splines'

## For programmatic use:
topic <- "family"; pkg_ref <- "stats"
help((topic), (pkg_ref))

---

help.request  

Send a Post to R-help

**Description**

Prompts the user to check they have done all that is expected of them before sending a post to the R-help mailing list, provides a template for the post with session information included and optionally sends the email (on Unix systems).

**Usage**

```r
help.request(subject = "",
              address = "r-help@R-project.org",
              file = "R.help.request", ...)
```

**Arguments**

- **subject**: subject of the email. Please do not use single quotes (') in the subject! Post separate help requests for multiple queries.
- **address**: recipient’s email address.
- **file**: filename to use (if needed) for setting up the email.
- **...**: additional named arguments such as method and ccaddress to pass to `create.post`.

**Details**

This function is not intended to replace the posting guide. Please read the guide before posting to R-help or using this function (see [https://www.r-project.org/posting-guide.html](https://www.r-project.org/posting-guide.html)).

The `help.request` function:

- asks whether the user has consulted relevant resources, stopping and opening the relevant URL if a negative response if given.
help.search

• checks whether the current version of R is being used and whether the add-on packages are up-to-date, giving the option of updating where necessary.

• asks whether the user has prepared appropriate (minimal, reproducible, self-contained, commented) example code ready to paste into the post.

Once this checklist has been completed a template post is prepared including current session information, and passed to create.post.

Value

Nothing useful.

Author(s)

Heather Turner, based on the then current code and help page of bug.report().

See Also

The posting guide (https://www.r-project.org/posting-guide.html), also sessionInfo() from which you may add to the help request.

create.post.

---

help.search Search the Help System

Description

Allows for searching the help system for documentation matching a given character string in the (file) name, alias, title, concept or keyword entries (or any combination thereof), using either fuzzy matching or regular expression matching. Names and titles of the matched help entries are displayed nicely formatted.

Vignette names, titles and keywords and demo names and titles may also be searched.

Usage

help.search(pattern, fields = c("alias", "concept", "title"),
    apropos, keyword, whatis, ignore.case = TRUE,
    package = NULL, lib.loc = NULL,
    help.db = getOption("help.db"),
    verbose = getOption("verbose"),
    rebuild = FALSE, agrep = NULL, use_UTF8 = FALSE,
    types = getOption("help.search.types")))

??pattern
field??pattern
Arguments

**pattern**
a character string to be matched in the specified fields. If this is given, the arguments `apropos`, `keyword`, and `whatis` are ignored.

**fields**
a character vector specifying the fields of the help database to be searched. The entries must be abbreviations of "name", "title", "alias", "concept", and "keyword", corresponding to the help page's (file) name, its title, the topics and concepts it provides documentation for, and the keywords it can be classified to. See below for details and how vignettes and demos are searched.

**apropos**
a character string to be matched in the help page topics and title.

**keyword**
a character string to be matched in the help page 'keywords'. ‘Keywords’ are really categories: the standard categories are listed in file `R.home("doc")/KEYWORDS` (see also the example) and some package writers have defined their own. If `keyword` is specified, `agrep` defaults to `FALSE`.

**whatis**
a character string to be matched in the help page topics.

**ignore.case**
a logical. If `TRUE`, case is ignored during matching; if `FALSE`, pattern matching is case sensitive.

**package**
a character vector with the names of packages to search through, or `NULL` in which case all available packages in the library trees specified by `lib.loc` are searched.

**lib.loc**
a character vector describing the location of R library trees to search through, or `NULL`. The default value of `NULL` corresponds to all libraries currently known.

**help.db**
a character string giving the file path to a previously built and saved help database, or `NULL`.

**verbose**
logical; if `TRUE`, the search process is traced. Integer values are also accepted, with `TRUE` being equivalent to 2, and 1 being less verbose. On Windows a progress bar is shown during rebuilding, and on Unix a heartbeat is shown for `verbose = 1` and a package-by-package list for `verbose >= 2`.

**rebuild**
a logical indicating whether the help database should be rebuilt. This will be done automatically if `lib.loc` or the search path is changed, or if `package` is used and a value is not found.

**agrep**
if `NULL` (the default unless `keyword` is used) and the character string to be matched consists of alphanumeric characters, whitespace or a dash only, approximate (fuzzy) matching via `agrep` is used unless the string has fewer than 5 characters; otherwise, it is taken to contain a regular expression to be matched via `grep`. If `FALSE`, approximate matching is not used. Otherwise, one can give a numeric or a list specifying the maximal distance for the approximate match, see argument `max.distance` in the documentation for `agrep`.

**use_UTF8**
logical: should results be given in UTF-8 encoding? Also changes the meaning of regexps in `agrep` to be Perl regexps.

**types**
a character vector listing the types of documentation to search. The entries must be abbreviations of "vignette" "help" or "demo". Results will be presented in the order specified.

**field**
a single value of `fields` to search.

Details

Upon installation of a package, a pre-built help.search index is serialized as ‘hsearch.rds’ in the ‘Meta’ directory (provided the package has any help pages). Vignettes are also indexed in the ‘Meta/vignette.rds’ file. These files are used to create the help search database via `hsearch_db`. 
The arguments `apropos` and `whatis` play a role similar to the Unix commands with the same names. Searching with `agrep = FALSE` will be several times faster than the default (once the database is built). However, approximate searches should be fast enough (around a second with 5000 packages installed).

If possible, the help database is saved in memory for use by subsequent calls in the session.

Note that currently the aliases in the matching help files are not displayed.

As with `?`, in `??` the pattern may be prefixed with a package name followed by `::` or `:::` to limit the search to that package.

For help files, `\keyword` entries which are not among the standard keywords as listed in file `KEYWORDS` in the R documentation directory are taken as concepts. For standard keyword entries different from `internal`, the corresponding descriptions from file `KEYWORDS` are additionally taken as concepts. All `\concept` entries used as concepts.

Vignettes are searched as follows. The "name" and "alias" are both the base of the vignette filename, and the "concept" entries are taken from the `\VignetteKeyword` entries. Vignettes are not classified using the help system "keyword" classifications. Demos are handled similarly to vignettes, without the "concept" search.

Value

The results are returned in a list object of class "hsearch", which has a print method for nicely formatting the results of the query. This mechanism is experimental, and may change in future versions of R.

In R.app on macOS, this will show up a browser with selectable items. On exiting this browser, the help pages for the selected items will be shown in separate help windows.

The internal format of the class is undocumented and subject to change.

See Also

`hsearch_db` for more information on the help search database employed, and for utilities to inspect available concepts and keywords.

`help`, `help.start` for starting the hypertext (currently HTML) version of R’s online documentation, which offers a similar search mechanism.

`RSiteSearch` to access an on-line search of R resources.

`apropos` uses regexps and has nice examples.

Examples

```r
help.search("linear models")  # In case you forgot how to fit linear models
help.search("non-existent topic")

??utils::help  # All the topics matching "help" in the utils package

help.search("print")  # All help pages with topics or title matching 'print'
help.search(apropos = "print")  # The same

help.search(keyword = "hplot")  # All help pages documenting high-level plots.
file.show(file.path(R.home("doc"), "KEYWORDS"))  # show all keywords
```
## Help pages with documented topics starting with 'try'.

help.search("\btry", fields = "alias")

---

**help.start**  
**Hypertext Documentation**

### Description

Start the hypertext (currently HTML) version of R's online documentation.

### Usage

```r
help.start(update = FALSE, gui = "irrelevant",  
            browser = getOption("browser"), remote = NULL)
```

### Arguments

- **update**  
  logical: should this attempt to update the package index to reflect the currently available packages. (Not attempted if remote is non-NULL.)

- **gui**  
  just for compatibility with S-PLUS.

- **browser**  
  the name of the program to be used as hypertext browser. It should be in the PATH, or a full path specified. Alternatively, it can be an R function which will be called with a URL as its only argument. This option is normally unset on Windows, when the file-association mechanism will be used.

- **remote**  
  A character string giving a valid URL for the `R_HOME` directory on a remote location.

### Details

Unless `remote` is specified this requires the HTTP server to be available (it will be started if possible: see `startDynamicHelp`).

One of the links on the index page is the HTML package index, `R.home("docs")/html/packages.html`, which can be remade by `make.packages.html()`. For local operation, the HTTP server will remake a temporary version of this list when the link is first clicked, and each time thereafter check if updating is needed (if `.libPaths` has changed or any of the directories has been changed). This can be slow, and using update = TRUE will ensure that the packages list is updated before launching the index page.

Argument `remote` can be used to point to HTML help published by another R installation: it will typically only show packages from the main library of that installation.

### See Also

- `help()` for on- and off-line help in other formats.
- `browseURL` for how the help file is displayed.
- `RSiteSearch` to access an on-line search of R resources.
Examples

help.start()
## Not run:
if(.Platform$OS.type == "unix") # includes Mac
## the 'remote' arg can be tested by
help.start(remote = paste0("file://", R.home()))
## End(Not run)

hsearch-utils  
Help Search Utilities

Description

Utilities for searching the help system.

Usage

hsearch_db(package = NULL, lib.loc = NULL,
types = getOption("help.search.types"),
verbose = getOption("verbose"),
rebuild = FALSE, use_UTF8 = FALSE)

hsearch_db_concepts(db = hsearch_db())
hsearch_db_keywords(db = hsearch_db())

Arguments

package  a character vector with the names of packages to search through, or NULL in which case all available packages in the library trees specified by lib.loc are searched.
lib.loc  a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known.
types  a character vector listing the types of documentation to search. See help.search for details.
verbose  a logical controlling the verbosity of building the help search database. See help.search for details.
rebuild  a logical indicating whether the help search database should be rebuilt. See help.search for details.
use_UTF8  logical: should results be given in UTF-8 encoding?
db  a help search database as obtained by calls to hsearch_db().

Details

hsearch_db() builds and caches the help search database for subsequent use by help.search. (In fact, re-builds only when forced (rebuild = TRUE) or “necessary”.)

The format of the help search database is still experimental, and may change in future versions. Currently, it consists of four tables: one with base information about all documentation objects found, including their names and titles and unique ids; three more tables contain the individual aliases, concepts and keywords together with the ids of the documentation objects they belong to.
Separating out the latter three tables accounts for the fact that a single documentation object may provide several of these entries, and allows for efficient searching.

See the details in `help_search` for how searchable entries are interpreted according to help type. `hsearch_db_concepts()` and `hsearch_db_keywords()` extract all concepts or keywords, respectively, from a help search database, and return these in a data frame together with their total frequencies and the numbers of packages they are used in, with entries sorted in decreasing total frequency.

**Examples**

```r
db <- hsearch_db()
## Total numbers of documentation objects, aliases, keywords and concepts (using the current format):
sapply(db, NROW)
## Can also be obtained from print method:
db
## 10 most frequent concepts:
head(hsearch_db_concepts(), 10)
## 10 most frequent keywords:
head(hsearch_db_keywords(), 10)
```

---

**INSTALL**

**Install Add-on Packages**

**Description**

Utility for installing add-on packages.

**Usage**

```r
R CMD INSTALL [options] [-l lib] pkgs
```

**Arguments**

- **pkgs**: a space-separated list with the path names of the packages to be installed. See ‘Details’.
- **lib**: the path name of the R library tree to install to. Also accepted in the form ‘--library=lib’. Paths including spaces should be quoted, using the conventions for the shell in use.
- **options**: a space-separated list of options through which in particular the process for building the help files can be controlled. Use `R CMD INSTALL --help` for the full current list of options.

**Details**

This will stop at the first error, so if you want all the pkgs to be tried, call this via a shell loop.

If used as `R CMD INSTALL pkgs` without explicitly specifying `lib`, packages are installed into the library tree rooted at the first directory in the library path which would be used by R run in the current environment.

To install into the library tree `lib`, use `R CMD INSTALL -l lib pkgs`. This prepends `lib` to the library path for duration of the install, so required packages in the installation directory will be found (and used in preference to those in other libraries).
Both lib and the elements of pkgs may be absolute or relative path names of directories. pkgs may also contain names of package archive files: these are then extracted to a temporary directory. These are tarballs containing a single directory, optionally compressed by gzip, bzip2, xz or compress. Finally, binary package archive files (as created by R CMD INSTALL --build) can be supplied.

Tarballs are by default unpackaged by the internal `untar` function: if needed an external `tar` command can be specified by the environment variable `R_INSTALL_TAR`: please ensure that it can handle the type of compression used on the tarball. (This is sometimes needed for tarballs containing invalid or unsupported sections, and can be faster on very large tarballs. Setting `R_INSTALL_TAR` to `‘tar.exe’` has been needed to overcome permissions issues on some Windows systems.)

The package sources can be cleaned up prior to installation by `‘--preclean’` or after by `‘--clean’`: cleaning is essential if the sources are to be used with more than one architecture or platform.

Some package sources contain a `‘configure’` script that can be passed arguments or variables via the option `‘--configure-args’` and `‘--configure-vars’`, respectively, if necessary. The latter is useful in particular if libraries or header files needed for the package are in non-system directories. In this case, one can use the configure variables `LIBS` and `CPPFLAGS` to specify these locations (and set these via `‘--configure-vars’`), see section ‘Configuration variables’ in ‘R Installation and Administration’ for more information. (If these are used more than once on the command line they are concatenated.) The configure mechanism can be bypassed using the option `‘--no-configure’`.

If the attempt to install the package fails, leftovers are removed. If the package was already installed, the old version is restored. This happens either if a command encounters an error or if the install is interrupted from the keyboard: after cleaning up the script terminates.

For details of the locking which is done, see the section ‘Locking’ in the help for `install.packages`.

Option `‘--build’` can be used to tar up the installed package for distribution as a binary package (as used on macOS). This is done by `utils::tar` unless environment variable `R_INSTALL_TAR` is set.

By default a package is installed with static HTML help pages if and only if R was: use options `‘--html’` and `‘--no-html’` to override this.

Packages are not by default installed keeping the source formatting (see the `keep.source` argument to `source`): this can be enabled by the option `‘--with-keep.source’` or by setting environment variable `R_KEEP_PKG_SOURCE` to `yes`.

Specifying the `‘--install-tests’` option copies the contents of the ‘tests’ directory into the package installation. If the `R_ALWAYS_INSTALL_TESTS` environment variable is set to a true value, the tests will be installed even if `‘--install-tests’` is omitted.

Use `R CMD INSTALL --help` for concise usage information, including all the available options.

Sub-architectures

An R installation can support more than one sub-architecture: currently this is most commonly used for 32- and 64-bit builds on Windows.

For such installations, the default behaviour is to try to install source packages for all installed sub-architectures unless the package has a configure script or a `‘src/Makefile’` (or `‘src/Makefile.win’` on Windows), when only compiled code for the sub-architecture running R CMD INSTALL is installed.

To install a source package with compiled code only for the sub-architecture used by R CMD INSTALL, use `‘--no-multiarch’`. To install just the compiled code for another sub-architecture, use `‘--libs-only’`. 
There are two ways to install for all available sub-architectures. If the configure script is known to work for both Windows architectures, use flag ‘--force-biarch’ (and packages can specify this via a ‘Biarch: yes’ field in their DESCRIPTION files). Second, a single tarball can be installed with

```
R CMD INSTALL --merge-multiarch mypkg_version.tar.gz
```

### Staged installation

The default way to install source packages changed in R 3.6.0, so packages are first installed to a temporary location and then (if successful) moved to the destination library directory. Some older packages were written in ways that assume direct installation to the destination library.

Staged installation can currently be overridden by having a line ‘StagedInstall: no’ in the package’s DESCRIPTION file, via flag ‘--no-staged-install’ or by setting environment variable R_INSTALL_STAGED to a false value (e.g. ‘false’ or ‘no’).

Staged installation requires either ‘--pkglock’ or ‘--lock’, one of which is used by default.

**Note**

The options do not have to precede ‘pkgs’ on the command line, although it will be more legible if they do. All the options are processed before any packages, and where options have conflicting effects the last one will win.

Some parts of the operation of INSTALL depend on the R temporary directory (see tempdir, usually under ‘/tmp’) having both write and execution access to the account running R. This is usually the case, but if ‘/tmp’ has been mounted as noexec, environment variable TMPDIR may need to be set to a directory from which execution is allowed.

### See Also

`REMOVE`, `.libPaths` for information on using several library trees; `install.packages` for R-level installation of packages; `update.packages` for automatic update of packages using the Internet or a local repository.

The section on ‘Add-on packages’ in ‘R Installation and Administration’ and the chapter on ‘Creating R packages’ in ‘Writing R Extensions’ via `RShowDoc` or in the ‘doc/manual’ subdirectory of the R source tree.
clean = FALSE, Ncpus = getOption("Ncpus", 1L),
verbose = getOption("verbose"),
libs_only = FALSE, INSTALL_opts, quiet = FALSE,
keep_outputs = FALSE, ...)

Arguments

**pkgs**
character vector of the names of packages whose current versions should be downloaded from the repositories.
If `repos = NULL`, a character vector of file paths,
on **Windows**, file paths of `.zip` files containing binary builds of packages. 
(http:// and file:// URLs are also accepted and the files will be downloaded and installed from local copies.) Source directories or file paths or URLs of archives may be specified with type = "source", but some packages need suitable tools installed (see the 'Details' section).
On **Unix-alikes**, these file paths can be source directories or archives or binary package archive files (as created by `R CMD build --binary`). (http:// and file:// URLs are also accepted and the files will be downloaded and installed from local copies.) On a CRAN build of R for macOS these can be `.tgz` files containing binary package archives. Tilde-expansion will be done on file paths.
If this is missing, a listbox of available packages is presented where possible in an interactive R session.

**lib**
character vector giving the library directories where to install the packages. Recycled as needed. If missing, defaults to the first element of `.libPaths()`.

**repos**
character vector, the base URL(s) of the repositories to use, e.g., the URL of a CRAN mirror such as "https://cloud.r-project.org". For more details on supported URL schemes see `url`.
Can be `NULL` to install from local files, directories or URLs: this will be inferred by extension from `pkgs` if of length one.

**contriburl**
URL(s) of the contrib sections of the repositories. Use this argument if your repository mirror is incomplete, e.g., because you mirrored only the 'contrib' section, or only have binary packages. Overrides argument `repos`. Incompatible with type = "both".

**method**
download method, see `download.file`. Unused if a non-NULL available is supplied.

**available**
a matrix as returned by `available.packages` listing packages available at the repositories, or `NULL` when the function makes an internal call to `available.packages`. Incompatible with type = "both".

**destdir**
directory where downloaded packages are stored. If it is `NULL` (the default) a subdirectory `downloaded_packages` of the session temporary directory will be used (and the files will be deleted at the end of the session).

**dependencies**
logical indicating whether to also install uninstalled packages which these packages depend on/link to/import/suggest (and so on recursively). Not used if `repos = NULL`. Can also be a character vector, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Only supported if `lib` is of length one (or missing), so it is unambiguous where to install the dependent packages. If this is not the case it is ignored, with a warning.
The default, NA, means c("Depends", "Imports", "LinkingTo").

TRUE means to use c("Depends", "Imports", "LinkingTo", "Suggests")

for pkgs and c("Depends", "Imports", "LinkingTo") for added dependencies: this installs all the packages needed to run pkgs, their examples, tests and vignettes (if the package author specified them correctly).

In all of these, "LinkingTo" is omitted for binary packages.

type: character, indicating the type of package to download and install. Will be "source" except on Windows and some macOS builds: see the section on 'Binary packages' for those.

configure.args: (Used only for source installs.) A character vector or a named list. If a character vector with no names is supplied, the elements are concatenated into a single string (separated by a space) and used as the value for the 'configure-args' flag in the call to R CMD INSTALL. If the character vector has names these are assumed to identify values for 'configure-args' for individual packages. This allows one to specify settings for an entire collection of packages which will be used if any of those packages are to be installed. (These settings can therefore be re-used and act as default settings.)

A named list can be used also to the same effect, and that allows multi-element character strings for each package which are concatenated to a single string to be used as the value for 'configure-args'.

configure.vars: (Used only for source installs.) Analogous to configure.args for flag 'configure-vars', which is used to set environment variables for the configure run.

clean: a logical value indicating whether to add the 'clean' flag to the call to R CMD INSTALL. This is sometimes used to perform additional operations at the end of the package installation in addition to removing intermediate files.

Ncpus: the number of parallel processes to use for a parallel install of more than one source package. Values greater than one are supported if the make command specified by Sys.getenv("MAKE", "make") accepts argument -k -j Ncpus.

verbose: a logical indicating if some "progress report" should be given.

libs_only: a logical value: should the 'libs-only' option be used to install only additional sub-architectures for source installs? (See also INSTALL_opts.) This can also be used on Windows to install just the DLL(s) from a binary package, e.g. to add 64-bit DLLs to a 32-bit install.

INSTALL_opts: an optional character vector of additional option(s) to be passed to R CMD INSTALL for a source package install. E.g., c("--html", "--no-multiarch", "--no-test-load").

Can also be a named list of character vectors to be used as additional options, with names the respective package names.

quiet: logical: if true, reduce the amount of output. This is not passed to available.packages() in case that is called, on purpose.

keep_outputs: a logical: if true, keep the outputs from installing source packages in the current working directory, with the names of the output files the package names with '.out' appended. Alternatively, a character string giving the directory in which to save the outputs. Ignored when installing from local files.

... Arguments to be passed to download.file, available.packages, or to the functions for binary installs on macOS and Windows (which accept an argument "lock": see the section on 'Locking').
**Details**

This is the main function to install packages. It takes a vector of names and a destination library, downloads the packages from the repositories and installs them. (If the library is omitted it defaults to the first directory in `.libPaths()`, with a message if there is more than one.) If `lib` is omitted or is of length one and is not a (group) writable directory, in interactive use the code offers to create a personal library tree (the first element of `Sys.getenv("R_LIBS_USER")`) and install there.

Detection of a writable directory is problematic on Windows: see the ‘Note’ section.

For installs from a repository an attempt is made to install the packages in an order that respects their dependencies. This does assume that all the entries in `lib` are on the default library path for installs (set by environment variable `R_LIBS`).

You are advised to run `update.packages` before `install.packages` to ensure that any already installed dependencies have their latest versions.

**Value**

Invisible `NULL`.

**Binary packages**

This section applies only to platforms where binary packages are available: Windows and CRAN builds for macOS.

R packages are primarily distributed as source packages, but binary packages (a packaging up of the installed package) are also supported, and the type most commonly used on Windows and by the CRAN builds for macOS. This function can install either type, either by downloading a file from a repository or from a local file.

Possible values of `type` are (currently) "source", "mac.binary", and "win.binary": the appropriate binary type where supported can also be selected as "binary".

For a binary install from a repository, the function checks for the availability of a source package on the same repository, and reports if the source package has a later version, or is available but no binary version is. This check can be suppressed by using

```r
options(install.packages.check.source = "no")
```

and should be if there is a partial repository containing only binary files.

An alternative (and the current default) is "both" which means ‘use binary if available and current, otherwise try source’. The action if there are source packages which are preferred but may contain code which needs to be compiled is controlled by `getOption("install.packages.compile.from.source")`. `type = "both"` will be silently changed to "binary" if either contriburl or available is specified.

Using packages with `type = "source"` always works provided the package contains no C/C++/Fortran code that needs compilation. Otherwise,

**on Windows**, you will need to have installed the Rtools collection as described in the ‘R for Windows FAQ’ and you must have the `PATH` environment variable set up as required by Rtools.

For a 32/64-bit installation of R on Windows, a small minority of packages with compiled code need either `INSTALL_opts = "--force-biarch"` or `INSTALL_opts = "--merge-multiarch"` for a source installation. (It is safe to always set the latter when installing from a repository or tarballs, although it will be a little slower.)

When installing a package on Windows, `install.packages` will abort the install if it detects that the package is already installed and is currently in use. In some circumstances (e.g.,
multiple instances of R running at the same time and sharing a library) it will not detect a problem, but the installation may fail as Windows locks files in use.

**On Unix-alikes**, when the package contains C/C++/Fortran code that needs compilation, suitable compilers and related tools need to be installed. On macOS you need to have installed the ‘Command-line tools for Xcode’ (see the ‘R Installation and Administration’ manual) and if needed by the package a Fortran compiler, and have them in your path.

**Locking**

There are various options for locking: these differ between source and binary installs.

By default for a source install, the library directory is ‘locked’ by creating a directory ‘00LOCK’ within it. This has two purposes: it prevents any other process installing into that library concurrently, and is used to store any previous version of the package to restore on error. A finer-grained locking is provided by the option ‘--pkglock’ which creates a separate lock for each package: this allows enough freedom for parallel installation. Per-package locking is the default when installing a single package, and for multiple packages when Ncpus > 1L. Finally locking (and restoration on error) can be suppressed by ‘--no-lock’.

For a macOS binary install, no locking is done by default. Setting argument lock to TRUE (it defaults to the value of `getOption("install.lock", FALSE)`) will use per-directory locking as described for source installs. For Windows binary install, per-directory locking is used by default (lock defaults to the value of `getOption("install.lock", TRUE)`). If the value is "pkglock" per-package locking will be used.

If package locking is used on Windows with libs_only = TRUE and the installation fails, the package will be restored to its previous state.

Note that it is possible for the package installation to fail so badly that the lock directory is not removed: this inhibits any further installs to the library directory (or for --pkglock, of the package) until the lock directory is removed manually.

**Parallel installs**

Parallel installs are attempted if pkgs has length greater than one and Ncpus > 1. It makes use of a parallel make, so the make specified (default make) when R was built must be capable of supporting make -j n: GNU make, dmake and pmake do, but Solaris make and older FreeBSD make do not: if necessary environment variable MAKE can be set for the current session to select a suitable make.

install.packages needs to be able to compute all the dependencies of pkgs from available, including if one element of pkgs depends indirectly on another. This means that if for example you are installing CRAN packages which depend on Bioconductor packages which in turn depend on CRAN packages, available needs to cover both CRAN and Bioconductor packages.

**Timeouts**

A limit on the elapsed time for each call to R CMD INSTALL (so for source installs) can be set via environment variable `_R_INSTALL_PACKAGES_ELAPSED_TIMEOUT_:` in seconds (or in minutes or hours with optional suffix ‘m’ or ‘h’, suffix ‘s’ being allowed for the default seconds) with 0 meaning no limit.

For non-parallel installs this is implemented via the timeout argument of system2: for parallel installs via the OS’s timeout command. (The one tested is from GNU coreutils, commonly available on Linux but not other Unix-alikes. If no such command is available the timeout request is ignored, with a warning. On Windows, one needs to specify a suitable timeout command via environment variable R_TIMEOUT because ‘c:/Windows/system32/timeout.exe’ is not.) For parallel installs a ‘Error 124’ message from make indicates that timeout occurred.
Timeouts during installation might leave lock directories behind and not restore previous versions.

**Version requirements on source installs**

If you are not running an up-to-date version of R you may see a message like

```
package 'RODBC' is not available (for R version 3.5.3)
```

One possibility is that the package is not available in any of the selected repositories; another is that is available but only for current or recent versions of R. For CRAN packages take a look at the package’s CRAN page (e.g., `https://cran.r-project.org/package=RODBC`). If that indicates in the ‘Depends’ field a dependence on a later version of R you will need to look in the ‘Old sources’ section and select the URL of a version of comparable age to your R. Then you can supply that URL as the first argument of `install.packages()`: you may need to first manually install its dependencies.

For other repositories, using `available.packages(filters = "OS_type")[pkgname, ]` will show if the package is available for any R version (for your OS).

**Note**

**On Unix-alikes:** Some binary distributions of R have INSTALL in a separate bundle, e.g. an R-devel RPM. `install.packages` will give an error if called with type = "source" on such a system.

Some binary Linux distributions of R can be installed on a machine without the tools needed to install packages: a possible remedy is to do a complete install of R which should bring in all those tools as dependencies.

**On Windows:** `install.packages` tries to detect if you have write permission on the library directories specified, but Windows reports unreliably. If there is only one library directory (the default), R tries to find out by creating a test directory, but even this need not be the whole story: you may have permission to write in a library directory but lack permission to write binary files (such as `.dll` files) there. See the ‘R for Windows FAQ’ for workarounds.

**See Also**

`update.packages`, `available.packages`, `download.packages`, `installed.packages`, `contrib.url`.

See `download.file` for how to handle proxies and other options to monitor file transfers.

`untar` for manually unpacking source package tarballs.

`INSTALL, REMOVE, remove.packages, library, .packages, read.dcf`

The ‘R Installation and Administration’ manual for how to set up a repository.

**Examples**

```R
## Not run:
## A Linux example for Fedora's layout of udunits2 headers.
install.packages(c("ncdf4", "RNetCDF"),
               configure.args = c(RNetCDF = "--with-netcdf-include=/usr/include/udunits2"))

## End(Not run)
```
installed.packages  

Find Installed Packages

Description

Find (or retrieve) details of all packages installed in the specified libraries.

Usage

```r
installed.packages(lib.loc = NULL, priority = NULL,
                    noCache = FALSE, fields = NULL,
                    subarch = .Platform$r_arch, ...)
```

Arguments

- **lib.loc**: character vector describing the location of R library trees to search through, or NULL for all known trees (see `.libPaths`).
- **priority**: character vector or NULL (default). If non-null, used to select packages; "high" is equivalent to c("base", "recommended"). To select all packages without an assigned priority use priority = NA_character_.
- **noCache**: Do not use cached information, nor cache it.
- **fields**: a character vector giving the fields to extract from each package’s ‘DESCRIPTION’ file in addition to the default ones, or NULL (default). Unavailable fields result in NA values.
- **subarch**: character string or NULL. If non-null and non-empty, used to select packages which are installed for that sub-architecture.
- **...**: allows unused arguments to be passed down from other functions.

Details

`installed.packages` scans the ‘DESCRIPTION’ files of each package found along `lib.loc` and returns a matrix of package names, library paths and version numbers.

The information found is cached (by library) for the R session and specified `fields` argument, and updated only if the top-level library directory has been altered, for example by installing or removing a package. If the cached information becomes confused, it can be avoided by specifying `noCache = TRUE`.

Value

A matrix with one row per package, row names the package names and column names (currently) "Package", "LibPath", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "OS_type", "License" and "Built" (the R version the package was built under). Additional columns can be specified using the `fields` argument.
Note

This needs to read several files per installed package, which will be slow on Windows and on some network-mounted file systems.

It will be slow when thousands of packages are installed, so do not use it to find out if a named package is installed (use find.package or system.file) nor to find out if a package is usable (call requireNamespace or require and check the return value) nor to find details of a small number of packages (use packageDescription).

See Also

update.packages, install.packages, INSTALL, REMOVE.

Examples

## confine search to .Library for speed
str(ip <- installed.packages(.Library, priority = "high"))
  ip[, c(1,3:5)]
PLIC <- installed.packages(.Library, priority = "high", fields = "License")
## what licenses are there:
table(PLIC[, "License"])

## Recommended setup (by many pros):
## Keep packages that come with R (priority="high") and all others separate!
## Consequently, .Library, R's "system" library, shouldn't have any
## non-'high'-priority packages:
pSys <- installed.packages(.Library, priority = NA_character_)
length(pSys) == 0 # TRUE under such a setup

isS3method

Is 'method' the Name of an S3 Method?

Description

Checks if method is the name of a valid / registered S3 method. Alternatively, when f and class are specified, it is checked if f is the name of an S3 generic function and paste(f, class, sep=".") is a valid S3 method.

Usage

isS3method(method, f, class, envir = parent.frame())

Arguments

method a character string, typically of the form "<fn>.<class>". If omitted, f and
  class have to be specified instead.
f optional character string, typically specifying an S3 generic function. Used,
  when method is not specified.
class optional character string, typically specifying an S3 class name. Used, when
  method is not specified.
envir the environment in which the method and its generic are searched first, as in
  getS3method().
isS3stdGeneric

Check if a Function Acts as an S3 Generic

Description

Determines whether f acts as a standard S3-style generic function.

Usage

isS3stdGeneric(f)

Arguments

f  
a function object

Details

A closure is considered a standard S3 generic if the first expression in its body calls UseMethod. Functions which perform operations before calling UseMethod will not be considered “standard” S3 generics.

If f is currently being traced, i.e., inheriting from class "traceable", the definition of the original untraced version of the function is used instead.

Value

If f is an S3 generic, a logical containing TRUE with the name of the S3 generic (the string passed to UseMethod). Otherwise, FALSE (unnamed).

Examples

isS3method("t")                 # FALSE - it is an S3 generic
isS3method("t.default")        # TRUE
isS3method("t.ts")             # TRUE
isS3method("t.test")           # FALSE
isS3method("t.data.frame")     # TRUE
isS3method("t.lm")             # FALSE - not existing
isS3method("t.foo.bar")        # FALSE - not existing

### S3 methods with "4 parts" in their name:

ff <- c("as.list", "as.matrix", "is.na", "row.names", "row.names<-")
for(m in ff) if(isS3method(m)) stop("wrongly declared an S3 method: ", m)
(m4 <- paste(ff, "data.frame", sep="."))
for(m in m4) if(!isS3method(m)) stop("not an S3 method: ", m)
Create Executable Programs on Unix-alikes

Description
Front-end for creating executable programs on unix-alikes, i.e., not on Windows.

Usage
```
R CMD LINK [options] linkcmd
```

Arguments
- **linkcmd**: a list of commands to link together suitable object files (include library objects) to create the executable program.
- **options**: further options to control the linking, or for obtaining information about usage and version.

Details
The linker front-end is useful in particular when linking against the R shared or static library: see the examples.
The actual linking command is constructed by the version of libtool installed at ‘R_HOME/bin’.
`R CMD LINK --help` gives usage information.

Note
Some binary distributions of R have LINK in a separate bundle, e.g. an R-devel RPM.
This is not available on Windows.

See Also
- `COMPIL`E.

Examples
```r
## Not run: ## examples of front-ends linked against R.
## First a C program
CC=`R CMD config CC`
R CMD LINK $CC -o foo.o `R CMD config --ldflags`

## if Fortran code has been compiled into ForFoo.o
FLIBS=`R CMD config FLIBS`
R CMD LINK $CC -o foo.o ForFoo.o `R CMD config --ldflags` $FLIBS

## And for a C++ front-end
CXX=`R CMD config CXX`
R CMD COMPILE foo.cc
R CMD LINK $CXX -o foo.o `R CMD config --ldflags`

## End(Not run)
```
localeToCharset  

Select a Suitable Encoding Name from a Locale Name

Description

This function aims to find a suitable coding for the locale named, by default the current locale, and if it is a UTF-8 locale a suitable single-byte encoding.

Usage

```r
localeToCharset(locale = Sys.getlocale("LC_CTYPE"))
```

Arguments

- `locale` character string naming a locale.

Details

The operation differs by OS.

**On Windows**, a locale is specified like "English_United Kingdom.1252". The final component gives the codepage, and this defines the encoding.

**On Unix-alikes**: Locale names are normally like `es_MX.iso88591`. If final component indicates an encoding and it is not `utf8` we just need to look up the equivalent encoding name. Otherwise, the language (here `es`) is used to choose a primary or fallback encoding.

In the C locale the answer will be "ASCII".

Value

A character vector naming an encoding and possibly a fallback single-encoding, NA if unknown.

Note

The encoding names are those used by `libiconv`, and ought also to work with glibc but maybe not with commercial Unixen.

See Also

`Sys.getlocale`, `iconv`.

Examples

```r
localeToCharset()
```
List Objects and their Structure

**Description**

`ls.str` and `lsf.str` are variations of `ls` applying `str()` to each matched name: see section Value.

**Usage**

```r
ls.str(pos = -1, name, envir, all.names = FALSE, pattern, mode = "any")
lsf.str(pos = -1, envir, ...)
```

```r
## S3 method for class 'ls_str'
print(x, max.level = 1, give.attr = FALSE, ...,
digits = max(1, getOption("str")$digits.d))
```

**Arguments**

- `pos` integer indicating search path position, or `-1` for the current environment.
- `name` optional name indicating search path position, see `ls`.
- `envir` environment to use, see `ls`.
- `all.names` logical indicating if names which begin with a `.` are omitted; see `ls`.
- `pattern` a regular expression passed to `ls`. Only names matching `pattern` are considered.
- `max.level` maximal level of nesting which is applied for displaying nested structures, e.g., a list containing sub lists. Default `1`: Display only the first nested level.
- `give.attr` logical; if `TRUE` (default), show attributes as sub structures.
- `mode` character specifying the mode of objects to consider. Passed to `exists` and `get`.
- `x` an object of class "ls_str".
- `...` further arguments to pass. `lsf.str` passes them to `ls.str` which passes them on to `ls`. The (non-exported) print method `print.ls_str` passes them to `str`.
- `digits` the number of significant digits to use for printing.

**Value**

`ls.str` and `lsf.str` return an object of class "ls_str", basically the character vector of matching names (functions only for `lsf.str`), similarly to `ls`, with a `print()` method that calls `str()` on each object.

**Author(s)**

Martin Maechler

**See Also**

`str`, `summary`, `args`
Examples

require(stats)

lsf.str()  # how do the functions look like which I am using?
ls.str(mode = "list")  # what are the structured objects I have defined?

## create a few objects
example(glm, echo = FALSE)
ll <- as.list(LETTERS)
print(ls.str(), max.level = 0)# don't show details

## which base functions have "file" in their name ?
lsf.str(pos = length(search()), pattern = "file")

## demonstrating that ls.str() works inside functions
## ["browser/debug mode"]: tt <- function(x, y = 1) { aa <- 7; r <- x + y; ls.str() } (nms <- sapply(strsplit(capture.output(tt(2))," *: *"), `[`, 1)) stopifnot(nms == c("aa", "r", "x", "y"))

Description

Show the name and email address of the maintainer of a package.

Usage

maintainer(pkg)

Arguments

pkg  Character string. The name of a single package.

Details

Accesses the package description to return the name and email address of the maintainer.

Questions about contributed packages should often be addressed to the package maintainer; questions about base packages should usually be addressed to the R-help or R-devel mailing lists. Bug reports should be submitted using the bug.report function.

Value

A character string giving the name and email address of the maintainer of the package, or NA if no such package is installed.

Author(s)

David Scott <d.scott@auckland.ac.nz> from code on R-help originally due to Charlie Sharpsteen <source@sharpsteen.net>; multiple corrections by R-core.
References


See Also

packageDescription, bug.report

Examples

maintainer("MASS")
**Examples**

```r
## Not run:
make.packages.html()
# this can be slow for large numbers of installed packages.

## End(Not run)
```

---

**make.socket**  
*Create a Socket Connection*

**Description**

With `server = FALSE` attempts to open a client socket to the specified port and host. With `server = TRUE` the R process listens on the specified port for a connection and then returns a server socket. It is a good idea to use `on.exit` to ensure that a socket is closed, as you only get 64 of them.

**Usage**

```r
make.socket(host = "localhost", port, fail = TRUE, server = FALSE)
```

**Arguments**

- **host**  
  name of remote host
- **port**  
  port to connect to/listen on
- **fail**  
  failure to connect is an error?
- **server**  
  a server socket?

**Value**

An object of class "socket", a list with components:

- **socket**  
  socket number. This is for internal use. On a Unix-alike it is a file descriptor.
- **port**  
  port number of the connection.
- **host**  
  name of remote computer.

**Warning**

I don’t know if the connecting host name returned when `server = TRUE` can be trusted. I suspect not.

**Author(s)**

Thomas Lumley

**References**

Adapted from Luke Tierney’s code for XLISP-Stat, in turn based on code from Robbins and Robbins “Practical UNIX Programming”.

---


See Also

`close.socket, read.socket`.

Compiling in support for sockets was optional prior to R 3.3.0: see `capabilities("sockets")` to see if it is available.

Examples

daytime <- function(host = "localhost")(    a <- make.socket(host, 13)    on.exit(close.socket(a))    read.socket(a)  )## Official time (UTC) from US Naval Observatory## Not run: daytime("tick.usno.navy.mil")

---

**menu**  

*Menu Interaction Function*

Description

`menu` presents the user with a menu of choices labelled from 1 to the number of choices. To exit without choosing an item one can select ‘0’.

Usage

`menu(choices, graphics = FALSE, title = NULL)`

Arguments

- `choices`  
a character vector of choices
- `graphics`  
a logical indicating whether a graphics menu should be used if available.
- `title`  
a character string to be used as the title of the menu. NULL is also accepted.

Details

If `graphics = TRUE` and a windowing system is available (Windows, macOS or X11 via Tcl/Tk) a listbox widget is used, otherwise a text menu. It is an error to use `menu` in a non-interactive session.

Ten or fewer items will be displayed in a single column, more in multiple columns if possible within the current display width.

No title is displayed if `title` is NULL or "".

Value

The number corresponding to the selected item, or 0 if no choice was made.

References

See Also

`select.list`, which is used to implement the graphical menu, and allows multiple selections.

Examples

```r
## Not run:
switch(menu(c("List letters", "List LETTERS")) + 1,
        cat("Nothing done\n"), letters, LETTERS)
## End(Not run)
```

Description

List all available methods for a S3 and S4 generic function, or all methods for an S3 or S4 class.

Usage

```r
methods(generic.function, class, dropPath = FALSE)
.S3methods(generic.function, class, envir = parent.frame(),
          dropPath = FALSE)
```

Arguments

- `generic.function` a generic function, or a character string naming a generic function.
- `class` a symbol or character string naming a class: only used if `generic.function` is not supplied.
- `envir` the environment in which to look for the definition of the generic function, when the generic function is passed as a character string.
- `dropPath` a `logical` indicating if the `search()` path, apart from `.GlobalEnv` and `package:base` (i.e., `baseenv()`), should be skipped when searching for method definitions. The default `FALSE` is back compatible and typically desired for printing, with or without asterisk; `dropPath=TRUE` has been hard coded in R 4.3.0 and is faster for non-small `search()` paths.
- `x` typically the result of `methods(...)`, an R object of S3 class "MethodsFunction", see ‘Value’ below.
- `byclass` an optional `logical` allowing to override the "byclass" attribute determining how the result is printed, see ‘Details’.
- `...` potentially further arguments passed to and from `methods`; unused currently.
methods() finds S3 and S4 methods associated with either the generic.function or class argument. Methods are found in all packages on the current search() path. .S3methods() finds only S3 methods, .S4methods() finds only S4 methods.

When invoked with the generic.function argument, the "byclass" attribute (see Details) is FALSE, and the print method by default displays the signatures (full names) of S3 and S4 methods. S3 methods are printed by pasting the generic function and class together, separated by a ".", as generic.class. The S3 method name is followed by an asterisk * if the method definition is not exported from the package namespace in which the method is defined. S4 method signatures are printed as generic,class-method; S4 allows for multiple dispatch, so there may be several classes in the signature generic,A,B-method.

When invoked with the class argument, "byclass" is TRUE, and the print method by default displays the names of the generic functions associated with the class, generic.

The source code for all functions is available. For S3 functions exported from the namespace, enter the method at the command line as generic.class. For S3 functions not exported from the namespace, see getAnywhere or getS3method. For S4 methods, see getMethod.

Help is available for each method, in addition to each generic. For interactive help, use the documentation shortcut ? with the name of the generic and tab completion, ?"generic<tab>" to select the method for which help is desired.

The S3 functions listed are those which are named like methods and may not actually be methods (known exceptions are discarded in the code).

Value

An object of class "MethodsFunction", a character vector of method names with "byclass" and "info" attributes. The "byclass" attribute is a logical indicating if the results were obtained with argument class defined. The "info" attribute is a data frame with columns:

- **generic** character vector of the names of the generic.
- **visible** logical(), is the method “visible” to the user? When true, it typically is exported from the namespace of the package in which it is defined, and the package is attach()ed to the search() path.
- **isS4** logical(), true when the method is an S4 method.
- **from** a factor, the location or package name where the method was found.

Note

The original methods function was written by Martin Maechler.

References


See Also

S3Methods, class, getS3method.

For S4, getMethod, showMethods, Introduction or Methods_Details.
mirrorAdmin

Managing Repository Mirrors

Description

Functions helping to maintain CRAN, some of them may also be useful for administrators of other repository networks.

Usage

mirror2html(mirrors = NULL, file = "mirrors.html", head = "mirrors-head.html", foot = "mirrors-foot.html")
checkCRAN(method)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mirrors</td>
<td>A data frame, by default the CRAN list of mirrors is used.</td>
</tr>
<tr>
<td>file</td>
<td>A connection or a character string.</td>
</tr>
<tr>
<td>head</td>
<td>Name of optional header file.</td>
</tr>
<tr>
<td>foot</td>
<td>Name of optional footer file.</td>
</tr>
<tr>
<td>method</td>
<td>Download method, see download.file.</td>
</tr>
</tbody>
</table>
modifyList

Recursively Modify Elements of a List

Description

Modifies a possibly nested list recursively by changing a subset of elements at each level to match a second list.

Usage

modifyList(x, val, keep.null = FALSE)

Arguments

x          A named list, possibly empty.
val        A named list with components to replace corresponding components in x.
keep.null  If TRUE, NULL elements in val become NULL elements in x. Otherwise, the corresponding element, if present, is deleted from x.

Value

A modified version of x, with the modifications determined as follows (here, list elements are identified by their names). Elements in val which are missing from x are added to x. For elements that are common to both but are not both lists themselves, the component in x is replaced (or possibly deleted, depending on the value of keep.null) by the one in val. For common elements that are in both lists, x[[name]] is replaced by modifyList(x[[name]], val[[name]]).

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

Examples

foo <- list(a = 1, b = list(c = "a", d = FALSE))
bar <- modifyList(foo, list(e = 2, b = list(d = TRUE)))
str(foo)
str(bar)
**Build and Query R or Package News Information**

**Description**

Build and query the news data base for R or add-on packages.

**Usage**

```r
news(query, package = "R", lib.loc = NULL, format = NULL,
reader = NULL, db = NULL)
```

### S3 method for class 'news_db'

```r
print(x, doBrowse = interactive(),
browser = getOption("browser"), ...)
```

**Arguments**

- `query` an expression for selecting news entries
- `package` a character string giving the name of an installed add-on package, or "R" or "R-3" or "R-2".
- `lib.loc` a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known.
- `format` Not yet used.
- `reader` Not yet used.
- `db, x` a news db obtained from `news()`.
- `doBrowse` logical specifying that the news should be opened in the browser (by `browseURL`, accessible as via `help.start`) instead of printed to the console.
- `browser` the browser to be used, see `browseURL`.
- `...` potentially further arguments passed to `print()`.

**Details**

If `package` is "R" (default), a news db is built with the news since the 4.0.0 release of R (corresponding to R's top-level 'NEWS' file). For "R-3" or "R-2", news for R 3.x.y or R 2.x.y respectively. Otherwise, if the given add-on package can be found in the given libraries, it is attempted to read its news in structured form from files `inst/NEWS.Rd`, `NEWS.md` (since R version 3.6.0, needs packages `commonmark` and `xml2` to be available), 'NEWS' or 'inst/NEWS' (in that order).

File `inst/NEWS.Rd` should be an Rd file given the entries as Rd `itemize` lists, grouped according to version using section elements with names starting with a suitable prefix (e.g. “Changes in version”) followed by a space and the version number, and optionally followed by a space and a parenthesized ISO 8601 (%Y-%m-%d, see `strptime`) format date, and possibly further grouped according to categories using `subsection` elements named as the categories. At the very end of `\section{..}`, the date may also be specified as (%Y-%m-%d, <note>), i.e., including parentheses.

File `NEWS.md` should contain the news in Markdown (following the CommonMark (https://commonmark.org/) specification), with the primary heading level giving the version number after a prefix followed by a space, and optionally followed by a space and a parenthesized ISO 8601...
format date. Where available, secondary heading are taken to indicate categories. To accommodate for common practice, news entries are only split down to the category level.

The plain text `NEWS` files in add-on packages use a variety of different formats; the default news reader should be capable to extract individual news entries from a majority of packages from the standard repositories, which use (slight variations of) the following format:

- Entries are grouped according to version, with version header “Changes in version” at the beginning of a line, followed by a version number, optionally followed by an ISO 8601 format date, possibly parenthesized.
- Entries may be grouped according to category, with a category header (different from a version header) starting at the beginning of a line.
- Entries are written as itemize-type lists, using one of ‘o’, ‘*’, ‘-‘ or ‘+’ as item tag. Entries must be indented, and ideally use a common indentation for the item texts.

Additional formats and readers may be supported in the future.

Package tools provides an (internal) utility function news2Rd to convert plain text `NEWS` files to Rd. For `NEWS` files in a format which can successfully be handled by the default reader, package maintainers can use tools::news2Rd(dir, "NEWS.Rd"), possibly with additional argument codify = TRUE, with dir a character string specifying the path to a package's root directory. Upon success, the 'NEWS.Rd' file can further be improved and then be moved to the 'inst' subdirectory of the package source directory.

The news db built is a character data frame inheriting from "news_db" with variables Version, Category, Date and Text, where the last contains the entry texts read, and the other variables may be NA if they were missing or could not be determined.

Using query, one can select news entries from the db. If missing or NULL, the complete db is returned. Otherwise, query should be an expression involving (a subset of) the variables Version, Category, Date and Text, and when evaluated within the db returning a logical vector with length the number of entries in the db. The entries for which evaluation gave TRUE are selected. When evaluating, Version and Date are coerced to numeric_version and Date objects, respectively, so that the comparison operators for these classes can be employed.

Value

A data frame inheriting from class "news_db", with attributes "package" (and "subset" if the query lead to proper subsetting).

Examples

```r
## Build a db of all R news entries.
db <- news()

## Bug fixes with PR number in 4.0.0.
db4 <- news(Version == "4.0.0" & grepl("BUG", Category) & grepl("PR#", Text),
            db = db)
nrow(db4)

## print db4 to show in an HTML browser.

## News from a date range ('Matrix' is there in a regular R installation):
if(length(iM <- find.package("Matrix", quiet = TRUE)) && nzchar(iM)) {
dM <- news(package="Matrix")
}
```
nsl

Look up the IP Address by Hostname (on Unix-alikes)

Description

Interface to the system gethostbyname, currently available only on unix-alikes, i.e., not on Windows.

Usage

nsl(hostname)

Arguments

hostname the name of the host.

Details

This was included as a test of internet connectivity, to fail if the node running R is not connected. It will also return NULL if BSD networking is not supported, including the header file ‘arpa/inet.h’. This function is not available on Windows.

Value

The IP address, as a character string, or NULL if the call fails.

Examples

if(.Platform$OS.type == "unix") # includes Mac
print( nsl("www.r-project.org") )
object.size  
Report the Space Allocated for an Object

Description

Provides an estimate of the memory that is being used to store an R object.

Usage

```r
object.size(x)
```

## S3 method for class 'object.size'
format(x, units = "b", standard = "auto", digits = 1L, ...)

## S3 method for class 'object.size'
print(x, quote = FALSE, units = "b", standard = "auto",
digits = 1L, ...)

Arguments

- **x**: an R object.
- **quote**: logical, indicating whether or not the result should be printed with surrounding quotes.
- **units**: the units to be used in formatting and printing the size. Allowed values for the different standards are

For all standards, `unit = "auto"` is also allowed. If `standard = "auto"`, any of the "legacy" and IEC units are allowed. See ‘Formatting and printing object sizes’ for details.

- **standard**: the byte-size unit standard to be used. A character string, possibly abbreviated from "legacy", "IEC", "SI" and "auto". See ‘Formatting and printing object sizes’ for details.
- **digits**: the number of digits after the decimal point, passed to `round`.
- **...**: arguments to be passed to or from other methods.

Details

Exactly which parts of the memory allocation should be attributed to which object is not clear-cut. This function merely provides a rough indication: it should be reasonably accurate for atomic vectors, but does not detect if elements of a list are shared, for example. (Sharing amongst elements of a character vector is taken into account, but not that between character vectors in a single object.)

The calculation is of the size of the object, and excludes the space needed to store its name in the symbol table.
Associated space (e.g., the environment of a function and what the pointer in a EXTPTSRXP points to) is not included in the calculation.

Object sizes are larger on 64-bit builds than 32-bit ones, but will very likely be the same on different platforms with the same word length and pointer size.

Sizes of objects using a compact internal representation may be over-estimated.

**Value**

An object of class "object_size" with a length-one double value, an estimate of the memory allocation attributable to the object in bytes.

**Formatting and printing object sizes**

Object sizes can be formatted using byte-size units from R’s legacy standard, the IEC standard, or the SI standard. As illustrated by below tables, the legacy and IEC standards use binary units (multiples of 1024), whereas the SI standard uses decimal units (multiples of 1000).

For methods format and print, argument standard specifies which standard to use and argument units specifies which byte-size unit to use. units = "auto" chooses the largest units in which the result is one or more (before rounding). Byte sizes are rounded to digits decimal places. standard = "auto" chooses the standard based on units, if possible, otherwise, the legacy standard is used.

**Summary of R’s legacy and IEC units:**

<table>
<thead>
<tr>
<th>object size</th>
<th>legacy</th>
<th>IEC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1 bytes</td>
<td>1 B</td>
</tr>
<tr>
<td>1024</td>
<td>1 Kb</td>
<td>1 KiB</td>
</tr>
<tr>
<td>1024^2</td>
<td>1 Mb</td>
<td>1 MiB</td>
</tr>
<tr>
<td>1024^3</td>
<td>1 Gb</td>
<td>1 GiB</td>
</tr>
<tr>
<td>1024^4</td>
<td>1 Tb</td>
<td>1 TiB</td>
</tr>
<tr>
<td>1024^5</td>
<td>1 Pb</td>
<td>1 PiB</td>
</tr>
<tr>
<td>1024^6</td>
<td></td>
<td>1 EiB</td>
</tr>
<tr>
<td>1024^7</td>
<td></td>
<td>1 ZiB</td>
</tr>
<tr>
<td>1024^8</td>
<td></td>
<td>1 YiB</td>
</tr>
</tbody>
</table>

**Summary of SI units:**

<table>
<thead>
<tr>
<th>object size</th>
<th>SI</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1 B</td>
</tr>
<tr>
<td>1000</td>
<td>1 kB</td>
</tr>
<tr>
<td>1000^2</td>
<td>1 MB</td>
</tr>
<tr>
<td>1000^3</td>
<td>1 GB</td>
</tr>
<tr>
<td>1000^4</td>
<td>1 TB</td>
</tr>
<tr>
<td>1000^5</td>
<td>1 PB</td>
</tr>
<tr>
<td>1000^6</td>
<td>1 EB</td>
</tr>
<tr>
<td>1000^7</td>
<td>1 ZB</td>
</tr>
<tr>
<td>1000^8</td>
<td>1 YB</td>
</tr>
<tr>
<td>1000^9</td>
<td>1 RB</td>
</tr>
<tr>
<td>1000^10</td>
<td>1 QB</td>
</tr>
</tbody>
</table>

**Author(s)**

R Core; Henrik Bengtsson for the non-legacy standards.
References


See Also

Memory-limits for the design limitations on object size.

Examples

```r
object.size(letters)
object.size(ls)
format(object.size(library), units = "auto")

sl <- object.size(rep(letters, 1000))

print(sl)  # 209288 bytes
print(sl, units = "auto")  # 204.4 Kb
print(sl, units = "auto", standard = "IEC")  # 204.4 KiB
print(sl, units = "auto", standard = "SI")  # 209.3 kB

(fsl <- sapply(c("Kb", "KB", "KiB"),
               function(u) format(sl, units = u)))

stopifnot(identical(  # assert that all three are the same:
    unique(substr(as.vector(fsl), 1,5)),
    format(round(as.vector(sl)/1024, 1))))

## find the 10 largest objects in the base package
z <- sapply(ls("package:base"), function(x)
    object.size(get(x, envir = baseenv())))

if(interactive()) {
    as.matrix(rev(sort(z))[1:10])
} else # (more constant over time):
    names(rev(sort(z))[1:10])
```

package.skeleton

Create a Skeleton for a New Source Package

Description

package.skeleton automates some of the setup for a new source package. It creates directories, saves functions, data, and R code files to appropriate places, and creates skeleton help files and a ‘Read-and-delete-me’ file describing further steps in packaging.

Usage

```r
package.skeleton(name = "anRpackage", list,
                  environment = .GlobalEnv,
                  path = ".", force = FALSE,
                  code_files = character(), encoding = "unknown")
```
Arguments

name character string: the package name and directory name for your package. Must be a valid package name.

list character vector naming the $R$ objects to put in the package. Usually, at most one of list, environment, or code_files will be supplied. See 'Details'.

environment an environment where objects are looked for. See 'Details'.

path path to put the package directory in.

force If FALSE will not overwrite an existing directory.

code_files a character vector with the paths to $R$ code files to build the package around. See 'Details'.

encoding optionally a character string with an encoding for an optional Encoding: line in ‘DESCRIPTION’ when non-ASCII characters will be used; typically one of "latin1", "latin2", or "UTF-8"; see the WRE manual.

Details

The arguments list, environment, and code_files provide alternative ways to initialize the package. If code_files is supplied, the files so named will be sourced to form the environment, then used to generate the package skeleton. Otherwise list defaults to the objects in environment (including those whose names start with .), but can be supplied to select a subset of the objects in that environment.

Stubs of help files are generated for functions, data objects, and S4 classes and methods, using the prompt, promptClass, and promptMethods functions. If an object from another package is intended to be imported and re-exported without changes, the promptImport function should be used after package.skeleton to generate a simple help file linking to the original one.

The package sources are placed in subdirectory name of path. If code_files is supplied, these files are copied; otherwise, objects will be dumped into individual source files. The file names in code_files should have suffix ".R" and be in the current working directory.

The filenames created for source and documentation try to be valid for all OSes known to run $R$. Invalid characters are replaced by ‘_’, invalid names are preceded by ‘zz’, names are converted to lower case (to avoid case collisions on case-insensitive file systems) and finally the converted names are made unique by make.unique(sep = "_"). This can be done for code and help files but not data files (which are looked for by name). Also, the code and help files should have names starting with an ASCII letter or digit, and this is checked and if necessary z prepended.

Functions with names starting with a dot are placed in file ‘$R$/name−internal.R’.

When you are done, delete the ‘Read-and-delete-me’ file, as it should not be distributed.

Value

Used for its side-effects.

References

Read the ‘Writing R Extensions’ manual for more details.

Once you have created a source package you need to install it: see the ‘R Installation and Administration’ manual, INSTALL and install.packages.
packageDescription

See Also

prompt.promptClass, and promptMethods.

package_native_routine_registration_skeleton for helping in preparing packages with compiled code.

Examples

require(stats)
## two functions and two "data sets":
f <- function(x, y) x+y
g <- function(x, y) x-y
d <- data.frame(a = 1, b = 2)
e <- rnorm(1000)
package.skeleton(list = c("f","g","d","e"), name = "mypkg")

packageDescription

Package Description

Description

Parses and returns the 'DESCRIPTION' file of a package as a "packageDescription".

Utility functions return (transformed) parts of that.

Usage

packageDescription(pkg, lib.loc = NULL, fields = NULL,
drop = TRUE, encoding = ")
packageVersion(pkg, lib.loc = NULL)
packageDate(pkg, lib.loc = NULL,
date.fields = c("Date", "Packaged", "Date/Publication", "Built"),
tryFormats = c("%Y-%m-%d", "%Y/%m/%d", "%d", "%m/%d/%Y"),
desc = packageDescription(pkg, lib.loc=lib.loc, fields=date.fields))
asDateBuilt(built)

Arguments

pkg a character string with the package name.
lib.loc a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages and namespaces are searched before the libraries.
fields a character vector giving the tags of fields to return (if other fields occur in the file they are ignored).
drop If TRUE and the length of fields is 1, then a single character string with the value of the respective field is returned instead of an object of class "packageDescription".
encoding If there is an Encoding field, to what encoding should re-encoding be attempted? If NA, no re-encoding. The other values are as used by iconv, so the default "" indicates the encoding of the current locale.
packageDescription

date.fields character vector of field tags to be tried. The first for which as.Date(.) is not NA will be returned. (Partly experimental, see Note.)

tryFormats date formats to try, see as.Date.character().

desc optionally, a named list with components named from date.fields; where the default is fine, a complete packageDescription() maybe specified as well.

built for asDateBuilt(), a character string as from packageDescription(*, fields="Built").

Details

A package will not be `found` unless it has a `DESCRIPTION` file which contains a valid Version field. Different warnings are given when no package directory is found and when there is a suitable directory but no valid `DESCRIPTION` file.

An attached environment named to look like a package (e.g., package:utils2) will be ignored.

packageVersion() is a convenience shortcut, allowing things like if (packageVersion("MASS") < "7.3") { do.things }.

For packageDate(), if desc is valid, both pkg and lib.loc are not made use of.

Value

If a `DESCRIPTION` file for the given package is found and can successfully be read, packageDescription returns an object of class "packageDescription", which is a named list with the values of the (given) fields as elements and the tags as names, unless drop = TRUE.

If parsing the `DESCRIPTION` file was not successful, it returns a named list of NAs with the field tags as names if fields is not null, and NA otherwise.

packageVersion() returns a (length-one) object of class "package_version".

packageDate() will return a "Date" object from as.Date() or NA.

asDateBuilt(built) returns a "Date" object or signals an error if built is invalid.

Note

The default behavior of packageDate(), notably for date.fields, is somewhat experimental and may change.

See Also

read.dcf

Examples

packageDescription("stats")
packageDescription("stats", fields = c("Package", "Version"))

packageDescription("stats", fields = "Version")
packageDescription("stats", fields = "Version", drop = FALSE)

if(requireNamespace("MASS") && packageVersion("MASS") < "7.3.29")
message("you need to update "MASS"")

pu <- packageDate("utils")
str(pu)
packageName

Find Package Associated with an Environment

Description

Many environments are associated with a package; this function attempts to determine that package.

Usage

packageName(env = parent.frame())

Arguments

env  The environment whose name we seek.

Details

Environment env would be associated with a package if `topenv(env)` is the namespace environment for that package. Thus when env is the environment associated with functions inside a package, or local functions defined within them, packageName will normally return the package name.

Not all environments are associated with a package: for example, the global environment, or the evaluation frames of functions defined there. packageName will return NULL in these cases.

Value

A length one character vector containing the name of the package, or NULL if there is no name.

See Also

`getPackageName` is a more elaborate function that can construct a name if none is found.

Examples

packageName()
packageName(environment(mean))
packageStatus  Package Management Tools

Description
Summarize information about installed packages and packages available at various repositories, and automatically upgrade outdated packages.

Usage
packageStatus(lib.loc = NULL, repositories = NULL, method,
    type = getOption("pkgType"), ...)

## S3 method for class 'packageStatus'
summary(object, ...)

## S3 method for class 'packageStatus'
update(object, lib.loc = levels(object$inst$LibPath),
    repositories = levels(object$avail$Repository), ...)

## S3 method for class 'packageStatus'
upgrade(object, ask = TRUE, ...)

Arguments
lib.loc  a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known.
repositories  a character vector of URLs describing the location of R package repositories on the Internet or on the local machine. If specified as NULL, derive appropriate URLs from option "repos".
method  Download method, see download.file.
type  type of package distribution: see install.packages.
object  an object of class "packageStatus" as returned by packageStatus.
ask  if TRUE, the user is prompted which packages should be upgraded and which not.
...  for packageStatus: arguments to be passed to available.packages and installed.packages.
for the upgrade method, arguments to be passed to install.packages for other methods: currently not used.

Details
The URLs in repositories should be full paths to the appropriate contrib sections of the repositories. The default is contrib.url(getOption("repos")).

There are print and summary methods for the "packageStatus" objects: the print method gives a brief tabular summary and the summary method prints the results.

The update method updates the "packageStatus" object. The upgrade method is similar to update.packages: it offers to install the current versions of those packages which are not currently up-to-date.
An object of class "packageStatus". This is a list with two components

- `inst`: a data frame with columns as the `matrix` returned by `installed.packages` plus "Status", a factor with levels c("ok", "upgrade", "unavailable"). Only the newest version of each package is reported, in the first repository in which it appears.

- `avail`: a data frame with columns as the `matrix` returned by `available.packages` plus "Status", a factor with levels c("installed", "not installed").

For the summary method the result is also of class "summary.packageStatus" with additional components

- `Libs`: a list with one element for each library
- `Repos`: a list with one element for each repository

with the elements being lists of character vectors of package name for each status.

**See Also**

`installed.packages, available.packages`

**Examples**

```r
## Not run:
x <- packageStatus()
prompt(x)
summary(x)
upgrade(x)
x <- update(x)
prompt(x)
## End(Not run)
```

---

**Invoke a Pager on an R Object**

**Description**

Displays a representation of the object named by `x` in a pager via `file.show`.

**Usage**

`page(x, method = c("dput", "print"), ...)`

**Arguments**

- `x`: An R object, or a character string naming an object.
- `method`: The default method is to dump the object via `dput`. An alternative is to use `print` and capture the output to be shown in the pager. Can be abbreviated.
- `...`: additional arguments for `dput, print` or `file.show` (such as `title`).
Details

If \( x \) is a length-one character vector, it is used as the name of an object to look up in the environment from which page is called. All other objects are displayed directly.

A default value of title is passed to file.show if one is not supplied in ....

See Also

file.show, edit, fix.

To go to a new page when graphing, see frame.

Examples

```r
## Not run: ## four ways to look at the code of 'page'
page(page)       # as an object
page("page")     # a character string
v <- "page"; page(v) # a length-one character vector
page(utils::page) # a call

## End(Not run)
```

Description

A class and utility methods for holding information about persons like name and email address.

Usage

```r
person(given = NULL, family = NULL, middle = NULL,
       email = NULL, role = NULL, comment = NULL,
       first = NULL, last = NULL)

as.person(x)
## Default S3 method:
as.person(x)

## S3 method for class 'person'
format(x,
       include = c("given", "family", "email", "role", "comment"),
       braces = list(given = "", family = "", email = c("<", ">"),
                     role = c("[", "]"), comment = c("(",")")),
       collapse = list(given = " " ,family = " " , email = " " , "role = " , " , comment = " , ")
       ...
       style = c("text", "R")
)

## S3 method for class 'person'
toBibtex(object, escape = FALSE, ...)
```
Arguments

given a character vector with the *given* names, or a list thereof.
family a character string with the *family* name, or a list thereof.
middle a character string with the collapsed middle name(s). Deprecated, see Details.
email a character string (or vector) giving an e-mail address (each), or a list thereof.
role a character vector specifying the role(s) of the person (see Details), or a list thereof.
comment a character string (or vector) providing comments, or a list thereof.
first a character string giving the first name. Deprecated, see Details.
last a character string giving the last name. Deprecated, see Details.
x an object for the as.person generic; a character string for the as.person default method; an object of class "person" otherwise.
include a character vector giving the fields to be included when formatting.
braces a list of characters (see Details).
collapse a list of characters (see Details).
... currently not used.
style a character string specifying the print style, with "R" yielding formatting as R code.
object an R object inhering from class "person".
escape a logical indicating whether non-ASCII characters should be translated to LaTeX escape sequences.

Details

Objects of class "person" can hold information about an arbitrary positive number of persons. These can be obtained by one call to person() with list arguments, or by first creating objects representing single persons and combining these via c().

The format() method collapses information about persons into character vectors (one string for each person): the fields in include are selected, each collapsed to a string using the respective element of collapse and subsequently "embraced" using the respective element of braces, and finally collapsed into one string separated by white space. If braces and/or collapse do not specify characters for all fields, the defaults shown in the usage are imputed. If collapse is FALSE or NA the corresponding field is not collapsed but only the first element is used. The print() method calls the format() method and prints the result, the toBibtex() method creates a suitable BibTeX representation.

Person objects can be subscripted by fields (using $) or by position (using []).
as.person() is a generic function. Its default method tries to reverse the default person formatting, and can also handle formatted person entries collapsed by comma or "and" (with appropriate white space).

Personal names are rather tricky, e.g., https://en.wikipedia.org/wiki/Personal_name.

The current implementation (starting from R 2.12.0) of the "person" class uses the notions of *given* (including middle names) and *family* names, as specified by given and family respectively. Earlier versions used a scheme based on first, middle and last names, as appropriate for most of Western culture where the given name precedes the family name, but not universal, as some other cultures place it after the family name, or use no family name. To smooth the transition to the new scheme, arguments first, middle and last are still supported, but their use is deprecated and they must
not be given in combination with the corresponding new style arguments. For persons which are not
natural persons (e.g., institutions, companies, etc.) it is appropriate to use given (but not family)
for the name, e.g., person("R Core Team", role = "aut").

The new scheme also adds the possibility of specifying roles based on a subset of the MARC
Code List for Relators (https://www.loc.gov/marc/relators/relaterm.html). When giving
the roles of persons in the context of authoring R packages, the following usage is suggested.

"aut" (Author) Use for full authors who have made substantial contributions to the package and
should show up in the package citation.

"com" (Compiler) Use for persons who collected code (potentially in other languages) but did not
make further substantial contributions to the package.

"cph" (Copyright holder) Use for all copyright holders. This is a legal concept so should use the
legal name of an institution or corporate body.

"cre" (Creator) Use for the package maintainer.

"ctb" (Contributor) Use for authors who have made smaller contributions (such as code patches
etc.) but should not show up in the package citation.

"ctr" (Contractor) Use for authors who have been contracted to write (parts of) the package and
hence do not own intellectual property.

"dtc" (Data contributor) Use for persons who contributed data sets for the package.

"fnd" (Funder) Use for persons or organizations that furnished financial support for the develop-
ment of the package.

"rev" (Reviewer) Use for persons or organizations responsible for reviewing (parts of) the pack-
age.

"ths" (Thesis advisor) If the package is part of a thesis, use for the thesis advisor.

"trl" (Translator) If the R code is a translation from another language (typically S), use for the
translator to R.

In the old scheme, person objects were used for single persons, and a separate "personList" class
with corresponding creator personList() for collections of these. The new scheme employs a
single class for information about an arbitrary positive number of persons, eliminating the need for
the personList mechanism.

The comment field can be used for “arbitrary” additional information about persons. Elements
named "ORCID" will be taken to give ORCID identifiers (see https://orcid.org/ for more infor-
mation), and be displayed as the corresponding URIs by the print() and format() methods (see
Examples below).

Value

person() and as.person() return objects of class "person".

See Also

citation

Examples

## Create a person object directly ...
p1 <- person("Karl", "Pearson", email = "pearson@stats.heaven")

## ... or convert a string.
p2 <- as.person("Ronald Aylmer Fisher")

## Combining and subsetting.
p <- c(p1, p2)
p[1]
p[-1]

## Extracting fields.
p$family
p$email
p[1]$email

## Specifying package authors, example from "boot":
## AC is the first author [aut] who wrote the S original.
## BR is the second author [aut], who translated the code to R [trl],
## and maintains the package [cre].
b <- c(person("Angelo", "Canty", role = "aut", comment =
  "S original, <http://statwww.epfl.ch/davison/BMA/library.html>"),
  person(c("Brian", "D."), "Ripley", role = c("aut", "trl", "cre"),
  comment = "R port", email = "ripley@stats.ox.ac.uk")
)
b

## Formatting.
format(b)

format(b, include = c("family", "given", "role"),
  braces = list(family = c("", ","), role = c("(Role(s): ", ")")))

## Conversion to BibTeX author field.
paste(format(b, include = c("given", "family"), collapse = " and ")
toBibtex(b)

## ORCID identifiers.
(p3 <- person("Achim", "Zeileis",
  comment = c(ORCID = "0000-0003-0918-3766")))

---

**personList**

Collections of Persons (Older Interface)

**Description**

Old interface providing functionality for information about collections of persons. Since R 2.14.0 person objects can be combined with the corresponding `c` method which supersedes the `personList` function.

**Usage**

```r
personList(...) as.personList(x)
```

**Arguments**

- `...` person objects (inheriting from class "person")
- `x` an object the elements of which are coercible via `as.person`
PkgUtils

Value

a person object (inheriting from class "person")

See Also

person for the new functionality for representing and manipulating information about persons.

Utilities for Building and Checking Add-on Packages

Description

Utilities for checking whether the sources of an R add-on package work correctly, and for building a source package from them.

Usage

R CMD check [options] pkgdirs
R CMD build [options] pkgdirs

Arguments

pkgdirs

a list of names of directories with sources of R add-on packages. For check these can also be the filenames of compressed tar archives with extension '.tar.gz', '.tgz', '.tar.bz2' or '.tar.xz'.

options

further options to control the processing, or for obtaining information about usage and version of the utility.

Details

R CMD check checks R add-on packages from their sources, performing a wide variety of diagnostic checks.

R CMD build builds R source tarballs. The name(s) of the packages are taken from the 'DESCRIPTION' files and not from the directory names. This works entirely on a copy of the supplied source directories.

Use R CMD foo --help to obtain usage information on utility foo.

The defaults for some of the options to R CMD build can be set by environment variables _R_BUILD_RESAVE_DATA_ and _R_BUILD_COMPACT_VIGNETTES_: see ‘Writing R Extensions’. Many of the checks in R CMD check can be turned off or on by environment variables: see Chapter ‘Tools’ of the ‘R Internals’ manual.

By default R CMD build uses the "internal" option to tar to prepare the tarball. An external tar program can be specified by the R_BUILD_TAR environment variable. This may be substantially faster for very large packages, and can be needed for packages with long path names (over 100 bytes) or very large files (over 8GB): however, the resulting tarball may not be portable.

R CMD check by default unpacks tarballs by the internal untar function: if needed an external tar command can be specified by the environment variable R_INSTALL_TAR; please ensure that it can handle the type of compression used on the tarball. (This is sometimes needed for tarballs containing invalid or unsupported sections, and can be faster on very large tarballs. Setting R_INSTALL_TAR to 'tar.exe' has been needed to overcome permissions issues on some Windows systems.)
Note

Only on Windows: They make use of a temporary directory specified by the environment variable 
TMPDIR and defaulting to ‘c:/TEMP’. Do ensure that if set forward slashes are used.

See Also

The sections on ‘Checking and building packages’ and ‘Processing Rd format’ in ‘Writing R Ex-
tensions’ (see on Unix-alikes the ‘doc/manual’ subdirectory of the R source tree, on Windows, see 
the Manuals sub-menu of the Help menu on the console).

---

process.events  Trigger Event Handling

Description

R front ends like the Windows GUI handle key presses and mouse clicks through “events” generated 
by the OS. These are processed automatically by R at intervals during computations, but in some 
cases it may be desirable to trigger immediate event handling. The process.events function does 
that.

Usage

process.events()

Details

This is a simple wrapper for the C API function R_ProcessEvents. As such, it is possible that it 
will not return if the user has signalled to interrupt the calculation.

Value

NULL is returned invisibly.

Author(s)

Duncan Murdoch

See Also

See ‘Writing R Extensions’ and the ‘R for Windows FAQ’ for more discussion of the 
R_ProcessEvents function.
Produce Prototype of an R Documentation File

Description
Facilitate the constructing of files documenting \texttt{R} objects.

Usage
\begin{verbatim}
prompt(object, filename = NULL, name = NULL, ...)

## Default S3 method:
prompt(object, filename = NULL, name = NULL,
       force.function = FALSE, ...)

## S3 method for class 'data.frame'
prompt(object, filename = NULL, name = NULL, ...)

promptImport(object, filename = NULL, name = NULL,
             importedFrom = NULL, importPage = name, ...)
\end{verbatim}

Arguments
\begin{description}
\item[object] an \texttt{R} object, typically a function for the default method. Can be \texttt{missing} when name is specified.
\item[filename] usually, a \texttt{connection} or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is name followed by ".\texttt{Rd}". Can also be \texttt{NA} (see below).
\item[name] a character string specifying the name of the object.
\item[force.function] a logical. If \texttt{TRUE}, treat object as function in any case.
\item[...] further arguments passed to or from other methods.
\item[importedFrom] a character string naming the package from which \texttt{object} was imported. De-
\item[importPage] a character string naming the help page in the package from which \texttt{object} was imported.
\end{description}

Details
Unless \texttt{filename} is \texttt{NA}, a documentation shell for \texttt{object} is written to the file specified by \texttt{filename}, and a message about this is given. For function objects, this shell contains the proper function and argument names. \texttt{R} documentation files thus created still need to be edited and moved into the ‘\texttt{man}’ subdirectory of the package containing the object to be documented.

If \texttt{filename} is \texttt{NA}, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to \texttt{cat(unlist(x), file = filename, sep = "\textbackslash n")}, where \texttt{x} is the list-style representation.

When \texttt{prompt} is used in \texttt{for} loops or scripts, the explicit name specification will be useful.

The \texttt{importPage} argument for \texttt{promptImport} needs to give the base of the name of the help file of the original help page. For example, the \texttt{approx} function is documented in ‘\texttt{approxfun.Rd}’ in the \texttt{stats} package, so if it were imported and re-exported it should have \texttt{importPage = “approxfun”}. Objects that are imported from other packages are not normally documented unless re-exported.
Value

If filename is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

Warning

The default filename may not be a valid filename under limited file systems (e.g., those on Windows).

Currently, calling prompt on a non-function object assumes that the object is in fact a data set and hence documents it as such. This may change in future versions of R. Use promptData to create documentation skeletons for data sets.

Note

The documentation file produced by prompt.data.frame does not have the same format as many of the data frame documentation files in the base package. We are trying to settle on a preferred format for the documentation.

Author(s)

Douglas Bates for prompt.data.frame

References


See Also

promptData, help and the chapter on ‘Writing R documentation’ in ‘Writing R Extensions’ (see the ‘doc/manual’ subdirectory of the R source tree).

For creation of many help pages (for a package), see package.skeleton.

To prompt the user for input, see readline.

Examples

require(graphics)
prompt(plot.default)
prompt(interactive, force.function = TRUE)
unlink("plot.default.Rd")
unlink("interactive.Rd")
prompt(women) # data.frame
unlink("women.Rd")
prompt(sunspots) # non-data.frame data
unlink("sunspots.Rd")

## Not run:
## Create a help file for each function in the .GlobalEnv:
for(f in ls()) if(is.function(get(f))) prompt(name = f)
promptData

Generate Outline Documentation for a Data Set

Description
Generates a shell of documentation for a data set.

Usage
promptData(object, filename = NULL, name = NULL)

Arguments

object
an R object to be documented as a data set.

filename
usually, a connection or a character string giving the name of the file to which
the documentation shell should be written. The default corresponds to a file
whose name is name followed by ".Rd". Can also be NA (see below).

name
a character string specifying the name of the object.

Details
Unless filename is NA, a documentation shell for object is written to the file specified by
filename, and a message about this is given.
If filename is NA, a list-style representation of the documentation shell is created and returned.
Writing the shell to a file amounts to cat(unlist(x), file = filename, sep = "\n"), where x is
the list-style representation.
Currently, only data frames are handled explicitly by the code.

Value
If filename is NA, a list-style representation of the documentation shell. Otherwise, the name of the
file written to is returned invisibly.

See Also
prompt

Examples
promptData(sunspots)
unlink("sunspots.Rd")
promptPackage  Generate a Shell for Documentation of a Package

Description

Generates a prototype of a package overview help page using Rd macros that dynamically extract information from package metadata when building the package.

Usage

promptPackage(package, lib.loc = NULL, filename = NULL, name = NULL, final = FALSE)

Arguments

package  a character string with the name of the package to be documented.
lib.loc  ignored.
filename  usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is name followed by ".Rd". Can also be NA (see below).
name  a character string specifying the name of the help topic; defaults to '\texttt{<pkgname>-package}', which is the required \code{\alias} for the overview help page.
final  a logical value indicating whether to attempt to create a usable version of the help topic, rather than just a shell.

Details

Unless \code{filename} is NA, a documentation shell for \code{package} is written to the file specified by \code{filename}, and a message about this is given.

If \code{filename} is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to \code{cat(unlist(x), file = filename, sep = "\n")}, where \code{x} is the list-style representation.

If \code{final} is \code{TRUE}, the generated documentation will not include the place-holder slots for manual editing, it will be usable as-is. In most cases a manually edited file is preferable (but \code{final = TRUE} is certainly less work).

Value

If \code{filename} is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

See Also

prompt.package.skeleton
Examples

```r
filename <- tempfile()
promptPackage("utils", filename = filename)
file.show(filename)
unlink(filename)
```

Description

These functions provide access to documentation. Documentation on a topic with name `name` (typically, an R object or a data set) can be displayed by either `help("name")` or `?name`.

Usage

`?topic`

`type?topic`

Arguments

- **topic**: Usually, a `name` or character string specifying the topic for which help is sought. Alternatively, a function call to ask for documentation on a corresponding S4 method: see the section on S4 method documentation. The calls `pkg:::topic` and `pkg:::topic` are treated specially, and look for help on `topic` in package `pkg`.

- **type**: the special type of documentation to use for this topic; for example, if the type is `class`, documentation is provided for the class with name `topic`. See the Section ‘S4 Method Documentation’ for the uses of `type` to get help on formal methods, including `methods?function` and `method?call`.

Details

This is a shortcut to `help` and uses its default type of help.

Some topics need to be quoted (by `backticks`) or given as a character string. There include those which cannot syntactically appear on their own such as unary and binary operators, function and control-flow reserved words (including `if`, `else for`, `in`, `repeat`, `while`, `break` and `next`). The other reserved words can be used as if they were names, for example `TRUE`, `NA` and `Inf`.

S4 Method Documentation

Authors of formal (‘S4’) methods can provide documentation on specific methods, as well as overall documentation on the methods of a particular function. The "?" operator allows access to this documentation in three ways.

The expression `methods?f` will look for the overall documentation methods for the function `f`. Currently, this means the documentation file containing the alias `f`-methods.

There are two different ways to look for documentation on a particular method. The first is to supply the `topic` argument in the form of a function call, omitting the type argument. The effect is to look for documentation on the method that would be used if this function call were actually evaluated.
See the examples below. If the function is not a generic (no S4 methods are defined for it), the help reverts to documentation on the function name.

The "?" operator can also be called with doc_type supplied as method; in this case also, the topic argument is a function call, but the arguments are now interpreted as specifying the class of the argument, not the actual expression that will appear in a real call to the function. See the examples below.

The first approach will be tedious if the actual call involves complicated expressions, and may be slow if the arguments take a long time to evaluate. The second approach avoids these issues, but you do have to know what the classes of the actual arguments will be when they are evaluated.

Both approaches make use of any inherited methods; the signature of the method to be looked up is found by using selectMethod (see the documentation for getMethod). A limitation is that methods in packages (as opposed to regular functions) will only be found if the package exporting them is on the search list, even if it is specified explicitly using the ?package::generic() notation.

References


See Also

help

?? for finding help pages on a vague topic.

Examples

?lapply

?"for" # but quotes/backticks are needed

?`+`

?women # information about data set "women"

## Not run:

require(methods)

## define a S4 generic function and some methods

combo <- function(x, y) c(x, y)

setGeneric("combo")

setMethod("combo", c("numeric", "numeric"), function(x, y) x+y)

## assume we have written some documentation

## for combo, and its methods ....

?combo # produces the function documentation

methods?combo # looks for the overall methods documentation

method?combo("numeric", "numeric") # documentation for the method above

?combo(1:10, rnorm(10)) # ... the same method, selected according to
# the arguments (one integer, the other numeric)

?combo(1:10, letters) # documentation for the default method

## End(Not run)
Description

This page documents a mechanism to generate relevant completions from a partially completed command line. It is not intended to be useful by itself, but rather in conjunction with other mechanisms that use it as a backend. The functions listed in the usage section provide a simple control and query mechanism. The actual interface consists of a few unexported functions described further down.

Usage

```r
rc.settings(ops, ns, args, dots, func, ipck, S3, data, help,
            argdb, fuzzy, quotes, files)
rc.status()
rc.getOption(name)
rc.options(...)```

```r
.DollarNames(x, pattern)
.AtNames(x, pattern)
```

```r
## Default S3 method:
.DollarNames(x, pattern = ")")
## S3 method for class 'list'
.DollarNames(x, pattern = ")")
## S3 method for class 'environment'
.DollarNames(x, pattern = ")")
## Default S3 method:
.AtNames(x, pattern = ")")
```

```r
findMatches(pattern, values, fuzzy)
```

Arguments

- **ops** Logical flag. Activates completion after the $ and @ operators.
- **ns** Logical flag. Controls namespace related completions.
- **args** Logical flag. Enables completion of function arguments.
- **dots** Logical flag. If disabled, drops ... from list of function arguments. Relevant only if args is enabled.
- **func** Logical flag. Enables detection of functions. If enabled, a customizable extension ("(" by default) is appended to function names. The process of determining whether a potential completion is a function requires evaluation, including for lazy loaded symbols. This is undesirable for large objects, because of potentially wasteful use of memory in addition to the time overhead associated with loading. For this reason, this feature is disabled by default.
- **S3** Logical flag. When args = TRUE, activates completion on arguments of all S3 methods (otherwise just the generic, which usually has very few arguments).
Logical flag. Enables completion of installed package names inside `library` and `require`.

data
Logical flag. Enables completion of data sets (including those already visible) inside `data`.

help
Logical flag. Enables completion of help requests starting with a question mark, by looking inside help index files.

argdb
Logical flag. When `args = TRUE`, completion is attempted on function arguments. Generally, the list of valid arguments is determined by dynamic calls to `args`. While this gives results that are technically correct, the use of the ... argument often hides some useful arguments. To give more flexibility in this regard, an optional table of valid arguments names for specific functions is retained internally. Setting `argdb = TRUE` enables preferential lookup in this internal data base for functions with an entry in it. Of course, this is useful only when the data base contains information about the function of interest. Some functions are already included, and more can be added by the user through the unexported function `.addFunctionInfo` (see below).

fuzzy
Logical flag. Enables fuzzy matching, where close but non-exact matches (e.g., with different case) are considered if no exact matches are found. This feature is experimental and the details can change. In `findMatches`, this argument defaults to the current setting.

quotes
Logical flag. Enables completion in R code when inside quotes. This normally leads to filename completion, but can be otherwise depending on context (for example, when the open quote is preceded by `?`), help completion is invoked. Setting this to `FALSE` relegates completion to the underlying completion frontend, which may do its own processing (for example, `readline` on Unix-alikes will do filename completion).

files
Logical flag. Deprecated. Use quotes instead.

name, ...
user-settable options. Currently valid names are

```r
function.suffix: default "("  
funarg.suffix: default "="  
package.suffix: default "::"
```

Usage is similar to that of `options`.

x
An R object for which valid names after "$" are computed and returned.

pattern
A regular expression. Only matching names are returned.

values
character string giving set of candidate values in which matches are to be found.

Details

There are several types of completion, some of which can be disabled using `rc.settings`. The arguments of `rc.settings` are all logical flags, turning specific optional completion features on and off. All settings are on by default except `ipck`, `func`, and `fuzzy`. Turn more off if your CPU cycles are valuable; you will still retain basic completion.

The most basic level, which can not be turned off once the completion functionality is activated, provides completion on names visible on the search path, along with a few special keywords (e.g., `TRUE`). This type of completion is not attempted if the partial ‘word’ (a.k.a. token) being completed is empty (since there would be too many completions). The more advanced types of completion are described below.
Completion after extractors $ and @: When the ops setting is turned on, completion after $ and @ is attempted. This requires the prefix to be evaluated, which is attempted unless it involves an explicit function call (implicit function calls involving the use of [], $, etc do not inhibit evaluation).

Valid completions after the $ and @ extractors are determined by the generic functions .DollarNames and .AtNames respectively. A few basic methods are provided, and more can be written for custom classes. The findMatches function can be useful for this purpose.

Completion inside namespaces: When the ns setting is turned on, completion inside namespaces is attempted when a token is preceded by the :: or :::: operators. Additionally, the basic completion mechanism is extended to include all loaded namespaces, i.e., foopkg:: becomes a valid completion of foo if "foopkg" is a loaded namespace.

The completion of package namespaces applies only to already loaded namespaces, i.e. if MASS is not loaded, MAS will not complete to MASS::. However, attempted completion inside an apparent namespace will attempt to load the namespace if it is not already loaded, e.g. trying to complete on MASS::fr will load MASS if it is not already loaded.

Completion for help items: When the help setting is turned on, completion on help topics is attempted when a token is preceded by ?. Prefixes (such as class, method) are supported, as well as quoted help topics containing special characters.

Completion of function arguments: When the args setting is turned on, completion on function arguments is attempted whenever deemed appropriate. The mechanism used will currently fail if the relevant function (at the point where completion is requested) was entered on a previous prompt (which implies in particular that the current line is being typed in response to a continuation prompt, usually +). Note that separation by newlines is fine.

The list of possible argument completions that is generated can be misleading. There is no problem for non-generic functions (except that ... is listed as a completion; this is intentional as it signals the fact that the function can accept further arguments). However, for generic functions, it is practically impossible to give a reliable argument list without evaluating arguments (and not even then, in some cases), which is risky (in addition to being difficult to code, which is the real reason it hasn’t even been tried), especially when that argument is itself an in-line function call. Our compromise is to consider arguments of all currently available methods of that generic. This has two drawbacks. First, not all listed completions may be appropriate in the call currently being constructed. Second, for generics with many methods (like print and plot), many matches will need to be considered, which may take a noticeable amount of time. Despite these drawbacks, we believe this behaviour to be more useful than the only other practical alternative, which is to list arguments of the generic only.

Only S3 methods are currently supported in this fashion, and that can be turned off using the S3 setting.

Since arguments can be unnamed in R function calls, other types of completion are also appropriate whenever argument completion is. Since there are usually many many more visible objects than formal arguments of any particular function, possible argument completions are often buried in a bunch of other possibilities. However, recall that basic completion is suppressed for blank tokens. This can be useful to list possible arguments of a function. For example, trying to complete seq([TAB]) and seq(from = 1, [TAB]) will both list only the arguments of seq (or any of its methods), whereas trying to complete seq(length([TAB]) will list both the length.out argument and the length( function as possible completions. Note that no attempt is made to remove arguments already supplied, as that would incur a further speed penalty.

Special functions: For a few special functions (library, data, etc), the first argument is treated specially, in the sense that normal completion is suppressed, and some function specific completions are enabled if so requested by the settings. The ipck setting, which controls whether library and require will complete on installed packages, is disabled by default because
the first call to `installed.packages` is potentially time consuming (e.g., when packages are installed on a remote network file server). Note, however, that the results of a call to `installed.packages` is cached, so subsequent calls are usually fast, so turning this option on is not particularly onerous even in such situations.

`findMatches` is an utility function that is used internally to determine matches. It can be used for writing methods for `.DollarNames` or `.AtNames`, the main benefit being that it will take the current fuzzy setting into account.

**Value**

If `rc.settings` is called without any arguments, it returns the current settings as a named logical vector. Otherwise, it returns `NULL` invisibly.

`rc.status` returns, as a list, the contents of an internal (unexported) environment that is used to record the results of the last completion attempt. This can be useful for debugging. For such use, one must resist the temptation to use completion when typing the call to `rc.status` itself, as that then becomes the last attempt by the time the call is executed.

The items of primary interest in the returned list are:

- `comps` The possible completions generated by the last call to `.completeToken`, as a character vector.
- `token` The token that was (or, is to be) completed, as set by the last call to `.assignToken` (possibly inside a call to `.guessTokenFromLine`).
- `linebuffer` The full line, as set by the last call to `.assignLinebuffer`.
- `start` The start position of the token in the line buffer, as set by the last call to `.assignStart`.
- `end` The end position of the token in the line buffer, as set by the last call to `.assignEnd`.
- `fileName` Logical, indicating whether the cursor is currently inside quotes.
- `fguess` The name of the function the cursor is currently inside.
- `isFirstArg` Logical. If cursor is inside a function, is it the first argument?

In addition, the components `settings` and `options` give the current values of settings and options respectively.

`rc.getOption` and `rc.options` behave much like `getOption` and `options` respectively.

`findMatches` returns values that match the input pattern, taking the fuzzy flag into account.

**Unexported API**

There are several unexported functions in the package. Of these, a few are special because they provide the API through which other mechanisms can make use of the facilities provided by this package (they are unexported because they are not meant to be called directly by users). The usage of these functions are:

```r
.assignToken(text)
.assignLinebuffer(line)
.assignStart(start)
.assignEnd(end)
.completeToken()
```
.retrieveCompletions()
.getFileComp()

guessTokenFromLine()
.win32consoleCompletion(linebuffer, cursorPosition,
    check.repeat = TRUE,
    minlength = -1)

.addFunctionInfo(...)

The first four functions set up a completion attempt by specifying the token to be completed (text), and indicating where (start and end, which should be integers) the token is placed within the complete line typed so far (line).

Potential completions of the token are generated by .completeToken, and the completions can be retrieved as an R character vector using .retrieveCompletions. It is possible for the user to specify a replacement for this function by setting rc.options("custom.completer"); if not NULL, this function is called to compute potential completions. This facility is meant to help in situations where completing as R code is not appropriate. See source code for more details.

If the cursor is inside quotes, completion may be suppressed. The function .getFileComp can be used after a call to .completeToken to determine if this is the case (returns TRUE), and alternative completions generated as deemed useful. In most cases, filename completion is a reasonable fallback.

The .guessTokenFromLine function is provided for use with backends that do not already break a line into tokens. It requires the linebuffer and endpoint (cursor position) to be already set, and itself sets the token and the start position. It returns the token as a character string.

The .win32consoleCompletion is similar in spirit, but is more geared towards the Windows GUI (or rather, any front-end that has no completion facilities of its own). It requires the linebuffer and cursor position as arguments, and returns a list with three components, addition, possible and comps. If there is an unambiguous extension at the current position, addition contains the additional text that should be inserted at the cursor. If there is more than one possibility, these are available either as a character vector of preformatted strings in possible, or as a single string in comps. possible consists of lines formatted using the current width option, so that printing them on the console one line at a time will be a reasonable way to list them. comps is a space separated (collapsed) list of the same completions, in case the front-end wishes to display it in some other fashion.

The minlength argument can be used to suppress completion when the token is too short (which can be useful if the front-end is set up to try completion on every keypress). If check.repeat is TRUE, it is detected if the same completion is being requested more than once in a row, and ambiguous completions are returned only in that case. This is an attempt to emulate GNU Readline behaviour, where a single TAB completes up to any unambiguous part, and multiple possibilities are reported only on two consecutive TABs.

As the various front-end interfaces evolve, the details of these functions are likely to change as well.

The function .addFunctionInfo can be used to add information about the permitted argument names for specific functions. Multiple named arguments are allowed in calls to it, where the tags are names of functions and values are character vectors representing valid arguments. When the argdb setting is TRUE, these are used as a source of valid argument names for the relevant functions.

Note

If you are uncomfortable with unsolicited evaluation of pieces of code, you should set ops = FALSE. Otherwise, trying to complete foo@ba will evaluate foo, trying to complete foo[i, 1:10]$ba will
evaluate `foo[i, 1:10]`, etc. This should not be too bad, as explicit function calls (involving parentheses) are not evaluated in this manner. However, this will affect promises and lazy loaded symbols.

**Author(s)**

Deepayan Sarkar, <deepayan.sarkar@r-project.org>

---

### read.DIF

**Data Input from Spreadsheet**

**Description**

Reads a file in Data Interchange Format (DIF) and creates a data frame from it. DIF is a format for data matrices such as single spreadsheets.

**Usage**

```r
read.DIF(file, header = FALSE,
          dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"),
          row.names, col.names, as.is = !stringsAsFactors,
          na.strings = "NA", colClasses = NA, nrow = -1,
          skip = 0, check.names = TRUE, blank.lines.skip = TRUE,
          stringsAsFactors = FALSE,
          transpose = FALSE, fileEncoding = "")
```

**Arguments**

- **file**: the name of the file which the data are to be read from, or a `connection`, or a complete URL. The name "clipboard" may also be used on Windows, in which case `read.DIF("clipboard")` will look for a DIF format entry in the Windows clipboard.
- **header**: a logical value indicating whether the spreadsheet contains the names of the variables as its first line. If missing, the value is determined from the file format: `header` is set to `TRUE` if and only if the first row contains only character values and the top left cell is empty.
- **dec**: the character used in the file for decimal points.
- **numerals**: string indicating how to convert numbers whose conversion to double precision would lose accuracy, see `type.convert`.
- **row.names**: a vector of row names. This can be a vector giving the actual row names, or a single number giving the column of the table which contains the row names, or character string giving the name of the table column containing the row names. If there is a header and the first row contains one fewer field than the number of columns, the first column in the input is used for the row names. Otherwise if `row.names` is missing, the rows are numbered. Using `row.names = NULL` forces row numbering.
- **col.names**: a vector of optional names for the variables. The default is to use "V" followed by the column number.
controls conversion of character variables (insofar as they are not converted to logical, numeric or complex) to factors, if not otherwise specified by colClasses. Its value is either a vector of logicals (values are recycled if necessary), or a vector of numeric or character indices which specify which columns should not be converted to factors.

Note: In releases prior to R 2.12.1, cells marked as being of character type were converted to logical, numeric or complex using type.convert as in read.table.

Note: to suppress all conversions including those of numeric columns, set colClasses = "character".

Note that as.is is specified per column (not per variable) and so includes the column of row names (if any) and any columns to be skipped.

a character vector of strings which are to be interpreted as NA values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields.

colonClasses character. A vector of classes to be assumed for the columns. Recycled as necessary, or if the character vector is named, unspecified values are taken to be NA.

Possible values are NA (when type.convert is used), "NULL" (when the column is skipped), one of the atomic vector classes (logical, integer, numeric, complex, character, raw), or "factor", "Date" or "POSIXt". Otherwise there needs to be an as method (from package methods) for conversion from "character" to the specified formal class.

Note that colClasses is specified per column (not per variable) and so includes the column of row names (if any).

the maximum number of rows to read in. Negative values are ignored.

the number of lines of the data file to skip before beginning to read data.

logical. If TRUE then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by make.names) so that they are, and also to ensure that there are no duplicates.

logical: if TRUE blank lines in the input are ignored.

 logical: should character vectors be converted to factors?

logical, indicating if the row and column interpretation should be transposed. Microsoft’s Excel has been known to produce (non-standard conforming) DIF files which would need transpose = TRUE to be read correctly.

character string: if non-empty declares the encoding used on a file (not a connection or clipboard) so the character data can be re-encoded. See the ‘Encoding’ section of the help for file, the ‘R Data Import/Export’ manual and ‘Note’.

A data frame (data.frame) containing a representation of the data in the file. Empty input is an error unless col.names is specified, when a 0-row data frame is returned: similarly giving just a header line if header = TRUE results in a 0-row data frame.
Note

The columns referred to in as.is and colClasses include the column of row names (if any). Less memory will be used if colClasses is specified as one of the six atomic vector classes.

Author(s)

R Core; transpose option by Christoph Buser, ETH Zurich

References

The DIF format specification can be found by searching on http://www.wotsit.org/; the optional header fields are ignored. See also https://en.wikipedia.org/wiki/Data_Interchange_Format.

The term is likely to lead to confusion: Windows will have a ‘Windows Data Interchange Format (DIF) data format’ as part of its WinFX system, which may or may not be compatible.

See Also

The R Data Import/Export manual.

Examples

```r
## read.DIF() may need transpose = TRUE for a file exported from Excel
udir <- system.file("misc", package = "utils")
dd <- read.DIF(file.path(udir, "exDIF.dif"), header = TRUE, transpose = TRUE)
dc <- read.csv(file.path(udir, "exDIF.csv"), header = TRUE)
stopifnot(identical(dd, dc), dim(dd) == c(4,2))
```

---

read.fortran  Read Fixed-Format Data in a Fortran-like Style

Description

Read fixed-format data files using Fortran-style format specifications.

Usage

```r
read.fortran(file, format, ..., as.is = TRUE, colClasses = NA)
```

Arguments

- **file**: File or connection to read from.
- **format**: Character vector or list of vectors. See ‘Details’ below.
- **...**: Other arguments for `read.fwf`.
- **as.is**: Keep characters as characters?
- **colClasses**: Variable classes to override defaults. See `read.table` for details.
Details

The format for a field is of one of the following forms: rFl.d, rDl.d, rXl, rAl, rIl, where l is the number of columns, d is the number of decimal places, and r is the number of repeats. F and D are numeric formats, A is character, I is integer, and X indicates columns to be skipped. The repeat code r and decimal place code d are always optional. The length code l is required except for X formats when r is present.

For a single-line record, format should be a character vector. For a multiline record it should be a list with a character vector for each line.

Skipped (X) columns are not passed to read.fwf, so colClasses, col.names, and similar arguments passed to read.fwf should not reference these columns.

Value

A data frame

Note

read.fortran does not use actual Fortran input routines, so the formats are at best rough approximations to the Fortran ones. In particular, specifying d > 0 in the F or D format will shift the decimal d places to the left, even if it is explicitly specified in the input file.

See Also

read.fwf, read.table, read.csv

Examples

ff <- tempfile()
cat(file = ff, "123456", "987654", sep = "\n")
read.fortran(ff, c("F2.1","F2.0","I2"))
read.fortran(ff, c("2F1.0","2X","2A1"))
unlink(ff)
cat(file = ff, "123456AB", "987654CD", sep = "\n")
read.fortran(ff, list(c("2F3.1","A2"), c("3I2","2X")))
unlink(ff)
# Note that the first number is read differently than Fortran would
# read it:
cat(file = ff, "12.3456", "1234567", sep = "\n")
read.fortran(ff, "F7.4")
unlink(ff)
Arguments

- **file**: the name of the file which the data are to be read from. Alternatively, `file` can be a `connection`, which will be opened if necessary, and if so closed at the end of the function call.
- **widths**: integer vector, giving the widths of the fixed-width fields (of one line), or list of integer vectors giving widths for multiline records.
- **header**: a logical value indicating whether the file contains the names of the variables as its first line. If present, the names must be delimited by `sep`.
- **sep**: character; the separator used internally; should be a character that does not occur in the file (except in the header).
- **skip**: number of initial lines to skip; see `read.table`.
- **row.names**: see `read.table`.
- **col.names**: see `read.table`.
- **n**: the maximum number of records (lines) to be read, defaulting to no limit.
- **buffersize**: Maximum number of lines to read at one time.
- **fileEncoding**: character string: if non-empty declares the encoding used on a file (not a connection) so the character data can be re-encoded. See the ‘Encoding’ section of the help for `file`, the ‘R Data Import/Export’ manual and ‘Note’.
- **...**: further arguments to be passed to `read.table`. Useful such arguments include `as.is`, `na.strings`, `colClasses` and `strip.white`.

Details

Multiline records are concatenated to a single line before processing. Fields that are of zero-width or are wholly beyond the end of the line in `file` are replaced by `NA`.

Negative-width fields are used to indicate columns to be skipped, e.g., `-5` to skip 5 columns. These fields are not seen by `read.table` and so should not be included in a `col.names` or `colClasses` argument (nor in the header line, if present).

Reducing the `buffersize` argument may reduce memory use when reading large files with long lines. Increasing `buffersize` may result in faster processing when enough memory is available.

Note that `read.fwf` (not `read.table`) reads the supplied file, so the latter's argument `encoding` will not be useful.

Value

A `data.frame` as produced by `read.table` which is called internally.

Author(s)

Brian Ripley for R version: originally in Perl by Kurt Hornik.

See Also

- `scan` and `read.table`.
- `read.fortran` for another style of fixed-format files.
Examples

```r
ff <- tempfile()
cat(file = ff, "123456", "987654", sep = "\n")
read.fwf(ff, widths = c(1,2,3)) #> 1 23 456 \ 9 87 654
read.fwf(ff, widths = c(1,-2,3)) #> 1 456 \ 9 654
unlink(ff)
cat(file = ff, "123", "987654", sep = "\n")
read.fwf(ff, widths = c(1,0, 2,3)) #> 1 NA 23 \ 9 NA 87 654
unlink(ff)
cat(file = ff, "123456", "987654", sep = "\n")
read.fwf(ff, widths = list(c(1,0, 2,3), c(2,2,2))) #> 1 NA 23 456 98 76 54
unlink(ff)
```

---

**read.socket**  
*Read from or Write to a Socket*

**Description**

`read.socket` reads a string from the specified socket, `write.socket` writes to the specified socket. There is very little error checking done by either.

**Usage**

```r
read.socket(socket, maxlen = 256L, loop = FALSE)
write.socket(socket, string)
```

**Arguments**

- `socket`: a socket object.
- `maxlen`: maximum length (in bytes) of string to read.
- `loop`: wait for ever if there is nothing to read?
- `string`: string to write to socket.

**Value**

- `read.socket` returns the string read as a length-one character vector.
- `write.socket` returns the number of bytes written.

**Author(s)**

Thomas Lumley

**See Also**

`close.socket`, `make.socket`
Examples

finger <- function(user, host = "localhost", port = 79, print = TRUE)
{
  if (!is.character(user))
    stop("user name must be a string")
  user <- paste(user, "\n")
  socket <- make.socket(host, port)
  on.exit(close.socket(socket))
  write.socket(socket, user)
  output <- character(0)
  repeat{
    ss <- read.socket(socket)
    if (ss == "") break
    output <- paste(output, ss)
  }
  close.socket(socket)
  if (print) cat(output)
  invisible(output)
}
## Not run:
finger("root") ## only works if your site provides a finger daemon
## End(Not run)

read.table

Data Input

Description

Reads a file in table format and creates a data frame from it, with cases corresponding to lines and variables to fields in the file.

Usage

read.table(file, header = FALSE, sep = "", quote = "\"",
            dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"),
            row.names, col.names, as.is = !stringsAsFactors, tryLogical = TRUE,
            na.strings = "NA", colClasses = NA, nrows = -1,
            skip = 0, check.names = TRUE, fill = !blank.lines.skip,
            strip.white = FALSE, blank.lines.skip = TRUE,
            comment.char = ":",
            allowEscapes = FALSE, flush = FALSE,
            stringsAsFactors = FALSE,
            fileEncoding = "", encoding = "unknown", text, skipNul = FALSE)

read.csv(file, header = TRUE, sep = ",", quote = "\"",
          dec = ".", fill = TRUE, comment.char = "", ...)

read.csv2(file, header = TRUE, sep = ";", quote = "\"",
           dec = ",", fill = TRUE, comment.char = "", ...)

read.delim(file, header = TRUE, sep = "\t", quote = "\"",
           dec = ".", fill = TRUE, comment.char = "", ...)
read.table

read.delim2(file, header = TRUE, sep = "\t", quote = "\"", dec = ",", fill = TRUE, comment.char = ",", ...)  

**Arguments**

- **file**  
  The name of the file which the data are to be read from. Each row of the table appears as one line of the file. If it does not contain an absolute path, the file name is relative to the current working directory, getwd(). Tilde-expansion is performed where supported. This can be a compressed file (see file). Alternatively, file can be a readable text-mode connection (which will be opened for reading if necessary, and if so closed (and hence destroyed) at the end of the function call). If stdin() is used, the prompts for lines may be somewhat confusing. Terminate input with a blank line or an EOF signal, Ctrl-D on Unix and Ctrl-Z on Windows. Any pushback on stdin() will be cleared before return.

  file can also be a complete URL. (For the supported URL schemes, see the 'URLs' section of the help for url.)

- **header**  
  A logical value indicating whether the file contains the names of the variables as its first line. If missing, the value is determined from the file format: header is set to TRUE if and only if the first row contains one fewer field than the number of columns.

- **sep**  
  The field separator character. Values on each line of the file are separated by this character. If sep = "" (the default for read.table) the separator is ‘white space’, that is one or more spaces, tabs, newlines or carriage returns.

- **quote**  
  The set of quoting characters. To disable quoting altogether, use quote = "". See scan for the behaviour on quotes embedded in quotes. Quoting is only considered for columns read as character, which is all of them unless colClasses is specified.

- **dec**  
  The character used in the file for decimal points.

- **row.names**  
  A vector of row names. This can be a vector giving the actual row names, or a single number giving the column of the table which contains the row names, or character string giving the name of the table column containing the row names.

  If there is a header and the first row contains one fewer field than the number of columns, the first column in the input is used for the row names. Otherwise if row.names is missing, the rows are numbered.

  Using row.names = NULL forces row numbering. Missing or NULL row.names generate row names that are considered to be ‘automatic’ (and not preserved by as.matrix).

- **col.names**  
  A vector of optional names for the variables. The default is to use "V" followed by the column number.

- **as.is**  
  Controls conversion of character variables (insofar as they are not converted to logical, numeric or complex) to factors, if not otherwise specified by colClasses. Its value is either a vector of logicals (values are recycled if necessary), or a vector of numeric or character indices which specify which columns should not be converted to factors.
Note: to suppress all conversions including those of numeric columns, set `colClasses = "character"`.

Note that `as.is` is specified per column (not per variable) and so includes the column of row names (if any) and any columns to be skipped.

`tryLogical` a logical determining if columns consisting entirely of "F", "T", "FALSE", and "TRUE" should be converted to logical: passed to `type.convert`, true by default.

`na.strings` a character vector of strings which are to be interpreted as NA values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields. Note that the test happens after white space is stripped from the input, so `na.strings` values may need their own white space stripped in advance.

`colClasses` character. A vector of classes to be assumed for the columns. If unnamed, recycled as necessary. If named, names are matched with unspecified values being taken to be NA.

Possible values are NA (the default, when `type.convert` is used), "NULL" (when the column is skipped), one of the atomic vector classes (logical, integer, numeric, complex, character, raw), or "factor", "Date" or "POSIXct". Otherwise there needs to be an as method (from package `methods`) for conversion from "character" to the specified formal class.

Note that `colClasses` is specified per column (not per variable) and so includes the column of row names (if any).

`nrows` integer: the maximum number of rows to read in. Negative and other invalid values are ignored.

`skip` integer: the number of lines of the data file to skip before beginning to read data.

`check.names` logical. If TRUE then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by `make.names`) so that they are, and also to ensure that there are no duplicates.

`fill` logical. If TRUE then in case the rows have unequal length, blank fields are implicitly added. See ‘Details’.

`strip.white` logical. Used only when `sep` has been specified, and allows the stripping of leading and trailing white space from unquoted character fields (numeric fields are always stripped). See `scan` for further details (including the exact meaning of ‘white space’), remembering that the columns may include the row names.

`blank.lines.skip` logical: if TRUE blank lines in the input are ignored.

`comment.char` character: a character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether.

`allowEscapes` logical. Should C-style escapes such as `\n` be processed or read verbatim (the default)? Note that if not within quotes these could be interpreted as a delimiter (but not as a comment character). For more details see `scan`.

`flush` logical: if TRUE, `scan` will flush to the end of the line after reading the last of the fields requested. This allows putting comments after the last field.

`stringsAsFactors` logical: should character vectors be converted to factors? Note that this is overridden by `as.is` and `colClasses`, both of which allow finer control.
### read.table

**fileEncoding**  character string: if non-empty declares the encoding used on a file (not a connection) so the character data can be re-encoded. See the ‘Encoding’ section of the help for file, the ‘R Data Import/Export’ manual and ‘Note’.

**encoding**  encoding to be assumed for input strings. It is used to mark character strings as known to be in Latin-1 or UTF-8 (see Encoding): it is not used to re-encode the input, but allows R to handle encoded strings in their native encoding (if one of those two). See ‘Value’ and ‘Note’.

**text**  character string: if file is not supplied and this is, then data are read from the value of text via a text connection. Notice that a literal string can be used to include (small) data sets within R code.

**skipNul**  logical: should nuls be skipped?

...  Further arguments to be passed to read.table.

### Details

This function is the principal means of reading tabular data into R.

Unless colClasses is specified, all columns are read as character columns and then converted using type.convert to logical, integer, numeric, complex or (depending on as.is) factor as appropriate. Quotes are (by default) interpreted in all fields, so a column of values like "42" will result in an integer column.

A field or line is ‘blank’ if it contains nothing (except whitespace if no separator is specified) before a comment character or the end of the field or line.

If row.names is not specified and the header line has one less entry than the number of columns, the first column is taken to be the row names. This allows data frames to be read in from the format in which they are printed. If row.names is specified and does not refer to the first column, that column is discarded from such files.

The number of data columns is determined by looking at the first five lines of input (or the whole input if it has less than five lines), or from the length of col.names if it is specified and is longer. This could conceivably be wrong if fill or blank.lines.skip are true, so specify col.names if necessary (as in the ‘Examples’).

read.csv and read.csv2 are identical to read.table except for the defaults. They are intended for reading ‘comma separated value’ files (`.csv`) or (read.csv2) the variant used in countries that use a comma as decimal point and a semicolon as field separator. Similarly, read.delim and read.delim2 are for reading delimited files, defaulting to the TAB character for the delimiter. Notice that header = TRUE and fill = TRUE in these variants, and that the comment character is disabled.

The rest of the line after a comment character is skipped; quotes are not processed in comments. Complete comment lines are allowed provided blank.lines.skip = TRUE; however, comment lines prior to the header must have the comment character in the first non-blank column.

Quoted fields with embedded newlines are supported except after a comment character. Embedded nuls are unsupported: skipping them (with skipNul = TRUE) may work.

### Value

A data frame (data.frame) containing a representation of the data in the file.

Empty input is an error unless col.names is specified, when a 0-row data frame is returned: similarly giving just a header line if header = TRUE results in a 0-row data frame. Note that in either case the columns will be logical unless colClasses was supplied.

Character strings in the result (including factor levels) will have a declared encoding if encoding is "latin1" or "UTF-8".
CSV files

See the help on *write.csv* for the various conventions for .csv files. The commonest form of CSV file with row names needs to be read with *read.csv(..., row.names = 1)* to use the names in the first column of the file as row names.

Memory usage

These functions can use a surprising amount of memory when reading large files. There is extensive discussion in the ‘R Data Import/Export’ manual, supplementing the notes here.

Less memory will be used if *colClasses* is specified as one of the six atomic vector classes. This can be particularly so when reading a column that takes many distinct numeric values, as storing each distinct value as a character string can take up to 14 times as much memory as storing it as an integer.

Using *nrows*, even as a mild over-estimate, will help memory usage.

Using *comment.char = ""* will be appreciably faster than the *read.table* default.

*read.table* is not the right tool for reading large matrices, especially those with many columns: it is designed to read *data frames* which may have columns of very different classes. Use *scan* instead for matrices.

Note

The columns referred to in *as.is* and *colClasses* include the column of row names (if any).

There are two approaches for reading input that is not in the local encoding. If the input is known to be UTF-8 or Latin1, use the *encoding* argument to declare that. If the input is in some other encoding, then it may be translated on input. The *fileEncoding* argument achieves this by setting up a connection to do the re-encoding into the current locale. Note that on Windows or other systems not running in a UTF-8 locale, this may not be possible.

References


See Also

The ‘R Data Import/Export’ manual.

*scan*, *type.convert*, *read.fwf* for reading fixed width formatted input; *write.table*; *data.frame*.

*count.fields* can be useful to determine problems with reading files which result in reports of incorrect record lengths (see the ‘Examples’ below).

[https://www.rfc-editor.org/rfc/rfc/rfc4180](https://www.rfc-editor.org/rfc/rfc/rfc4180) for the IANA definition of CSV files (which requires comma as separator and CRLF line endings).

Examples

```r
## using count.fields to handle unknown maximum number of fields
## when fill = TRUE
test1 <- c(1:5, "6,7", "8,9,10")
tf <- tempfile()
writeLines(test1, tf)
```
### Description

On Windows, read values of keys in the Windows Registry, and optionally whole hives.

### Usage

```r
readRegistry(key, hive = c("HLM", "HCR", "HCU", "HU", "HCC", "HPD"),
             maxdepth = 1, view = c("default", "32-bit", "64-bit"))
```

### Arguments

- **key**: character string, the path to the key in the Windows Registry.
- **hive**: The ‘hive’ containing the key. The abbreviations are for `HKEY_LOCAL_MACHINE`, `HKEY_CLASSES_ROOT`, `HKEY_CURRENT_USER`, `HKEY_USERS`, `HKEY_CURRENT_CONFIG` and `HKEY_PERFORMANCE_DATA`.
- **maxdepth**: How far to recurse into the subkeys of the key. By default only the values of the key and the names of subkeys are returned.
- **view**: On 64-bit Windows, the view of the Registry to be used: see ‘Details’.

### Details

Registry access is done using the security settings of the current R session: this means that some Registry keys may not be accessible even if they exist. This may result in NULL values in the object returned, and, possibly, empty element names.


### Value

A named list of values and subkeys (which may themselves be named lists). The default value (if any) precedes named values which precede subkeys, and both the latter sets are sorted alphabetically.
Note
This is only available on Windows.

Examples

```r
if(.Platform$OS.type == "windows") withAutoprint({
  ## only in HLM if set in an admin-mode install.
  try(readRegistry("SOFTWARE\R-core", maxdepth = 3))

  gmt <- file.path("SOFTWARE", "Microsoft", "Windows NT",
                   "CurrentVersion", "Time Zones",
                   "GMT Standard Time", fsep = "\")
  readRegistry(gmt, "HLM")
})
## Not run: ## on a 64-bit R need this to find 32-bit JAGS
readRegistry("SOFTWARE\JAGS", maxdepth = 3, view = "32")
## See if there is a 64-bit user install
readRegistry("SOFTWARE\R-core\R64", "HCU", maxdepth = 2)
## End(Not run)
```

---

recover  Browsing after an Error

Description

This function allows the user to browse directly on any of the currently active function calls, and is suitable as an error option. The expression `options(error = recover)` will make this the error option.

Usage

```r
recover()
```

Details

When called, `recover` prints the list of current calls, and prompts the user to select one of them. The standard R `browser` is then invoked from the corresponding environment; the user can type ordinary R language expressions to be evaluated in that environment.

When finished browsing in this call, type `c` to return to `recover` from the browser. Type another frame number to browse some more, or type `0` to exit `recover`.

The use of `recover` largely supersedes `dump.frames` as an error option, unless you really want to wait to look at the error. If `recover` is called in non-interactive mode, it behaves like `dump.frames`. For computations involving large amounts of data, `recover` has the advantage that it does not need to copy out all the environments in order to browse in them. If you do decide to quit interactive debugging, call `dump.frames` directly while browsing in any frame (see the examples).

Value

Nothing useful is returned. However, you can invoke `recover` directly from a function, rather than through the error option shown in the examples. In this case, execution continues after you type `0` to exit `recover`. 
Compatibility Note

The \texttt{R} \textit{recover} function can be used in the same way as the \texttt{S} function of the same name; therefore, the error option shown is a compatible way to specify the error action. However, the actual functions are essentially unrelated and interact quite differently with the user. The navigating commands \texttt{up} and \texttt{down} do not exist in the \texttt{R} version; instead, exit the browser and select another frame.

References

See the compatibility note above, however.

See Also

\texttt{browser} for details about the interactive computations; \texttt{options} for setting the error option; \texttt{dump.frames} to save the current environments for later debugging.

Examples

```r
## Not run:
options(error = recover) # setting the error option

### Example of interaction

> myFit <- lm(y ~ x, data = xy, weights = w)
Error in lm.wfit(x, y, w, offset = offset, ...) :
  missing or negative weights not allowed

Enter a frame number, or 0 to exit
1:lm(y ~ x, data = xy, weights = w)
2:lm.wfit(x, y, w, offset = offset, ...) 
Selection: 2
Called from: eval(expr, envir, enclos)
Browse[1]> objects() # all the objects in this frame
[1] "method" "n" "my" "offset" "tol" "w"
[7] "x" "y"
Browse[1]> w
[1] -0.5013844 1.3112515 0.2939348 -0.8983705 -0.1538642
[6] -0.9772989 0.7888790 -0.1919154 -0.3026882
Browse[1]> dump.frames() # save for offline debugging
Browse[1]> c # exit the browser

Enter a frame number, or 0 to exit
1:lm(y ~ x, data = xy, weights = w)
2:lm.wfit(x, y, w, offset = offset, ...) 
Selection: 0 # exit recover
>
```

## End(Not run)
relist

Allow Re-Listing an unlist()ed Object

Description

relist() is an S3 generic function with a few methods in order to allow easy inversion of unlist(obj) when that is used with an object obj of (S3) class "relistable".

Usage

relist(flesh, skeleton)
## Default S3 method:
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'factor'
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'list'
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'matrix'
relist(flesh, skeleton = attr(flesh, "skeleton"))

as.relistable(x)
is.relistable(x)

## S3 method for class 'relistable'
unlist(x, recursive = TRUE, use.names = TRUE)

Arguments

deflesh
a vector to be relisted
defskeleton
a list, the structure of which determines the structure of the result
defx
an R object, typically a list (or vector).
defrecursive
tical. Should unlisting be applied to list components of x?
defuse.names
logical. Should names be preserved?

Details

Some functions need many parameters, which are most easily represented in complex structures, e.g., nested lists. Unfortunately, many mathematical functions in R, including optim and nlm can only operate on functions whose domain is a vector. R has unlist() to convert nested list objects into a vector representation. relist(), its methods and the functionality mentioned here provide the inverse operation to convert vectors back to the convenient structural representation. This allows structured functions (such as optim()) to have simple mathematical interfaces.

For example, a likelihood function for a multivariate normal model needs a variance-covariance matrix and a mean vector. It would be most convenient to represent it as a list containing a vector and a matrix. A typical parameter might look like

list(mean = c(0, 1), vcov = cbind(c(1, 1), c(1, 0))).

However, optim cannot operate on functions that take lists as input; it only likes numeric vectors. The solution is conversion. Given a function mvdnorm(x, mean, vcov, log = FALSE) which computes the required probability density, then
relist takes two parameters: skeleton and flesh. Skeleton is a sample object that has the right shape but the wrong content. Flesh is a vector with the right content but the wrong shape. Invoking

relist(flesh, skeleton)

will put the content of flesh on the skeleton. You don’t need to specify skeleton explicitly if the skeleton is stored as an attribute inside flesh. In particular, if flesh was created from some object obj with unlist(as.relistable(obj)) then the skeleton attribute is automatically set. (Note that this does not apply to the example here, as optim is creating a new vector to pass to ll and not its par argument.)

As long as skeleton has the right shape, it should be an inverse of unlist. These equalities hold:

relist(unlist(x), x) == x
unlist(relist(y, skeleton)) == y

x <- as.relistable(x)
relist(unlist(x)) == x

Note however that the relisted object might not be identical to the skeleton because of implicit coercions performed during the unlisting step. All elements of the relisted objects have the same type as the unlisted object. NULL values are coerced to empty vectors of that type.

Value

an object of (S3) class "relistable" (and "list").

Author(s)

R Core, based on a code proposal by Andrew Clausen.

See Also

unlist

Examples

ir <- list(mean = c(0, 1), vcov = cbind(c(1, 1), c(1, 0)))
initial.param <- as.relistable(ir)
ll <- function(param.vector)
{
  param <- relist(param.vector, skeleton = ir)
  -sum(mvdnorm(x, mean = param$mean, vcov = param$vcov,
              log = TRUE))
}

optim(unlist(initial.param), ll)

relist takes two parameters: skeleton and flesh. Skeleton is a sample object that has the right shape but the wrong content. Flesh is a vector with the right content but the wrong shape. Invoking

relist(flesh, skeleton)

will put the content of flesh on the skeleton. You don’t need to specify skeleton explicitly if the skeleton is stored as an attribute inside flesh. In particular, if flesh was created from some object obj with unlist(as.relistable(obj)) then the skeleton attribute is automatically set. (Note that this does not apply to the example here, as optim is creating a new vector to pass to ll and not its par argument.)

As long as skeleton has the right shape, it should be an inverse of unlist. These equalities hold:

relist(unlist(x), x) == x
unlist(relist(y, skeleton)) == y

x <- as.relistable(x)
relist(unlist(x)) == x

Note however that the relisted object might not be identical to the skeleton because of implicit coercions performed during the unlisting step. All elements of the relisted objects have the same type as the unlisted object. NULL values are coerced to empty vectors of that type.

Value

an object of (S3) class "relistable" (and "list").

Author(s)

R Core, based on a code proposal by Andrew Clausen.

See Also

unlist

Examples

ir <- list(mean = c(0, 1), vcov = cbind(c(1, 1), c(1, 0)))
initial.param <- as.relistable(ir)
ul <- unlist(initial.param)
relist(ul)
stopifnot(identical(relist(ul), initial.param))
**REMOVE**  
*Remove Add-on Packages*

**Description**
Utility for removing add-on packages.

**Usage**
```r
R CMD REMOVE [options] [-l lib] pkgs
```

**Arguments**
- `pkgs`  
a space-separated list with the names of the packages to be removed.
- `lib`  
the path name of the R library tree to remove from. May be absolute or relative. Also accepted in the form `--library=lib`.
- `options`  
further options for help or version.

**Details**
If used as `R CMD REMOVE pkgs` without explicitly specifying `lib`, packages are removed from the library tree rooted at the first directory in the library path which would be used by R run in the current environment.

To remove from the library tree `lib` instead of the default one, use `R CMD REMOVE -l lib pkgs`.

Use `R CMD REMOVE --help` for more usage information.

**Note**
Some binary distributions of R have REMOVE in a separate bundle, e.g. an R-devel RPM.

**See Also**
- INSTALL
- remove.packages

---

**remove.packages**  
*Remove Installed Packages*

**Description**
Removes installed packages/bundles and updates index information as necessary.

**Usage**
```r
remove.packages(pkgs, lib)
```

**Arguments**
- `pkgs`  
a character vector with the names of the packages to be removed.
- `lib`  
a character vector giving the library directories to remove the packages from. If missing, defaults to the first element in `.libPaths()`.
removeSource

Remove Stored Source from a Function or Language Object

Description

When options("keep.source") is TRUE, a copy of the original source code to a function is stored with it. Similarly, parse() may keep formatted source for an expression. Such source reference attributes are removed from the object by removeSource().

Usage

removeSource(fn)

Arguments

fn a function or another language object (fulfilling is.language) from which to remove the source.

Details

This removes the "srcref" and related attributes, via recursive cleaning of body(fn) in the case of a function or the recursive language parts, otherwise.

Value

A copy of the fn object with the source removed.

See Also

is.language about language objects.
srcref for a description of source reference records, deparse for a description of how functions are deparsed.

Examples

## to make this act independently of the global 'options()' setting:
op <- options(keep.source = TRUE)
fn <- function(x) {
  x + 1 # A comment, kept as part of the source
}
fn
names(attributes(fn)) # "srcref" (only)
names(attributes(body(fn))) # "srcref" "srcfile" "wholeSrcref"
f2 <- removeSource(fn)
f2
stopifnot(length(attributes(fn)) > 0,
is.null(attributes(f2)),
is.null(attributes(body(f2))))
## Source attribute of parse()d expressions, have {"srcref", "srcfile", "wholeSrcref"}:
E <- parse(text ="a <- x^y # power") ; names(attributes(E ))
E. <- removeSource(E) ; names(attributes(E.))
stopifnot(length(attributes(E )) > 0,
is.null(attributes(E.)))
options(op) # reset to previous state

---

**RHOME**

**R Home Directory**

**Description**

Returns the location of the R home directory, which is the root of the installed R tree.

**Usage**

```
R RHOME
```

---

**roman**

**Roman Numerals**

**Description**

Simple manipulation of (a small set of) integer numbers as roman numerals.

**Usage**

```
as.roman(x)
.romans
r1 + r2
r1 <= r2
max(r1)
sum(r2)
```

**Arguments**

- **x** a numeric or character vector of arabic or roman numerals.
- **r1, r2** a roman number vector, i.e., of `class "roman"`. 
Details

\texttt{as.roman} creates objects of class "roman" which are internally represented as integers, and have suitable methods for printing, formatting, subsetting, coercion, etc, see \texttt{methods(class = "roman")}.

Arithmetic ("Arith"), Comparison ("Compare") and ("Logic"), i.e., all "Ops" group operations work as for regular numbers via R’s integer functionality.

Only numbers between 1 and 3899 have a unique representation as roman numbers, and hence others result in \texttt{as.roman(NA)}.

..romans is the basic dictionary, a named \texttt{character} vector.

References


Examples

## First five roman 'numbers'.
\begin{verbatim}
(y <- as.roman(1 : 5))
## Middle one.
y[3]
## Current year as a roman number.
(y <- as.roman(format(Sys.Date(), "%Y")))
## Today, and 10, 20, 30, and 100 years ago ...
y - 10*c(0:3,10)
## mixture of arabic and roman numbers :
\end{verbatim}

\begin{verbatim}
as.roman(c(NA, 1:3, ",", strrep("I", 1:6))) # + NA with a warning for "IIIIII"
cc <- c(NA, 1:3, strrep("I", 0:5))
(rc <- as.roman(cc)) # two NAs: 0 is not "roman"
(ic <- as.integer(rc)) # works automatically [without an explicit method]
\end{verbatim}

\begin{verbatim}
rNA <- as.roman(NA)
## simple consistency checks -- arithmetic when result is in \{1,2,...,3899\} :
stopifnot(identical(rc, as.roman(rc)), # as.roman(.) is "idempotent"
 identical(rc + rc + (3*rc), rc*5),
 identical(ic, c(NA, 1:3, NA, 1:5)),
 identical(as.integer(5*rc), 5L*ic),
 identical(as.numeric(rc), as.numeric(ic)),
 identical(rc[1], rNA),
 identical(as.roman(0), rNA),
 identical(as.roman(NA_character_), rNA),
 identical(as.list(rc), as.list(ic)))
\end{verbatim}

## Non-Arithmetic 'Ops':
\begin{verbatim}
stopifnot(exprs = {

  # Comparisons :
  identical(ic < 1:5, rc < 1:5)
  identical(ic < 1:5, rc < as.roman(1:5))

  # Logic [integers |- logical] :
  identical(rc & TRUE , ic & TRUE)
  identical(rc & FALSE, ic & FALSE)
  identical(rc | FALSE, ic | FALSE)
  identical(rc | NA , ic | NA)
})
\end{verbatim}
Rprof

Enable Profiling of R's Execution

Description

Enable or disable profiling of the execution of \texttt{R} expressions.

Usage

\begin{verbatim}
Rprof(filename = "Rprof.out", append = FALSE, interval = 0.02,
memory.profiling = FALSE, gc.profiling = FALSE,
line.profiling = FALSE, filter.callframes = FALSE,
umfiles = 100L, bufsize = 10000L)
\end{verbatim}

Arguments

- \texttt{filename} The file to be used for recording the profiling results. Set to \texttt{NULL} or "" to disable profiling.
- \texttt{append} logical: should the file be over-written or appended to?
- \texttt{interval} real: time interval between samples.
- \texttt{memory.profiling} logical: write memory use information to the file?
- \texttt{gc.profiling} logical: record whether GC is running?
- \texttt{line.profiling} logical: write line locations to the file?
- \texttt{filter.callframes} logical: filter out intervening call frames of the call tree. See the filtering out call frames section.
- \texttt{numfiles, bufsize} integers: line profiling memory allocation

Details

Enabling profiling automatically disables any existing profiling to another or the same file.

Profiling works by writing out the call stack every \texttt{interval} seconds, to the file specified. Either the \texttt{summaryRprof} function or the wrapper script \texttt{R CMD Rprof} can be used to process the output file to produce a summary of the usage; use \texttt{R CMD Rprof --help} for usage information.

How time is measured varies by platform:
On Windows: Exactly what the time interval measures is subtle: it is time that the \texttt{R} process is running and executing an \texttt{R} command. It is not however just CPU time, for if \texttt{readline()} is waiting for input, that counts (on Windows, but not on a Unix-alike).

Note that the timing interval cannot be too small, for the time spent in each profiling step is added to the interval. What is feasible is machine-dependent, but 10ms seemed as small as advisable on a 1GHz machine.

On Unix-alikes it is the CPU time of the \texttt{R} process, so for example excludes time when \texttt{R} is waiting for input or for processes run by \texttt{system} to return.

Note that the timing interval cannot usefully be too small: once the timer goes off, the information is not recorded until the next timing click (probably in the range 1–10 ms).

On Linux, the interval needs to be at least 10ms, on all other platforms at least 1ms. Shorter intervals will be rounded up with a warning.

Functions will only be recorded in the profile log if they put a context on the call stack (see \texttt{sys.calls}). Some primitive functions do not do so: specifically those which are of type "special" (see the ‘R Internals’ manual for more details).

Individual statements will be recorded in the profile log if \texttt{line.profiling} is \texttt{TRUE}, and if the code being executed was parsed with source references. See \texttt{parse} for a discussion of source references. By default the statement locations are not shown in \texttt{summaryRprof}, but see that help page for options to enable the display.

Filtering Out Call Frames

Lazy evaluation makes the call stack more complex because intervening call frames are created between the time arguments are applied to a function, and the time they are effectively evaluated. When the call stack is represented as a tree, these intervening frames appear as sibling nodes. For instance, evaluating \texttt{try(EXPR)} produces the following call tree, at the time \texttt{EXPR} gets evaluated:

```
1. +--\texttt{base::try(EXPR)}
  2. | \--\texttt{base::tryCatch(...)}
  3. |   \--\texttt{base::tryCatchList(expr, classes, parentenv, handlers)}
  4. |     \--\texttt{base::tryCatchOne(expr, names, parentenv, handlers[[1L]])}
  5. |     \--\texttt{base::doTryCatch(return(expr), name, parentenv, handler)}
  6. \--\texttt{EXPR}
```

Lines 2 to 5 are intervening call frames, the last of which finally triggered evaluation of \texttt{EXPR}. Setting \texttt{filter.callframes} to \texttt{TRUE} simplifies the profiler output by removing all sibling nodes of intervening frames.

The same kind of call frame filtering is applied with \texttt{eval()} frames. When you call \texttt{eval()}, two frames are pushed on the stack to ensure a continuity between frames. Say we have these definitions:

```r
calling <- function() evaluator(quote(called()), environment())
evaluator <- function(expr, env) eval(expr, env)
called <- function() \texttt{EXPR()}
```

calling() calls called() in its own environment, via eval(). The latter is called indirectly through evaluator(). The net effect of this code is identical to just calling called() directly, without the intermediaries. However, the full call stack looks like this:

```
1. calling()
2. \--evaluator(quote(called()), environment())
```
### Rprof

3. `\-base::eval(expr, env)`
4. `\-base::eval(expr, env)`
5. `\-called()`
6. `\-EXPR()`

When call frame filtering is turned on, the true calling environment of `called()` is looked up, and the filtered call stack looks like this:

1. `calling()`
5. `\-called()`
6. `\-EXPR()`

If the calling environment is not on the stack, the function called by `eval()` becomes a root node. Say we have:

```r
calling <- function() evaluator(quote(called()), new.env())
```

With call frame filtering we then get the following filtered call stack:

5. `called()`
6. `\-EXPR()`

#### Note

**On Unix-alikes:** Profiling is not available on all platforms. By default, support for profiling is compiled in if possible – configure R with `-disable-R-profiling` to change this. As R profiling uses the same mechanisms as C profiling, the two cannot be used together, so do not use `Rprof` in an executable built for C-level profiling.

**On Windows:** `filename` can be a UTF-8-encoded filepath that cannot be translated to the current locale.

The profiler interrupts R asynchronously, and it cannot allocate memory to store results as it runs. This affects line profiling, which needs to store an unknown number of file pathnames. The `numfiles` and `bufsize` arguments control the size of pre-allocated buffers to hold these results: the former counts the maximum number of paths, the latter counts the numbers of bytes in them. If the profiler runs out of space it will skip recording the line information for new files, and issue a warning when `Rprof(NULL)` is called to finish profiling.

#### See Also

The chapter on “Tidying and profiling R code” in ‘Writing R Extensions’ (see the ‘doc/manual’ subdirectory of the R source tree).

`summaryRprof` to analyse the output file.

`tracemem, Rprofmem` for other ways to track memory use.

#### Examples

```r
## Not run: Rprof()
## some code to be profiled
Rprof(NULL)
## some code NOT to be profiled
Rprof(append = TRUE)
## some code to be profiled
```
Rprofmem

Enable Profiling of R's Memory Use

Description

Enable or disable reporting of memory allocation in R.

Usage

Rprofmem(filename = "Rprofmem.out", append = FALSE, threshold = 0)

Arguments

filename
The file to be used for recording the memory allocations. Set to NULL or "" to disable reporting.

append
logical: should the file be over-written or appended to?

threshold
numeric: allocations on R’s “large vector” heap larger than this number of bytes will be reported.

Details

Enabling profiling automatically disables any existing profiling to another or the same file.

Profiling writes the call stack to the specified file every time malloc is called to allocate a large vector object or to allocate a page of memory for small objects. The size of a page of memory and the size above which malloc is used for vectors are compile-time constants, by default 2000 and 128 bytes respectively.

The profiler tracks allocations, some of which will be to previously used memory and will not increase the total memory use of R.

Value

None

Note

The memory profiler slows down R even when not in use, and so is a compile-time option. (It is enabled in a standard Windows build of R.)

The memory profiler can be used at the same time as other R and C profilers.

See Also

The R sampling profiler, Rprof also collects memory information.

tracemem traces duplications of specific objects.

The “Writing R Extensions” manual section on “Tidying and profiling R code”
### Examples

```r
## Not run:
## not supported unless R is compiled to support it.
Rprofmem("Rprofmem.out", threshold = 1000)
example(glm)
Rprofmem(NULL)
noquote(readLines("Rprofmem.out", n = 5))

## End(Not run)
```

### Description

This is an alternative front end for use in ‘#!’ scripts and other scripting applications.

### Usage

```r
Rscript [options] file [args]
Rscript [options] -e expr [-e expr2 ...] [args]
```

### Arguments

- **options**: a list of options, all beginning with ‘-’.
- **expr, expr2**: R expression(s), properly quoted.
- **file**: the name of a file containing R commands. ‘-’ indicates ‘stdin’.
- **args**: arguments to be passed to the script in file or expressions supplied via ‘-e’.

### Details

Rscript --help gives details of usage, and Rscript --version gives the version of Rscript.

Other invocations invoke the R front-end with selected options. This front-end is convenient for writing ‘#!’ scripts since it is an executable and takes file directly as an argument. Options ‘--no-echo --no-restore’ are always supplied; these imply ‘--no-save’. Arguments that contain spaces cannot be specified directly on the ‘#!’ line, because spaces and tabs are interpreted as delimiters and there is no way to protect them from this interpretation on the ‘#!’ line. (The standard Windows command line has no concept of ‘#!’ scripts, but Cygwin shells do.)

Either one or more ‘-e’ options or file should be supplied. When using ‘-e’ options be aware of the quoting rules in the shell used: see the examples.

The prescribed order of arguments is important: e.g. ‘--verbose’ specified after ‘-e’ will be part of args and passed to the expression; the same will happen to ‘-e’ specified after file.

Additional options accepted as part of options (before file or ‘-e’) are

- ‘--verbose’ gives details of what Rscript is doing.
- ‘--default-packages=list’ where list is a comma-separated list of package names or NULL. Sets the environment variable R_DEFAULT_PACKAGES which determines the packages loaded on startup.
Spaces are allowed in `expr` and `file` (but will need to be protected from the shell in use, if any, for example by enclosing the argument in quotes).

If ‘`--default-packages`’ is not used, then `Rscript` checks the environment variable `R_SCRIPT_DEFAULT_PACKAGES`. If this is set, then it takes precedence over `R_DEFAULT_PACKAGES`.

Normally the version of `R` is determined at installation, but this can be overridden by setting the environment variable `RHOME`.

`stdin()` refers to the input file, and `file("stdin")` to the stdin file stream of the process.

**Note**

`Rscript` is only supported on systems with the `execv` system call.

**Examples**

```r
## Not run:
Rscript -e 'date()' -e 'format(Sys.time(), "%a %b %d %X %Y")'

# Get the same initial packages in the same order as default R:
Rscript --default-packages=methods,datasets,utils,grDevices,graphics,stats -e 'sessionInfo()

## example #! script for a Unix-alike
## (arguments given on the #! line end up as [options] to Rscript, while
## arguments passed to the #! script end up as [args], so available to
## commandArgs())
#! /path/to/Rscript --vanilla --default-packages=utils
args <- commandArgs(TRUE)
res <- try(install.packages(args))
if(inherits(res, "try-error")) q(status=1) else q()

## End(Not run)
```

---

**RShowDoc**

*Show R Manuals and Other Documentation*

**Description**

Utility function to find and display **R** documentation.

**Usage**

```r
RShowDoc(what, type = c("pdf", "html", "txt"), package)
```

**Arguments**

- `what` a character string: see ‘Details’.
- `type` an optional character string giving the preferred format. Can be abbreviated.
- `package` an optional character string specifying the name of a package within which to look for documentation.
Details

what can specify one of several different sources of documentation, including the R manuals
(R-admin, R-data, R-exts, R-intro, R-ints, R-lang), NEWS, COPYING (the GPL licence), any of
the licenses in ‘share/licenses’, FAQ (also available as R-FAQ), and the files in ‘R_HOME/doc’.

Only on Windows, the R for Windows FAQ is specified by rw-FAQ.

If package is supplied, documentation is looked for in the ‘doc’ and top-level directories of an
installed package of that name.

If what is missing a brief usage message is printed.

The documentation types are tried in turn starting with the first specified in type (or "pdf" if none
is specified).

Value

A invisible character string given the path to the file found.

See Also

For displaying regular help files, help (or ?) and help.start.

For type = "txt", file.show is used. vignettes are nicely viewed via RShowDoc(*, package=).

Examples

RShowDoc("R-lang")
RShowDoc("FAQ", type = "html")
RShowDoc("frame", package = "grid")
RShowDoc("changes.txt", package = "grid")
RShowDoc("NEWS", package = "MASS")

RSiteSearch

Search for Key Words or Phrases in Documentation

Description

Search for key words or phrases in various documentation, such as R manuals, help pages of base
and CRAN packages, vignettes, task views and others, using the search engine at https://search.
r-project.org and view them in a web browser.

Usage

RSiteSearch(string,
    restrict = c("functions", "descriptions", "news", "Rfunctions",
        "Rmanuals", "READMEs", "views", "vignettes"),
    format,
    sortby = c("score", "date:late", "date:early", "subject",
        "subject:descending", "size", "size:descending"),
    matchesPerPage = 20,
    words = c("all", "any"))
RSiteSearch

Arguments

string  A character string specifying word(s) or phrase(s) to search. If the words are to be searched as one entity, enclose them either in (escaped) quotes or in braces.
restrict  A character vector, typically of length greater than one. Values can be abbreviated. Possible areas to search in: functions for help pages of CRAN packages, descriptions for extended descriptions of CRAN packages, news for package NEWS, Rfunctions for help pages of R base packages, R manuals for R manuals, READMEs for README files of CRAN packages, views for task views, vignettes for package vignettes.
format  deprecated.
sortby  character string (can be abbreviated) indicating how to sort the search results: (score, date:late for sorting by date with latest results first, date:early for earliest first, subject for captions in alphabetical order, subject:descending for reverse alphabetical order, size or size:descending for size.)
matchesPerPage  How many items to show per page.
words  Show results matching all words/phrases (default) or any of them.

Details

This function is designed to work with the search site at https://search.r-project.org.
Unique partial matches will work for all arguments. Each new browser window will stay open unless you close it.

Value

(Invisibly) the complete URL passed to the browser, including the query string.

Author(s)

Andy Liaw and Jonathan Baron and Gennadiy Starostin

See Also

help.search, help.start for local searches.
browseURL for how the help file is displayed.

Examples

# need Internet connection
## for phrase searching you may use (escaped) double quotes or brackets
RSiteSearch("(logistic regression) \"glm object\"")
RSiteSearch(""logistic regression"")

## Search in vignettes and help files of R base packages
## store the query string:
fullquery <- RSiteSearch("lattice", restrict = c("vignettes","Rfunctions"))
fullquery # a string of 112 characters
**Description**

`rtags` provides etags-like indexing capabilities for R code, using R's own parser.

**Usage**

```r
code here...
```  

**Arguments**

- `path`, `pattern`, `recursive`
  Arguments passed on to `list.files` to determine the files to be tagged. By default, these are all files with extension `.R`, `.r`, `.S`, and `.s` in the current directory. These arguments are ignored if `src` is specified.

- `src`
  A vector of file names to be indexed.

- `keep.re`
  A regular expression further restricting `src` (the files to be indexed). For example, specifying `keep.re = "/R/[^/]*/\R$"` will only retain files with extension `.R` inside a directory named `R`.

- `ofile`
  Passed on to `cat` as the file argument; typically the output file where the tags will be written ("TAGS" or "tags" by convention). By default, the output is written to the R console (unless redirected).

- `append`
  Logical, indicating whether the output should overwrite an existing file, or append to it.

- `verbose`
  Logical. If `TRUE`, file names are echoed to the R console as they are processed.

- `type`
  Character string specifying whether emacs style ("etags") or vi style ("ctags") tags are to be generated.

**Details**

Many text editors allow definitions of functions and other language objects to be quickly and easily located in source files through a tagging utility. This functionality requires the relevant source files to be preprocessed, producing an index (or tag) file containing the names and their corresponding locations. There are multiple tag file formats, the most popular being the vi-style ctags format and the emacs-style etags format. Tag files in these formats are usually generated by the ctags and etags utilities respectively. Unfortunately, these programs do not recognize R code syntax. They do allow tagging of arbitrary language files through regular expressions, but this too is insufficient.

The `rtags` function is intended to be a tagging utility for R code. It parses R code files (using R's parser) and produces tags in both ctags and etags formats. The support for vi-style ctags is rudimentary, and was adapted from a patch by Neal Fultz; see PR#17214.
It may be more convenient to use the command-line wrapper script `R CMD rtags`.

**Author(s)**

Deepayan Sarkar

**References**


**See Also**

`list.files`, `cat`

**Examples**

```r
## Not run:
rtags("/path/to/src/repository",
       pattern = "\.\*\.[RrSs]$",
       keep.re = "/R/",
       verbose = TRUE,
       ofile = "TAGS",
       append = FALSE,
       recursive = TRUE)

## End(Not run)
```

---

**Rtangle**

**R Driver for Stangle**

**Description**

A driver for Stangle that extracts R code chunks. Notably all `RtangleSetup()` arguments may be used as arguments in the `Stangle()` call.

**Usage**

```r
Rtangle()
RtangleSetup(file, syntax, output = NULL, annotate = TRUE,
               split = FALSE, quiet = FALSE, drop.evalFALSE = FALSE, ...)
```

**Arguments**

- **file**: name of Sweave source file. See the description of the corresponding argument of `Sweave`.
- **syntax**: an object of class `SweaveSyntax`.
- **output**: name of output file used unless `split = TRUE`: see ‘Details’.
- **annotate**: a logical or `function`. When true, as by default, code chunks are separated by comment lines specifying the names and line numbers of the code chunks. If `FALSE` the decorating comments are omitted. Alternatively, `annotate` may be a function, see section ‘Chunk annotation’.
split  split output into a file for each code chunk?
quiet logical to suppress all progress messages.
drop.evalFALSE logical; When false, as by default, all chunks with option eval = FALSE are commented out in the output; otherwise (drop.evalFALSE = TRUE) they are omitted entirely.
... additional named arguments setting defaults for further options listed in ‘Supported Options’.

Details
Unless split = TRUE, the default name of the output file is basename(file) with an extension corresponding to the Sweave syntax (e.g., ‘Rnw’, ‘Stex’) replaced by ‘R’. File names "stdout" and "stderr" are interpreted as the output and message connection respectively.
If splitting is selected (including by the options in the file), each chunk is written to a separate file with extension the name of the ‘engine’ (default ‘.R’).
Note that this driver does more than simply extract the code chunks verbatim, because chunks may re-use earlier chunks.

Chunk annotation (annotate)
By default annotate = TRUE, the annotation is of one of the forms

```
###################################################
### code chunk number 3: viewport
###################################################
```

```
###################################################
### code chunk number 18: grid.Rnw:647-648
###################################################
```

```
###################################################
### code chunk number 19: trellisdata (eval = FALSE)
###################################################
```

using either the chunk label (if present, i.e., when specified in the source) or the file name and line numbers.
annotate may be a function with formal arguments (options, chunk, output), e.g. to produce less dominant chunk annotations; see Rtangle()$runcode how it is called instead of the default.

Supported Options
Rtangle supports the following options for code chunks (the values in parentheses show the default values):

**engine**: character string ("R"). Only chunks with engine equal to "R" or "S" are processed.
**keep.source**: logical (TRUE). If keep. source == TRUE the original source is copied to the file. Otherwise, deparsed source is output.
**eval**: logical (TRUE). If FALSE, the code chunk is copied across but commented out.
**prefix** Used if split = TRUE. See prefix.string.
prefix.string: a character string, default is the name of the source file (without extension). Used if split = TRUE as the prefix for the filename if the chunk has no label, or if it has a label and prefix = TRUE. Note that this is used as part of filenames, so needs to be portable.

show.line.nos: logical (FALSE). Should the output be annotated with comments showing the line number of the first code line of the chunk?

Author(s)
Friedrich Leisch and R-core.

See Also
'Sweave User Manual', a vignette in the utils package.
Sweave, RweaveLatex

Examples

nmRnw <- "example-1.Rnw"
exfile <- system.file("Sweave", nmRnw, package = "utils")
## Create R source file
Stangle(exfile)
nmR <- sub("Rnw\$", "R", nmRnw) # the (default) R output file name
if(interactive()) file.show("example-1.R")

## Smaller R source file with custom annotation:
my.Ann <- function(options, chunk, output) {
cat("### chunk #", options$chunknr, ": ",
if(!is.null(ol <- options$label)) ol else .RtangleCodeLabel(chunk),
if(!options$eval) " (eval = FALSE)", 
"\n",
file = output, sep = "")
}
Stangle(exfile, annotate = my.Ann)
if(interactive()) file.show("example-1.R")
Stangle(exfile, annotate = my.Ann, drop.evalFALSE=TRUE)
if(interactive()) file.show("example-1.R")

RweaveLatex

RweaveLatex

R/LaTeX Driver for Sweave

Description
A driver for Sweave that translates R code chunks in \LaTeX\ files by “running them”, i.e., parse() and eval() each.

Usage

RweaveLatex()
RweaveLatexSetup(file, syntax, output = NULL, quiet = FALSE,
      debug = FALSE, stylepath, ...)
Arguments

- **file**: Name of Sweave source file. See the description of the corresponding argument of Sweave.
- **syntax**: An object of class SweaveSyntax.
- **output**: Name of output file. The default is to remove extension `.nw`, `.Rnw` or `.Snw` and to add extension `.tex`. Any directory paths in file are also removed such that the output is created in the current working directory.
- **quiet**: If TRUE all progress messages are suppressed.
- **debug**: If TRUE, input and output of all code chunks is copied to the console.
- **stylepath**: See ‘Details’.
- **...**: named values for the options listed in ‘Supported Options’.

Details

The \TeX file generated needs to contain the line `\usepackage{Sweave}`, and if this is not present in the Sweave source file (possibly in a comment), it is inserted by the RweaveLatex driver as last line before the `\begin{document}` statement. If `stylepath = TRUE`, a hard-coded path to the file ‘Sweave.sty’ in the R installation is set in place of Sweave. The hard-coded path makes the \TeX file less portable, but avoids the problem of installing the current version of ‘Sweave.sty’ to some place in your TeX input path. However, TeX may not be able to process the hard-coded path if it contains spaces (as it often will under Windows) or TeX special characters.

The default for `stylepath` is now taken from the environment variable `SWEAVE_STYLEPATH_DEFAULT`, or is FALSE if it is unset or empty. If set, it should be exactly TRUE or FALSE: any other values are taken as FALSE.

The simplest way for frequent Sweave users to ensure that ‘Sweave.sty’ is in the TeX input path is to add `R_HOME/share/texmf` as a ‘texmf tree’ (‘root directory’ in the parlance of the ‘MiKTeX settings’ utility).

By default, ‘Sweave.sty’ loads the ‘graphicx’ \TeX package and sets the width of all included graphics to:

```
\setkeys{Gin}{width=0.8\textwidth}.
```

This setting (defined in the ‘graphicx’ package) affects the width size option passed to the ‘\includegraphics{}’ directive for each plot file and in turn impacts the scaling of your plot files as they will appear in your final document.

Thus, for example, you may set width=3 in your figure chunk and the generated graphics files will be set to 3 inches in width. However, the width of your graphic in your final document will be set to `0.8\textwidth` and the height dimension will be scaled accordingly. Fonts and symbols will be similarly scaled in the final document.

You can adjust the default value by including the `\setkeys{Gin}{width=...}` directive in your `.Rnw` file after the `\begin{document}` directive and changing the width option value as you prefer, using standard \TeX measurement values.

If you wish to override this default behavior entirely, you can add a `\usepackage[nogin]{Sweave}` directive in your preamble. In this case, no size/scaling options will be passed to the ‘\includegraphics{}’ directive and the height and width options will determine both the runtime generated graphic file sizes and the size of the graphics in your final document.

‘Sweave.sty’ also supports the ‘[nofontenc]’ option, which skips the default inclusion of ‘\usepackage[T1]{fontenc}’ for pdf\TeX processing.
It also supports the ‘[inconsolata]’ option, to render monospaced text in \texttt{inconsolata}, the font used by default for \proglang{R} help pages.

The use of fancy quotes (see \code{sQuote}) can cause problems when setting \proglang{R} output in non-UTF-8 locales (note that pdf\TeX{} assumes UTF-8 by default since 2018). Either set \code{options(useFancyQuotes = \FALSE)} or arrange that \LaTeX{} is aware of the encoding used and ensure that typewriter fonts containing directional quotes are used.

Some \LaTeX{} graphics drivers do not include \texttt{.png} or \texttt{.jpg} in the list of known extensions. To enable them, add something like \texttt{\DeclareGraphicsExtensions{.png,.pdf,.jpg}} to the preamble of your document or check the behavior of your graphics driver. When both pdf and png are \TRUE{} both files will be produced by Sweave, and their order in the \texttt{\DeclareGraphicsExtensions} list determines which will be used by pdfLatex.

### Supported Options

\texttt{RweaveLatex} supports the following options for code chunks (the values in parentheses show the default values). Character string values should be quoted when passed from \proglang{Sweave} through \texttt{\ldots} but not when used in the header of a code chunk.

- **engine**: character string ("R"). Only chunks with \code{engine} equal to "R" or "S" are processed.
- **echo**: logical (\TRUE{}). Include \proglang{R} code in the output file?
- **keep.source**: logical (\TRUE{}). When echoing, if \TRUE{} the original source is copied to the file. Otherwise, deparsed source is echoed.
- **eval**: logical (\TRUE{}). If \FALSE{}, the code chunk is not evaluated, and hence no text nor graphical output produced.
- **results**: character string ("verbatim"). If "verbatim", the output of \proglang{R} commands is included in the verbatim-like \texttt{Soutput} environment. If "tex", the output is taken to be already proper \LaTeX{} markup and included as is. If "hide" then all output is completely suppressed (but the code executed during the weave). Values can be abbreviated.
- **print**: logical (\FALSE{}). If \TRUE{}, this forces auto-printing of all expressions.
- **term**: logical (\TRUE{}). If \TRUE{}, visibility of values emulates an interactive \proglang{R} session: values of assignments are not printed, values of single objects are printed. If \FALSE{}, output comes only from explicit \code{print} or similar statements.
- **split**: logical (\FALSE{}). If \TRUE{}, text output is written to separate files for each code chunk.
- **strip.white**: character string ("true"). If "true", blank lines at the beginning and end of output are removed. If "all", then all blank lines are removed from the output. If "false" then blank lines are retained.
  
  A 'blank line' is one that is empty or includes only whitespace (spaces and tabs).

  Note that blank lines in a code chunk will usually produce a prompt string rather than a blank line on output.

- **prefix**: logical (\TRUE{}). If \TRUE{} generated filenames of figures and output all have the common prefix given by the \code{prefix.string} option: otherwise only unlabelled chunks use the prefix.
- **prefix.string**: a character string, default is the name of the source file (without extension). Note that this is used as part of filenames, so needs to be portable.
- **include**: logical (\TRUE{}), indicating whether input statements for text output (if \code{split = \TRUE{}}) and \texttt{\includegraphics} statements for figures should be auto-generated. Use \code{include = \FALSE{}} if the output should appear in a different place than the code chunk (by placing the input line manually).
**fig:** logical (FALSE), indicating whether the code chunk produces graphical output. Note that only one figure per code chunk can be processed this way. The labels for figure chunks are used as part of the file names, so should preferably be alphanumeric.

**eps:** logical (FALSE), indicating whether EPS figures should be generated. Ignored if fig = FALSE.

**pdf:** logical (TRUE), indicating whether PDF figures should be generated. Ignored if fig = FALSE.

**pdf.version, pdf.encoding, pdf.compress:** passed to pdf to set the version, encoding and compression (or not). Defaults taken from pdf.options().

**png:** logical (FALSE), indicating whether PNG figures should be generated. Ignored if fig = FALSE. Only available in R ≥ 2.13.0.

**jpeg:** logical (FALSE), indicating whether JPEG figures should be generated. Ignored if fig = FALSE. Only available in R ≥ 2.13.0.

**grdevice:** character (NULL): see section ‘Custom Graphics Devices’. Ignored if fig = FALSE. Only available in R ≥ 2.13.0.

**width:** numeric (6), width of figures in inches. See ‘Details’.

**height:** numeric (6), height of figures in inches. See ‘Details’.

**resolution:** numeric (300), resolution in pixels per inch: used for PNG and JPEG graphics. Note that the default is a fairly high value, appropriate for high-quality plots. Something like 100 is a better choice for package vignettes.

**concordance:** logical (FALSE). Write a concordance file to link the input line numbers to the output line numbers.

**figs.only:** logical (FALSE). By default each figure chunk is run once, then re-run for each selected type of graphics. That will open a default graphics device for the first figure chunk and use that device for the first evaluation of all subsequent chunks. If this option is true, the figure chunk is run only for each selected type of graphics, for which a new graphics device is opened and then closed.

In addition, users can specify further options, either in the header of an individual code section or in a `\SweaveOpts{}` line in the document. For unknown options, their type is set at first use.

### Custom Graphics Devices

If option grdevice is supplied for a code chunk with both fig and eval true, the following call is made

```r
get(options$grdevice, envir = .GlobalEnv)(name=, width=,
   height=, options)
```

which should open a graphics device. The chunk’s code is then evaluated and dev.off is called. Normally a function of the name given will have been defined earlier in the Sweave document, e.g.

```r
<<results=hide>>=
my.Swd <- function(name, width, height, ...)
   grDevices::png(filename = paste(name, "png", sep = "."),
      width = width, height = height, res = 100,
      units = "in", type = "quartz", bg = "transparent")
@
```

Alternatively for R >= 3.4.0, if the function exists in a package (rather than the .GlobalEnv) it can be used by setting grdevice = "pkg::my.Swd" (or with ‘::’ instead of ‘::’ if the function is not exported).
Currently only one custom device can be used for each chunk, but different devices can be used for different chunks.

A replacement for `dev.off` can be provided as a function with suffix `.off`, e.g. `my.Swd.off()` or `pkg::my.Swd.off()`, respectively.

### Hook Functions

Before each code chunk is evaluated, zero or more hook functions can be executed. If `getOption("SweaveHooks")` is set, it is taken to be a named list of hook functions. For each logical option of a code chunk (echo, print, ...) a hook can be specified, which is executed if and only if the respective option is TRUE. Hooks must be named elements of the list returned by `getOption("SweaveHooks")` and be functions taking no arguments. E.g., if option "SweaveHooks" is defined as `list(fig = foo)`, and `foo` is a function, then it would be executed before the code in each figure chunk. This is especially useful to set defaults for the graphical parameters in a series of figure chunks.

Note that the user is free to define new Sweave logical options and associate arbitrary hooks with them. E.g., one could define a hook function for a new option called `clean` that removes all objects in the workspace. Then all code chunks specified with `clean = TRUE` would start operating on an empty workspace.

### Author(s)

Friedrich Leisch and R-core

### See Also

- `Sweave`, `Rtangle`
Details

There are system copies of these files in ‘R_HOME\etc’. Users can have personal copies of the files: these are looked for in the location given by the environment variable R_USER. The system files are read only if a corresponding personal file is not found.

If the environment variable R_USER is not set, the R system sets it to HOME if that is set (stripping any trailing slash), otherwise to the Windows ‘personal’ directory, otherwise to {HOMEDRIVE}{HOMEPATH} if HOMEDRIVE and HOMEDRIVE are both set otherwise to the working directory. This is as described in the file ‘rw-FAQ’.

Value

Each of the files contains details in its comments of how to set the values.

At the time of writing ‘Rdevga’ configured the mapping of font numbers to fonts, and ‘Rconsole’ configured the appearance (single or multiple document interface, toolbar, statusbar on MDI), size, font and colours of the GUI console, and whether resizing the console sets options("width").

The file ‘Rconsole’ also configures the internal pager. This shares the font and colours of the console, but can be sized separately.

‘Rconsole’ can also set the initial positions of the console and the graphics device, as well as the size and position of the MDI workspace in MDI mode.

loadRconsole is called for its side effect of loading new defaults. It returns no useful value.

Chinese/Japanese/Korean

Users of these languages will need to select a suitable font for the console (perhaps MS Mincho) and for the graphics device (although the default Arial has many East Asian characters). It is essential that the font selected for the console has double-width East Asian characters – many monospaced fonts do not.

Note

The GUI preferences item on the Edit menu brings up an dialog box which can be used to edit the console settings, and to save them to a file.

This is only available on Windows.

Author(s)

Guido Masarotto and R-core members

See Also

windows

Examples

if(.Platform$OS.type == "windows") withAutoprint({
  ruser <- Sys.getenv("R_USER")
  cat("\n\nLocation for personal configuration files is
R_USER = ",
    ruser, "\n\n", sep = "")
## see if there are personal configuration files
file.exists(file.path(ruser, c("Rconsole", "Rdevga")))
## show the configuration files used
savehistory <- function(file)
{
  ruser <- Sys.getenv("R_USER")
  path <- file.path(ruser, file)
  if(!file.exists(path)) path <- file.path(R.home(), "etc", file)
  file.show(path, header = path)
}

showConfig("Rconsole")

---

**savehistory**  
*Load or Save or Display the Commands History*

**Description**

Load or save or display the commands history.

**Usage**

```r
loadhistory(file = ".Rhistory")
savehistory(file = ".Rhistory")

history(max.show = 25, reverse = FALSE, pattern, ...)

timestamp(stamp = date(),
          prefix = "#------ ", suffix = " ------#",
          quiet = FALSE)
```

**Arguments**

- `file`  
The name of the file in which to save the history, or from which to load it. The path is relative to the current working directory.
- `max.show`  
The maximum number of lines to show. `Inf` will give all of the currently available history.
- `reverse`  
logical. If true, the lines are shown in reverse order. Note: this is not useful when there are continuation lines.
- `pattern`  
A character string to be matched against the lines of the history. When supplied, only _unique_ matching lines are shown.
- `...`  
Arguments to be passed to `grep` when doing the matching.
- `stamp`  
A value or vector of values to be written into the history.
- `prefix`  
A prefix to apply to each line.
- `suffix`  
A suffix to apply to each line.
- `quiet`  
If TRUE, suppress printing timestamp to the console.
Details

There are several history mechanisms available for the different R consoles, which work in similar but not identical ways. Notably, there are different implementations for Unix and Windows.

**Windows:** The functions described here work in Rgui and interactive Rterm but not in batch use of Rterm nor in embedded/DCOM versions.

**Unix-alikes:** The functions described here work under the readline command-line interface but may not otherwise (for example, in batch use or in an embedded application). Note that R can be built without readline.

R.app, the console on macOS, has a separate and largely incompatible history mechanism, which by default uses a file `.Rapp.history` and saves up to 250 entries. These functions are not currently implemented there.

The (readline on Unix-alikes) history mechanism is controlled by two environment variables: R_HISTSIZE controls the number of lines that are saved (default 512), and R_HISTFILE (default `.Rhistory`) sets the filename used for the loading/saving of history if requested at the beginning/end of a session (but not the default for loadhistory/savehistory). There is no limit on the number of lines of history retained during a session, so setting R_HISTSIZE to a large value has no penalty unless a large file is actually generated.

These environment variables are read at the time of saving, so can be altered within a session by the use of `Sys.setenv`.

On Unix-alikes: Note that readline history library saves files with permission 0600, that is with read/write permission for the user and not even read permission for any other account.

The timestamp function writes a timestamp (or other message) into the history and echos it to the console. On platforms that do not support a history mechanism only the console message is printed.

**Note**

If you want to save the history at the end of (almost) every interactive session (even those in which you do not save the workspace), you can put a call to `savehistory()` in `.Last`. See the examples.

**Examples**

```r
## Not run:
## Save the history in the home directory: note that it is not
## (by default) read from there but from the current directory
.Last <- function()
  if(interactive()) try(savehistory("~/.Rhistory"))

## End(Not run)
```

---

**select.list**

*Select Items from a List*

**Description**

Select item(s) from a character vector.

**Usage**

```r
select.list(choices, preselect = NULL, multiple = FALSE,
           title = NULL, graphics =getOption("menu.graphics"))
```
Arguments

- **choices**: a character vector of items.
- **preselect**: a character vector, or NULL. If non-null and if the string(s) appear in the list, the item(s) are selected initially.
- **multiple**: logical: can more than one item be selected?
- **title**: optional character string for window title, or NULL for no title.
- **graphics**: logical: should a graphical widget be used?

Details

The normal default is `graphics = TRUE`.

On **Windows**, this brings up a modal dialog box with a (scrollable) list of items, which can be selected by the mouse. If `multiple` is true, further items can be selected or deselected by holding the control key down whilst selecting, and shift-clicking can be used to select ranges.

Normal termination is via the ‘OK’ button or by hitting Enter or double-clicking an item. Selection can be aborted via the ‘Cancel’ button or pressing Escape.

Under the **macOS GUI**, this brings up a modal dialog box with a (scrollable) list of items, which can be selected by the mouse.

On **other Unix-like platforms** it will use a Tcl/Tk listbox widget if possible.

If `graphics` is FALSE or no graphical widget is available it displays a text list from which the user can choose by number(s). The `multiple = FALSE` case uses `menu`. Preselection is only supported for `multiple = TRUE`, where it is indicated by a “+” preceding the item.

It is an error to use `select.list` in a non-interactive session.

Value

A character vector of selected items. If `multiple` is false and no item was selected (or Cancel was used), "" is returned. If `multiple` is true and no item was selected (or Cancel was used) then a character vector of length 0 is returned.

See Also

- `menu`, `tk_select.list` for a graphical version using Tcl/Tk.

Examples

```r
## Not run:
select.list(sort(.packages(all.available = TRUE)))

## End(Not run)
```
Collect Information About the Current R Session

Description

Get and report version information about R, the OS and attached or loaded packages.

The print() and toLatex() methods (for a "sessionInfo" object) show the locale and timezone information by default, when locale or tzone are true. The system.codepage is only shown when it is not empty, i.e., only on Windows, and if it differs from code.page, see below or l10n_info().

Usage

sessionInfo(package = NULL)
## S3 method for class 'sessionInfo'
print(x, locale = TRUE, tzone = locale,
      RNG = !identical(x$RNGkind, .RNGdefaults), ...)
## S3 method for class 'sessionInfo'
toLatex(object, locale = TRUE, tzone = locale,
      RNG = !identical(object$RNGkind, .RNGdefaults), ...)

Arguments

package a character vector naming installed packages, or NULL (the default) meaning all attached packages.

x an object of class "sessionInfo".

object an object of class "sessionInfo".

locale show locale, by default tzone, and (on Windows) code page information?

tzone show time zone information?

RNG show information on RNGkind()? Defaults to true iff it differs from the R version’s default, i.e., RNGversion(*)

... currently not used.

Value

sessionInfo() returns an object of class "sessionInfo" which has print and toLatex methods. This is a list with components

R.version a list, the result of calling R.Version().

platform a character string describing the platform R was built under. Where subarchitectures are in use this is of the form 'platform/sub-arch (nn-bit)'.

running a character string (or possibly NULL), the same as osVersion, see below.

RNGkind a character vector, the result of calling RNGkind().

matprod a character string, the result of calling getOption("matprod").

BLAS a character string, the result of calling extSoftVersion()["BLAS"].

LAPACK a character string, the result of calling La_library().

LA_version a character string, the result of calling La_version().
locale  a character string, the result of calling `Sys.getlocale()`.

tzone  a character string, the result of calling `Sys.timezone()`.

tzcode_type  a character string indicating source (system/internal) of the date-time conversion and printing functions.

basePkgs  a character vector of base packages which are attached.

otherPkgs  (not always present): a named list of the results of calling `packageDescription` on other attached packages.

loadedOnly  (not always present): a named list of the results of calling `packageDescription` on packages whose namespaces are loaded but are not attached.

osVersion

`osVersion` is a character string (or possibly `NULL` on bizarre platforms) describing the OS and version which it is running under (as distinct from built under). This attempts to name a Linux distribution and give the OS name on an Apple Mac.

It is the same as `sessionInfo()$running` and created when loading the `utils` package.

Windows may report unexpected versions: see the help for `win.version`.

How OSes identify themselves and their versions can be arcane: where possible `osVersion` (and hence `sessionInfo()$running`) uses a human-readable form.

Where R was compiled under macOS 10.x (as the CRAN Intel distributions were prior to R 4.3.0) but running under ‘Big Sur’ or later, macOS reports itself as ‘10.16’ (which R recognizes as ‘Big Sur ...’) and not ‘11’, ‘12’,....

Note

The information on ‘loaded’ packages and namespaces is the current version installed at the location the package was loaded from: it can be wrong if another process has been changing packages during the session.

See Also

`R.version`, `R_compiled_by`

Examples

```r
sI <- sessionInfo()
sI
# The same, showing the RNGkind, but not the locale :
print(sI, RNG = TRUE, locale = FALSE)
toLatex(sI, locale = FALSE) # shortest; possibly desirable at end of report
```

Usage

setRepositories(graphics = getOption("menu.graphics"),
    ind = NULL, addURLs = character())

Arguments

graphics Logical. If true, use a graphical list: on Windows or macOS GUI use a list box, and on a Unix-alike if tcltk and an X server are available, use Tk widget. Otherwise use a text menu.

ind NULL or a vector of integer indices, which have the same effect as if they were entered at the prompt for graphics = FALSE.

addURLs A character vector of additional URLs: it is often helpful to use a named vector.

Details

The default list of known repositories is stored in the file ‘R_HOME/etc/repositories’. That file can be edited for a site, or a user can have a personal copy in the file pointed to by the environment variable R_REPOSITORIES, or if this is unset, NULL or does not exist, in ‘HOME/.R/repositories’, which will take precedence.

A Bioconductor mirror can be selected by setting options("BioC_mirror"), e.g. via chooseBioCmirror — the default value is "https://bioconductor.org". This version of R chooses Bioconductor version 3.18 by default, but that can be changed via the environment variable R_BIOC_VERSION.

The items that are preselected are those that are currently in options("repos") plus those marked as default in the list of known repositories.

The list of repositories offered depends on the setting of option "pkgType" as some repositories only offer a subset of types (e.g., only source packages or not macOS binary packages). Further, for binary packages some repositories (notably R-Forge) only offer packages for the current or recent versions of R. (Type “both” is equivalent to “source”.)

Repository ‘CRAN’ is treated specially: the value is taken from the current setting of getOption("repos") if this has an element "CRAN": this ensures mirror selection is sticky.

This function requires the R session to be interactive unless ind is supplied.

Value

This function is invoked mainly for its side effect of updating options("repos"). It returns (invisibly) the previous repos options setting (as a list with component repos) or NULL if no changes were applied.

Note

This does not set the list of repositories at startup: to do so set options(repos =) in a start up file (see help topic Startup) or via a customized ‘repositories’ file.

See Also

chooseCRANmirror, chooseBioCmirror, install.packages.
Examples

```r
## Not run:
setRepositories(addURLs =
c(CRANxtras = "https://www.stats.ox.ac.uk/pub/RWin"))
## End(Not run)
```

**setTitle**

### Set the Window Title or the Statusbar of the RGui in Windows

**Description**

Set or get the title of the R (i.e. RGui) window which will appear in the task bar, or set the statusbar (if in use).

**Usage**

```r
setWindowTitle(suffix, title = paste(getIdentification(), suffix))
getWindowTitle()
getIdentification()
setStatusBar(text)
```

**Arguments**

- `suffix`: a character string to form part of the title
- `title`: a character string forming the complete new title
- `text`: a character string of up to 255 characters, to be displayed in the status bar.

**Details**

- `setWindowTitle` appends `suffix` to the normal window identification (RGui, R Console or Rterm). Use `suffix = ""` to reset the title.
- `getWindowTitle` gets the current title.
- This sets the title of the frame in MDI mode, the title of the console for RGui --sdi, and the title of the window from which it was launched for Rterm. It has no effect in embedded uses of R.
- `getIdentification` returns the normal window identification.
- `setStatusBar` sets the text in the statusbar of an MDI frame: if this is not currently shown it is selected and shown.

**Value**

The first three functions return a length 1 character vector.
- `setTitle` returns the previous window title (invisibly).
- `getWindowTitle` and `getIdentification` return the current window title and the normal window identification, respectively.
Note

These functions are only available on Windows and only make sense when using the Rgui. E.g., in Rterm (and hence in ESS) the title is not visible (but can be set and gotten), and in a version of RStudio it has been "", invariably.

Examples

```r
if(.Platform$OS.type == "windows") withAutoprint({
  ## show the current working directory in the title, saving the old one
  oldtitle <- setWindowTitle(getwd())
  Sys.sleep(0.5)
  ## reset the title
  setWindowTitle(""")
  Sys.sleep(0.5)
  ## restore the original title
  setWindowTitle(title = oldtitle)
})
```

---

**SHLIB**

**Build Shared Object/DLL for Dynamic Loading**

Description

Compile the given source files and then link all specified object files into a shared object aka DLL which can be loaded into R using `dyn.load` or `library.dynam`.

Usage

```
R CMD SHLIB [options] [-o dllname] files
```

Arguments

- **files**: a list specifying the object files to be included in the shared object/DLL. You can also include the name of source files (for which the object files are automagically made from their sources) and library linking commands.

- **dllname**: the full name of the shared object/DLL to be built, including the extension (typically `.so` on Unix systems, and `.dll` on Windows). If not given, the basename of the object/DLL is taken from the basename of the first file.

- **options**: Further options to control the processing. Use `R CMD SHLIB --help` for a current list.

Details

`R CMD SHLIB` is the mechanism used by `INSTALL` to compile source code in packages. It will generate suitable compilation commands for C, C++, Objective C(++) and Fortran sources: Fortran 90/95 sources can also be used but it may not be possible to mix these with other languages (on most platforms it is possible to mix with C, but mixing with C++ rarely works).

Please consult section ‘Creating shared objects’ in the manual ‘Writing R Extensions’ for how to customize it (for example to add `cpp` flags and to add libraries to the link step) and for details of some of its quirks.
Items in files with extensions ‘.c’, ‘.cpp’, ‘.cc’, ‘.C’, ‘.f’, ‘.f90’, ‘.f95’, ‘.m’ (ObjC), ‘.M’ and ‘.mm’ (ObjC++) are regarded as source files, and those with extension ‘.o’ as object files. All other items are passed to the linker.

Objective C(++) support is optional when R was configured: their main usage is on macOS.

Note that the appropriate run-time libraries will be used when linking if C++, Fortran or Objective C(++) sources are supplied, but not for compiled object files from these languages.

Option ‘-n’ (also known as ‘--dry-run’) will show the commands that would be run without actually executing them.

Note

Some binary distributions of R have SHLIB in a separate bundle, e.g., an R-devel RPM.

See Also

COMPILE, dyn.load, library.dynam.

The ‘R Installation and Administration’ and ‘Writing R Extensions’ manuals, including the section on ‘Customizing compilation’ in the former.

Examples

```r
## Not run:
# To link against a library not on the system library paths:
R CMD SHLIB -o mylib.so a.f b.f -L/opt/acml3.5.0-gnu64/lib -lacml
## End(Not run)
```

---

**shortPathName**

Express File Paths in Short Form on Windows

**Description**

Convert file paths to the short form. This is an interface to the Windows API call GetShortPathNameW.

**Usage**

```r
shortPathName(path)
```

**Arguments**

- **path**: character vector of file paths.

**Details**

For most file systems, the short form is the ‘DOS’ form with 8+3 path components and no spaces, and this used to be guaranteed. But some file systems on recent versions of Windows do not have short path names when the long-name path will be returned instead.
Value

A character vector. The path separator will be \\.
If a file path does not exist, the supplied path will be returned with
slashes replaced by backslashes.

Note

This is only available on Windows.

See Also

normalizePath.

Examples

if(.Platform$OS.type == "windows") withAutoprint({
  cat(quote(shortPathName(c(R.home(), tempdir()))), sep = "\n")
})

Description

These functions extract information from source references.

Usage

getSrcFilename(x, full.names = FALSE, unique = TRUE)
getSrcDirectory(x, unique = TRUE)
gsrcref(x)
getSrcLocation(x, which = c("line", "column", "byte", "parse"),
  first = TRUE)

Arguments

x An object (typically a function) containing source references.
full.names Whether to include the full path in the filename result.
unique Whether to list only unique filenames/directories.
which Which part of a source reference to extract. Can be abbreviated.
first Whether to show the first (or last) location of the object.

Details

Each statement of a function will have its own source reference
if the "keep.source" option is TRUE. These functions retrieve all of them.
The components are as follows:

  line The line number where the object starts or ends.
column The column number where the object starts or ends. Horizontal tabs are converted to spaces.

byte As for "column", but counting bytes, which may differ in case of multibyte characters (and horizontal tabs).

parse As for "line", but this ignores #line directives.

Value
getSrcFilename and getSrcDirectory return character vectors holding the filename/directory.
getSrcRef returns a list of "srcRef" objects or NULL if there are none.
getSrcLocation returns an integer vector of the requested type of locations.

See Also
srcRef, getParseData

Examples

fn <- function(x) {
  x + 1 # A comment, kept as part of the source
}

# Show the temporary file directory
# where the example was saved

getSrcDirectory(fn)
getSrcLocation(fn, "line")

---

stack Stack or Unstack Vectors from a Data Frame or List

Description
Stacking vectors concatenates multiple vectors into a single vector along with a factor indicating where each observation originated. Unstacking reverses this operation.

Usage
stack(x, ...)
## Default S3 method:
stack(x, drop=FALSE, ...)
## S3 method for class 'data.frame'
stack(x, select, drop=FALSE, ...)

unstack(x, ...)
## Default S3 method:
unstack(x, form, ...)
## S3 method for class 'data.frame'
unstack(x, form, ...)
Arguments

x a list or data frame to be stacked or unstacked.
select an expression, indicating which variable(s) to select from a data frame.
form a two-sided formula whose left side evaluates to the vector to be unstacked and whose right side evaluates to the indicator of the groups to create. Defaults to formula(x) in the data frame method for unstack.
drop Whether to drop the unused levels from the “ind” column of the return value.
... further arguments passed to or from other methods.

Details

The stack function is used to transform data available as separate columns in a data frame or list into a single column that can be used in an analysis of variance model or other linear model. The unstack function reverses this operation.

Note that stack applies to vectors (as determined by is.vector): non-vector columns (e.g., factors) will be ignored with a warning. Where vectors of different types are selected they are concatenated by unlist whose help page explains how the type of the result is chosen.

These functions are generic: the supplied methods handle data frames and objects coercible to lists by as.list.

Value

unstack produces a list of columns according to the formula form. If all the columns have the same length, the resulting list is coerced to a data frame.

stack produces a data frame with two columns:

values the result of concatenating the selected vectors in x.
ind a factor indicating from which vector in x the observation originated.

Author(s)

Douglas Bates

See Also

lm, reshape

Examples

require(stats)
formula(PlantGrowth) # check the default formula
pg <- unstack(PlantGrowth) # unstack according to this formula
pg
stack(pg) # now put it back together
stack(pg, select = -ctrl) # omitting one vector
**str**  
*Compactly Display the Structure of an Arbitrary R Object*

**Description**

Compactly display the internal structure of an R object, a diagnostic function and an alternative to `summary` (and to some extent, `dput`). Ideally, only one line for each ‘basic’ structure is displayed. It is especially well suited to compactly display the (abbreviated) contents of (possibly nested) lists. The idea is to give reasonable output for any R object. It calls `args` for (non-primitive) function objects.

`strOptions()` is a convenience function for setting `options(str = .)`, see the examples.

**Usage**

```r
str(object, ...)  
```

### S3 method for class 'data.frame'

```r
str(object, ...)  
```

### Default S3 method:

```r
str(object, max.level = NA,  
vec.len = strO$vec.len, digits.d = strO$digits.d,  
nchar.max = 128, give.attr = TRUE,  
drop.deparse.attr = strO$drop.deparse.attr,  
give.head = TRUE, give.length = give.head,  
width = getOption("width"), nest.lev = 0,  
indent.str = paste(rep.int(" ", max(0, nest.lev + 1)),  
   collapse = ".."),  
comp.str = "$ ", no.list = FALSE, envir = baseenv(),  
strict.width = strO$strict.width,  
formatNum = strO$formatNum, list.len = strO$list.len,  
deparse.lines = strO$deparse.lines, ...)  
```

```r
strOptions(strict.width = "no", digits.d = 3, vec.len = 4,  
list.len = 99, deparse.lines = NULL,  
drop.deparse.attr = TRUE,  
formatNum = function(x, ...)  
   format(x, trim = TRUE, drop0trailing = TRUE, ...))  
```

**Arguments**

- **object** any R object about which you want to have some information.
- **max.level** maximal level of nesting which is applied for displaying nested structures, e.g., a list containing sub lists. Default NA: Display all nesting levels.
- **vec.len** numeric (>= 0) indicating how many ‘first few’ elements are displayed of each vector. The number is multiplied by different factors (from .5 to 3) depending on the kind of vector. The number is multiplied by different factors (from .5 to 3) depending on the kind of vector. Defaults to the vec.len component of option “str” (see `options`) which defaults to 4.
- **digits.d** number of digits for numerical components (as for `print`). Defaults to the digits.d component of option “str” which defaults to 3.
nchar.max  maximal number of characters to show for character strings. Longer strings are truncated, see length example below.
give.attr  logical; if TRUE (default), show attributes as sub structures.
drop.deparse.attr  logical; if TRUE (default), deparse(control = <S>) will not have "showAttributes" in <S>. Used to be hard coded to FALSE and hence can be set via strOptions() for back compatibility.
give.length  logical; if TRUE (default), indicate length (as [1:...]).
give.head  logical; if TRUE (default), give (possibly abbreviated) mode/class and length (as <type>[1:...]).
width  the page width to be used. The default is the currently active options("width"); note that this has only a weak effect, unless strict.width is not "no".
nest.lev  current nesting level in the recursive calls to str.
indent.str  the indentation string to use.
comp.str  string to be used for separating list components.
no.list  logical; if true, no 'list of . . .' nor the class are printed.
envir  the environment to be used for promise (see delayedAssign) objects only.
strict.width  string indicating if the width argument’s specification should be followed strictly, one of the values c("no", "cut", "wrap"), which can be abbreviated. Defaults to the strict.width component of option "str" (see options) which defaults to "no" for back compatibility reasons; "wrap" uses strwrap(*, width = width) whereas "cut" cuts directly to width. Note that a small vec.length may be better than setting strict.width = "wrap".
formatNum  a function such as format for formatting numeric vectors. It defaults to the formatNum component of option "str", see "Usage" of strOptions() above, which is almost back compatible to R <= 2.7.x, however, using formatC may be slightly better.
list.len  numeric; maximum number of list elements to display within a level.
deparse.lines  numeric or NULL as by default, determining the nlines argument to deparse() when object is a call. When NULL, the nchar.max and width arguments are used to determine a smart default.
...
... potential further arguments (required for Method/Generic reasons).

Value

str does not return anything, for efficiency reasons. The obvious side effect is output to the terminal.

Note

See the extensive annotated ‘Examples’ below.

The default method tries to “work always”, but needs to make some assumptions for the case when object has a class but no own str() method which is the typical case: There it relies on "[" and "[[" subsetting methods to be compatible with length(). When this is not the case, or when is.list(object) is TRUE, but length(object) differs from length(unclass(object)) it treats it as “irregular” and reports the contents of unclass(object) as “hidden list".
Author(s)

Martin Maechler <maechler@stat.math.ethz.ch> since 1990.

See Also

ls.str for listing objects with their structure; summary, args.

Examples

require(stats); require(grDevices); require(graphics)
## The following examples show some of 'str' capabilities
str(1:12)
str(ls)
str(args) # more useful than args(args) !
str(freeny)
str(str)
str(.Machine, digits.d = 20) # extra digits for identification of binary numbers
str(lsfit(1:9, 1:9))
str(lsfit(1:9, 1:9), max.level = 1)
str(lsfit(1:9, 1:9), width = 00, strict.width = "cut")
str(lsfit(1:9, 1:9), width = 00, strict.width = "wrap")
op <- options(); str(op) # save first;
   # otherwise internal options() is used.
need.dev <-
  !exists(".Device") || is.null(.Device) || .Device == "null device"
if(need.dev) postscript()
str(par())
if(need.dev) graphics.off()

ch <- letters[1:12]; is.na(ch) <- 3:5
str(ch) # character NA's

str(list(a = "A", L = as.list(1:100)), list.len = 9)
## .. [list output truncated] 

## Long strings, 'nchar.max', 'strict.width':
nchar(longch <- paste(rep(letters,100), collapse = " "))
str(longch)
str(longch, nchar.max = 52)
str(longch, strict.width = "wrap")

## Multibyte characters in strings:
## Truncation behavior (<> correct width measurement) for "long" non-ASCII:
idx <- c(65313:65338, 65345:65350)
fwch <- intToUtf8(idx) # full width character string: each has width 2
ch <- strtrim(paste(LETTERS, collapse="_"), 64)
(ncc <- c(c.ch = nchar(ch), w.ch = nchar(ch, "w"), c.fw = nchar(fwch), w.fw = nchar(fwch, "w")))
stopifnot(unname(ncc) == c(64,64, 32, 64))
## nchar.max: 1st line needs an increase of 2 in order to see 1 (in UTF-8!):
invisible(lapply(60:66, function(N) str(fwch, nchar.max = N)));
invisible(lapply(60:66, function(N) str(ch, nchar.max = N))) # "1 is 1" here

## Settings for narrow transcript:
op <- options(width = 60, 
              str = strOptions(strict.width = "wrap"))
str(lsfit(1:9,1:9))
str(options())
## reset to previous:
options(op)

str(quote( { A+B; list(C, D) } ))

## S4 classes :
require(stats4)
x <- 0:10; y <- c(26, 17, 13, 12, 20, 9, 8, 5, 4, 8)
ll <- function(ymax = 15, xh = 6)
  -sum(dpois(y, lambda=ymax/(1+x/xh), log=TRUE))
fit <- mle(ll)
str(fit)

---

strcapture

**Capture String Tokens into a data.frame**

**Description**

Given a character vector and a regular expression containing capture expressions, `strcapture` will extract the captured tokens into a tabular data structure, such as a data.frame, the type and structure of which is specified by a prototype object. The assumption is that the same number of tokens are captured from every input string.

**Usage**

`strcapture(pattern, x, proto, perl = FALSE, useBytes = FALSE)`

**Arguments**

- `pattern` The regular expression with the capture expressions.
- `x` A character vector in which to capture the tokens.
- `proto` A `data.frame` or S4 object that behaves like one. See details.
- `perl,useBytes` Arguments passed to `regexec`.

**Details**

The `proto` argument is typically a `data.frame`, with a column corresponding to each capture expression, in order. The captured character vector is coerced to the type of the column, and the column names are carried over to the return value. Any data in the prototype are ignored. See the examples.
summaryRprof

Value

A tabular data structure of the same type as proto, so typically a data.frame, containing a column for each capture expression. The column types and names are inherited from proto. Cases in x that do not match pattern have NA in every column.

See Also

regexec and regmatches for related low-level utilities.

Examples

x <- "chr1:1-1000"
pattern <- "(.\?):([[:digit:]]+)\-([[:digit:]]+)"
proto <- data.frame(chr=character(), start=integer(), end=integer())
strcapture(pattern, x, proto)

summaryRprof

Summarise Output of R Sampling Profiler

Description

Summarise the output of the Rprof function to show the amount of time used by different R functions.

Usage

summaryRprof(filename = "Rprof.out", chunksize = 5000, memory = c("none", "both", "tseries", "stats"), lines = c("hide", "show", "both"), index = 2, diff = TRUE, exclude = NULL, basenames = 1)

Arguments

filename Name of a file produced by Rprof().
chunksize Number of lines to read at a time.
memory Summaries for memory information. See ‘Memory profiling’ below. Can be abbreviated.
lines Summaries for line information. See ‘Line profiling’ below. Can be abbreviated.
index How to summarize the stack trace for memory information. See ‘Details’ below.
diff If TRUE memory summaries use change in memory rather than current memory.
exclude Functions to exclude when summarizing the stack trace for memory summaries.
basenames Number of components of the path to filenames to display.

Details

This function provides the analysis code for Rprof files used by R CMD Rprof.

As the profiling output file could be larger than available memory, it is read in blocks of chunksize lines. Increasing chunksize will make the function run faster if sufficient memory is available.
Value

If `memory = "none"` and `lines = "hide"`, a list with components

- `by.self` A data frame of timings sorted by 'self' time.
- `by.total` A data frame of timings sorted by 'total' time.
- `sample.interval` The sampling interval.
- `sampling.time` Total time of profiling run.

The first two components have columns 'self.time', 'self.pct', 'total.time' and 'total.pct', the times in seconds and percentages of the total time spent executing code in that function and code in that function or called from that function, respectively.

If `lines = "show"`, an additional component is added to the list:

- `by.line` A data frame of timings sorted by source location.

If `memory = "both"` the same list but with memory consumption in Mb in addition to the timings.

If `memory = "tseries"` a data frame giving memory statistics over time. Memory usage is in bytes.

If `memory = "stats"` a by object giving memory statistics by function. Memory usage is in bytes.

If no events were recorded, a zero-row data frame is returned.

Memory profiling

Options other than `memory = "none"` apply only to files produced by `Rprof(memory.profiling = TRUE)`.

When called with `memory.profiling = TRUE`, the profiler writes information on three aspects of memory use: vector memory in small blocks on the R heap, vector memory in large blocks (from `malloc`), memory in nodes on the R heap. It also records the number of calls to the internal function `duplicate` in the time interval. `duplicate` is called by C code when arguments need to be copied.

Note that the profiler does not track which function actually allocated the memory.

With `memory = "both"` the change in total memory (truncated at zero) is reported in addition to timing data.

With `memory = "tseries"` or `memory = "stats"` the index argument specifies how to summarize the stack trace. A positive number specifies that many calls from the bottom of the stack; a negative number specifies the number of calls from the top of the stack. With `memory = "tseries"` the index is used to construct labels and may be a vector to give multiple sets of labels. With `memory = "stats"` the index must be a single number and specifies how to aggregate the data to the maximum and average of the memory statistics. With both `memory = "tseries"` and `memory = "stats"` the argument `diff = TRUE` asks for summaries of the increase in memory use over the sampling interval and `diff = FALSE` asks for the memory use at the end of the interval.

Line profiling

If the code being run has source reference information retained (via `keep.source = TRUE` in `source` or `KeepSource = TRUE` in a package 'DESCRIPTION' file or some other way), then information about the origin of lines is recorded during profiling. By default this is not displayed, but the `lines` parameter can enable the display.

If `lines = "show"`, line locations will be used in preference to the usual function name information, and the results will be displayed ordered by location in addition to the other orderings.

If `lines = "both"`, line locations will be mixed with function names in a combined display.
Sweave

Automatic Generation of Reports

Description

Sweave provides a flexible framework for mixing text and R/S code for automatic report generation. The basic idea is to replace the code with its output, such that the final document only contains the text and the output of the statistical analysis: however, the source code can also be included.

Usage

Sweave(file, driver = RweaveLatex(),
  syntax = getOption("SweaveSyntax"), encoding = ",
  ...)  
Stangle(file, driver = Rtangle(),
  syntax = getOption("SweaveSyntax"), encoding = ",
  ...)

Arguments

file Path to Sweave source file. Note that this can be supplied without the extension, but the function will only proceed if there is exactly one Sweave file in the directory whose basename matches file.

driver the actual workhorse, (a function returning) a named list of five functions; for details, see Section 5 of the ‘Sweave User Manual’ available as vignette("Sweave").
syntax NULL or an object of class "SweaveSyntax" or a character string with its name. See the section ‘Syntax Definition’.
encoding The default encoding to assume for file.
...

Examples

## Not run:
## Rprof() is not available on all platforms
Rprof(tmp <- tempfile())
example(glm)
Rprof()
summaryRprof(tmp)
unlink(tmp)
## End(Not run)
Details

An Sweave source file contains both text in a markup language (like \LaTeXX) and \texttt{R} (or \texttt{S}) code. The code gets replaced by its output (text or graphs) in the final markup file. This allows a report to be re-generated if the input data change and documents the code to reproduce the analysis in the same file that also produces the report.

Sweave combines the documentation and code chunks (or their output) into a single document. \texttt{Stangle} extracts only the code from the Sweave file creating an \texttt{R} source file that can be run using \texttt{source}. (Code inside \\texttt{\Sexpr{}} statements is ignored by \texttt{Stangle}.)

\texttt{Stangle} is just a wrapper to \texttt{Sweave} specifying a different default driver. Alternative drivers can be used and are provided by various contributed packages.

Environment variable \texttt{SWEAVE\_OPTIONS} can be used to override the initial options set by the driver: it should be a comma-separated set of key=value items, as would be used in a \texttt{\SweaveOpts} statement in a document.

If the encoding is unspecified (the default), \texttt{non\textunderscore ASCII} source files must contain a line of the form
\begin{verbatim}
\usepackage[foo]{inputenc}
\end{verbatim}
(where \texttt{‘foo’} is typically \texttt{‘latin1’}, \texttt{‘latin2’}, \texttt{‘utf8’} or \texttt{‘cp1252’} or \texttt{‘cp1250’}) or a comment line
\begin{verbatim}
%\SweaveUTF8
\end{verbatim}
to declare UTF-8 input (the default encoding assumed by \texttt{pdflatex} since 2018), or they will give an error. Re-encoding can be turned off completely with argument \texttt{encoding = "bytes"}.

Syntax Definition

Sweave allows a flexible syntax framework for marking documentation and text chunks. The default is a noweb-style syntax, as alternative a \LaTeXX-style syntax can be used. (See the user manual for further details.)

If \texttt{syntax = NULL} (the default) then the available syntax objects are consulted in turn, and selected if their extension component matches (as a regexp) the file name. Objects \texttt{SweaveSyntaxNoweb} (with extension = "\.[rsRS]nw$") and \texttt{SweaveSyntaxLatex} (with extension = "\.[rsRS]tex$") are supplied, but users or packages can supply others with names matching the pattern \texttt{SweaveSyntax\*}.

Author(s)

Friedrich Leisch and R-core.

References


See Also

‘Sweave User Manual’, a vignette in the \texttt{utils} package.
\texttt{RweaveLatex}, \texttt{Rtangle}. Alternative Sweave drivers are in, for example, packages \texttt{weaver} (Bioconductor), \texttt{R2HTML}, and \texttt{ascii}.
\texttt{tools:::buildVignette} to process source files using Sweave or alternative vignette processing engines.
Examples

testfile <- system.file("Sweave", "Sweave-test-1.Rnw", package = "utils")

## enforce par(ask = FALSE)
options(device.ask.default = FALSE)

## create a LaTeX file - in the current working directory, getwd():
Sweave(testfile)

## This can be compiled to PDF by
## tools::texi2pdf("Sweave-test-1.tex")

## or outside R by
##
## ## R CMD texi2pdf Sweave-test-1.tex
## # on Unix-alikes which sets the appropriate TEXINPUTS path.
## ##
## ## On Windows,
## ## Rcmd texify --pdf Sweave-test-1.tex
## # if MiKTeX is available.

## create an R source file from the code chunks
Stangle(testfile)
## which can be sourced, e.g.
source("Sweave-test-1.R")

---

SweaveSyntConv  Convert Sweave Syntax

Description

This function converts the syntax of files in Sweave format to another Sweave syntax definition.

Usage

SweaveSyntConv(file, syntax, output = NULL)

Arguments

file  Name of Sweave source file.
syntax An object of class SweaveSyntax or a character string with its name giving the target syntax to which the file is converted.
output Name of output file, default is to remove the extension from the input file and to add the default extension of the target syntax. Any directory names in file are also removed such that the output is created in the current working directory.

Author(s)

Friedrich Leisch
tar

Create a Tar Archive

Description
Create a tar archive.

Usage
```
tar(tarfile, files = NULL, compression = c("none", "gzip", "bzip2", "xz"), compression_level = 6, tar = Sys.getenv("tar"), extra_flags = "")
```

Arguments
- **tarfile**: The pathname of the tar file: tilde expansion (see `path.expand`) will be performed. Alternatively, a connection that can be used for binary writes.
- **files**: A character vector of filepaths to be archived: the default is to archive all files under the current directory.
- **compression**: character string giving the type of compression to be used (default none). Can be abbreviated.
- **compression_level**: integer: the level of compression. Only used for the internal method.
- **tar**: character string: the path to the command to be used. If the command itself contains spaces it needs to be quoted (e.g., by `shQuote`) – but argument `tar` may also contain flags separated from the command by spaces.
- **extra_flags**: Any extra flags for an external tar.

See Also
- ‘Sweave User Manual’, a vignette in the **utils** package.
- **RweaveLatex**, **Rtangle**

Examples
```
testfile <- system.file("Sweave", "Sweave-test-1.Rnw", package = "utils")

## convert the file to latex syntax
SweaveSyntConv(testfile, SweaveSyntaxLatex)

## and run it through Sweave
Sweave("Sweave-test-1.Stex")
```
Details

This is either a wrapper for a `tar` command or uses an internal implementation in R. The latter is used if `tarfile` is a connection or if the argument `tar` is "internal" or "" (the ‘factory-fresh’ default). Note that whereas Unix-alike versions of R set the environment variable `TAR`, its value is not the default for this function.

Argument `extra_flags` is passed to an external `tar` and so is platform-dependent. Possibly useful values include ‘-h’ (follow symbolic links, also ‘-L’ on some platforms), ‘--acls’, ‘--exclude-backups’, ‘--exclude-vcs’ (and similar) and on Windows ‘--force-local’ (so drives can be included in filepaths). Rtools 4 and earlier included a tar which used ‘--force-local’, but Rtools 4.2 includes original GNU tar, which does not use it by default.

A convenient and robust way to set options for GNU tar is via environment variable `TAR_OPTIONS`. Appending ‘--force-local’ to `TAR` does not work with GNU tar due to restrictions on how some options can be mixed. The tar available on Windows 10 (libarchive’s bsdtar) supports drive letters by default. It does not support the ‘--force-local’, but ignores `TAR_OPTIONS`.

For GNU tar, ‘--format=ustar’ forces a more portable format. (The default is set at compilation and will be shown at the end of the output from `tar --help`: for version 1.30 ‘out-of-the-box’ it is ‘--format=gnu’, but the manual says the intention is to change to ‘--format=posix’ which is the same as `pax` – it was never part of the POSIX standard for `tar` and should not be used.) For libarchive’s bsdtar, ‘--format=ustar’ is more portable than the default.

One issue which can cause an external command to fail is a command line too long for the system shell: as from R 3.5.0 this is worked around if the external command is detected to be GNU tar or libarchive tar (aka bsdtar).

Note that `files = '.'` will usually not work with an external `tar` as that would expand the list of files after `tarfile` is created. (It does work with the default internal method.)

Value

The return code from `system` or 0 for the internal version, invisibly.

Portability

The ‘tar’ format no longer has an agreed standard! ‘Unix Standard Tar’ was part of POSIX 1003.1:1998 but has been removed in favour of `pax`, and in any case many common implementations diverged from the former standard.

Many R platforms use a version of GNU tar, but the behaviour seems to be changed with each version. macOS >= 10.6, FreeBSD and Windows 10 use bsdtar from the libarchive project (but for macOS a version from 2017 or earlier, 2010 for High Sierra), and commercial Unixes will have their own versions. bsdtar is available for many other platforms: macOS up to at least 10.9 had GNU tar as gnutar and other platforms, e.g. Solaris, have it as gtar: on a Unix-alike `configure` will try gnutar and gtar before tar.

Known problems arise from

• The handling of file paths of more than 100 bytes. These were unsupported in early versions of tar, and supported in one way by POSIX tar and in another by GNU tar and yet another by the POSIX `pax` command which recent tar programs often support. The internal implementation warns on paths of more than 100 bytes, uses the ‘ustar’ way from the 1998 POSIX standard which supports up to 256 bytes (depending on the path: in particular the final component is limited to 100 bytes) if possible, otherwise the GNU way (which is widely supported, including by `untar`).

Most formats do not record the encoding of file paths.
• (File) links. tar was developed on an OS that used hard links, and physical files that were referred to more than once in the list of files to be included were included only once, the remaining instances being added as links. Later a means to include symbolic links was added. The internal implementation supports symbolic links (on OSes that support them), only. Of course, the question arises as to how links should be unpacked on OSes that do not support them: for regular files file copies can be used.

Names of links in the ‘ustar’ format are restricted to 100 bytes. There is an GNU extension for arbitrarily long link names, but bsdtar ignores it. The internal method uses the GNU extension, with a warning.

• Header fields, in particular the padding to be used when fields are not full or not used. POSIX did define the correct behaviour but commonly used implementations did (and still do) not comply.

• File sizes. The ‘ustar’ format is restricted to 8GB per (uncompressed) file.

For portability, avoid file paths of more than 100 bytes and all links (especially hard links and symbolic links to directories).

The internal implementation writes only the blocks of 512 bytes required (including trailing blocks of nuls), unlike GNU tar which by default pads with ‘nul’ to a multiple of 20 blocks (10KB). Implementations which pad differ on whether the block padding should occur before or after compression (or both): padding was designed for improved performance on physical tape drives.

The ‘ustar’ format records file modification times to a resolution of 1 second: on file systems with higher resolution it is conventional to discard fractional seconds.

Compression

When an external tar command is used, compressing the tar archive requires that tar supports the ‘-z’, ‘-j’ or ‘-J’ flag, and may require the appropriate command (gzip, bzip2 or xz) to be available. For GNU tar, further compression programs can be specified by e.g. extra_flags = "-I lz4". Some versions of bsdtar accept options such as ‘--lz4’, ‘--lzop’ and ‘--lrzip’ or an external compressor via --use-compress-program lz4: these could be supplied in extra_flags.

NetBSD prior to 8.0 used flag ‘--xz’ rather than ‘-J’, so this should be used via extra_flags = "--xz" rather than compression = "xz". The commands from OpenBSD and the Heirloom Toolchest are not documented to support xz.

The tar programs in commercial Unixen such as AIX and Solaris do not support compression.

Note

For users of macOS. Apple’s file systems have a legacy concept of ‘resource forks’ dating from classic Mac OS and rarely used nowadays. Apple’s version of tar stores these as separate files in the tarball with names prefixed by ‘_’, and unpacks such files into resource forks (if possible): other ways of unpacking (including untar in R) unpack them as separate files.

When argument tar is set to the command tar on macOS, environment variable COPYFILE_DISABLE=1 is set, which for the system version of tar prevents these separate files being included in the tarball.

See Also


toLatex

2135

untar.

toLatex

Converting R Objects to BibTeX or LaTeX

Description
These methods convert R objects to character vectors with BibTeX or LaTeX markup.
Usage
toBibtex(object, ...)
toLatex(object, ...)
## S3 method for class 'Bibtex'
print(x, prefix = "", ...)
## S3 method for class 'Latex'
print(x, prefix = "", ...)
Arguments
object
x
prefix
...

object of a class for which a toBibtex or toLatex method exists.
object of class "Bibtex" or "Latex".
a character string which is printed at the beginning of each line, mostly used to
insert whitespace for indentation.
in the print methods, passed to writeLines.

Details
Objects of class "Bibtex" or "Latex" are simply character vectors where each element holds one
line of the corresponding BibTeX or LaTeX file.
See Also
citEntry and sessionInfo for examples

txtProgressBar

Text Progress Bar

Description
Text progress bar in the R console.
Usage
txtProgressBar(min = 0, max = 1, initial = 0, char = "=",
width = NA, title, label, style = 1, file = "")
getTxtProgressBar(pb)
setTxtProgressBar(pb, value, title = NULL, label = NULL)
## S3 method for class 'txtProgressBar'
close(con, ...)


Arguments

- **min, max** (finite) numeric values for the extremes of the progress bar. Must have min < max.
- **initial, value** initial or new value for the progress bar. See ‘Details’ for what happens with invalid values.
- **char** the character (or character string) to form the progress bar. Must have non-zero display width.
- **width** the width of the progress bar, as a multiple of the width of char. If NA, the default, the number of characters is that which fits into getOption("width").
- **style** the ‘style’ of the bar – see ‘Details’.
- **file** an open connection object or "" which indicates the console: stderr() might be useful here.
- **pb, con** an object of class "txtProgressBar".
- **title, label** ignored, for compatibility with other progress bars.
- **...** for consistency with the generic.

Details

`txtProgressBar` will display a progress bar on the R console (or a connection) via a text representation.

`setTxtProgressbar` will update the value. Missing (NA) and out-of-range values of value will be (silently) ignored. (Such values of initial cause the progress bar not to be displayed until a valid value is set.)

The progress bar should be closed when finished with: this outputs the final newline character.

**style = 1** and **style = 2** just shows a line of char. They differ in that **style = 2** redraws the line each time, which is useful if other code might be writing to the R console. **style = 3** marks the end of the range by | and gives a percentage to the right of the bar.

Value

For `txtProgressBar` an object of class "txtProgressBar".

For `getTxtProgressbar` and `setTxtProgressbar`, a length-one numeric vector giving the previous value (invisibly for `setTxtProgressbar`).

Note

Using **style 2** or **3** or reducing the value with **style = 1** uses \"\r\" to return to the left margin – the interpretation of carriage return is up to the terminal or console in which R is running, and this is liable to produce ugly output on a connection other than a terminal, including when stdout() is redirected to a file.

See Also

`winProgressBar` (Windows only), `tkProgressBar` (Unix-alike platforms).
type.convert

Examples

# slow
testit <- function(x = sort(runif(20)), ...) {
  pb <- txtProgressBar(...)
  for(i in c(0, x, 1)) {Sys.sleep(0.5); setTxtProgressBar(pb, i)}
  Sys.sleep(1)
  close(pb)
}
testit()
testit(runif(10))
testit(style = 3)
testit(char= '\u27a4')

---

type.convert  Convert Data to Appropriate Type

Description

Convert a data object to logical, integer, numeric, complex, character or factor as appropriate.

Usage

type.convert(x, ...)
## Default S3 method:
type.convert(x, na.strings = "NA", as.is, dec = ".", numerals = c("allow.loss", "warn.loss", "no.loss"), tryLogical = TRUE, ...)
## S3 method for class 'data.frame'
type.convert(x, ...)
## S3 method for class 'list'
type.convert(x, ...)

Arguments

x a vector, matrix, array, data frame, or list.
na.strings a vector of strings which are to be interpreted as NA values. Blank fields are also considered to be missing values in logical, integer, numeric or complex vectors.
as.is whether to store strings as plain character. When false, convert character vectors to factors. See 'Details'.
dec the character to be assumed for decimal points.
numerals string indicating how to convert numbers whose conversion to double precision would lose accuracy, typically when x has more digits than can be stored in a double. Can be abbreviated. Possible values are numerals = "allow.loss", default: the conversion happens with some accuracy loss.
numerals = "warn.loss": a warning about accuracy loss is signalled and the conversion happens as with numerals = "allow.loss".
numerals = "no.loss": x is not converted to a number, but to a factor or character, depending on as.is.
tryLogical  a logical determining if vectors consisting entirely of F, T, FALSE, TRUE and
na.strings should be converted to logical; true, by default.
...  arguments to be passed to or from methods.

Details

This helper function is used by read.table. When the data object x is a data frame or list, the
function is called recursively for each column or list element.

Given a vector, the function attempts to convert it to logical, integer, numeric or complex, and when
additionally as.is = FALSE (no longer the default!), converts a character vector to factor. The first
type that can accept all the non-missing values is chosen.

Vectors which are entirely missing values are converted to logical, since NA is primarily logical.

If tryLogical is true as by default, vectors containing just F, T, FALSE, TRUE and values from
na.strings are converted to logical. This may be surprising in a context where you have many
character columns with e.g., 1-letter strings and you happen to get one with only “F”. In such
cases tryLogical = FALSE is recommended.

Vectors containing optional whitespace followed by decimal constants representable as R integers
or values from na.strings are converted to integer. Other vectors containing optional whites-
pace followed by other decimal or hexadecimal constants (see NumericConstants), or NaN, Inf or
infinity (ignoring case) or values from na.strings are converted to numeric. Where converting
inputs to numeric or complex would result in loss of accuracy they can optionally be returned as
strings or (for as.is = FALSE) factors.

Since this is a helper function, the caller should always pass an appropriate value of as.is.

Value

An object like x but using another storage mode when appropriate.

Author(s)

R Core, with a contribution by Arni Magnusson

See Also

read.table, class, storage.mode.

Examples

## Numeric to integer
class(rivers)
x <- type.convert(rivers, as.is = TRUE)
class(x)

## Convert many columns
auto <- type.convert(mtcars, as.is = TRUE)
str(mtcars)
str(auto)

## Convert matrix
phones <- type.convert(WorldPhones, as.is = TRUE)
storage.mode(WorldPhones)
storage.mode(phones)
## Factor or character

```r
chr <- c("A", "B", "B", "A")
ch2 <- c("F", "F", "NA", "F")
(fac <- factor(chr))
type.convert(chr, as.is = FALSE) # -> factor
type.convert(fac, as.is = FALSE) # -> factor
type.convert(chr, as.is = TRUE) # -> character
type.convert(fac, as.is = TRUE) # -> character
type.convert(ch2, as.is = TRUE) # -> logical
type.convert(ch2, as.is = TRUE, tryLogical=FALSE) # -> character
```

## untar

### Extract or List Tar Archives

**Description**

Extract files from or list the contents of a tar archive.

**Usage**

```r
untar(tarfile, files = NULL, list = FALSE, exdir = ".",
       compressed = NA, extras = NULL, verbose = FALSE,
       restore_times = TRUE,
       support_old_tars = Sys.getenv("R_SUPPORT_OLD_TARS", FALSE),
       tar = Sys.getenv("TAR"))
```

**Arguments**

- **tarfile**
  - The pathname of the tar file: tilde expansion (see `path.expand`) will be performed. Alternatively, a `connection` that can be used for binary reads. For a `compressed` tarfile, and if a connection is to be used, that should be created by `gzfile(.)` (or `gzcon(.)` which currently only works for "gzip", whereas `gzfile()` works for all compressions available in `tar()`).

- **files**
  - A character vector of recorded filepaths to be extracted: the default is to extract all files.

- **list**
  - If TRUE, list the files (the equivalent of `tar -tf`). Otherwise extract the files (the equivalent of `tar -xf`).

- **exdir**
  - The directory to extract files to (the equivalent of `tar -C`). It will be created if necessary.

- **compressed**
  - (Deprecated in favour of auto-detection, used only for an external `tar` command.) Logical or character string. Values "gzip", "bzip2" and "xz" select that form of compression (and may be abbreviated to the first letter). TRUE indicates `gzip` compression, FALSE no known compression, and NA (the default) indicates that the type is to be inferred from the file header.

  The external command may ignore the selected compression type but detect a type automatically.

- **extras**
  - NULL or a character string: further command-line flags such as `'-p'` to be passed to an external `tar` program.

- **verbose**
  - logical: if true echo the command used for an external `tar` program.
restore_times logical. If true (default) restore file modification times. If false, the equivalent of the ‘-m’ flag. Times in tarballs are supposed to be in UTC, but tarballs have been submitted to CRAN with times in the future or far past: this argument allows such times to be discarded.

Note that file times in a tarball are stored with a resolution of 1 second, and can only be restored to the resolution supported by the file system (which on a FAT system is 2 seconds).

support_old_tars logical. If false (the default), the external tar command is assumed to be able handle compressed tarfiles and if compressed does not specify it, to automatically detect the type of compression. (The major implementations have done so since 2009; for GNU tar since version 1.22.)

If true, the R code calls an appropriate decompressor and pipes the output to tar, for compressed = NA examining the tarfile header to determine the type of compression.

tar character string: the path to the command to be used or "internal". If the command itself contains spaces it needs to be quoted – but tar can also contain flags separated from the command by spaces.

Details

This is either a wrapper for a tar command or for an internal implementation written in R. The latter is used if tarfile is a connection or if the argument tar is "internal" or "" (except on Windows, when tar.exe is tried first).

Unless otherwise stated three types of compression of the tar file are supported: gzip, bzip2 and xz.

What options are supported will depend on the tar implementation used: the "internal" one is intended to provide support for most in a platform-independent way.

GNU tar: Modern GNU tar versions support compressed archives and since 1.15 are able to detect the type of compression automatically: version 1.22 added support for xz compression.

On a Unix-alike, configure will set environment variable TAR, preferring GNU tar if found.

bsdTar: macOS 10.6 and later (and FreeBSD and some other OSes) have a tar from the libarchive project which detects all three forms of compression automagically (even if undocumented in macOS).

NetBSD: It is undocumented if NetBSD’s tar can detect compression automatically: for versions before 8 the flag for xz compression was ‘--xz’ not ‘-J’. So support_old_tars = TRUE is recommended (or use bsdTar if installed).

OpenBSD: OpenBSD’s tar does not detect compression automatically. It has no support for xz beyond reporting that the file is xz-compressed. So support_old_tars = TRUE is recommended.

Heirloom Toolchest: This tar does automatically detect gzip and bzip2 compression (undocumented) but has no support for xz compression.

Older support: Environment variable R_GZIPCMD gives the command to decompress gzip files, and R_BZIPCMD for bzip2 files. (On Unix-alikes these are set at installation if found.) xz is used if available: if not decompression is expected to fail.

Arguments compressed, extras and verbose are only used when an external tar is used.

Some external tar commands will detect some of lrzip, lzma, lz4, lzip and zstd compression in addition to gzip, bzip2 and xz. (For some external tar commands, compressed
unzip

Extract or List Zip Archives

Description

Extract files from or list a zip archive.

Usage

```r
unzip(zipfile, files = NULL, list = FALSE, overwrite = TRUE,
      junkpaths = FALSE, exdir = ".", unzip = "internal",
      setTimes = FALSE)
```
Arguments

zipfile The pathname of the zip file: tilde expansion (see path.expand) will be performed.

files A character vector of recorded filepaths to be extracted: the default is to extract all files.

list If TRUE, list the files and extract none. The equivalent of unzip -l.

overwrite If TRUE, overwrite existing files (the equivalent of unzip -o), otherwise ignore such files (the equivalent of unzip -n).

junkpaths If TRUE, use only the basename of the stored filepath when extracting. The equivalent of unzip -j.

exdir The directory to extract files to (the equivalent of unzip -d). It will be created if necessary.

unzip The method to be used. An alternative is to use getOption("unzip"), which on a Unix-alike may be set to the path to a unzip program.

setTimes logical. For the internal method only, should the file times be set based on the times in the zip file? (NB: this applies to included files, not to directories.)

Value

If list = TRUE, a data frame with columns Name (character) Length (the size of the uncompressed file, numeric) and Date (of class "POSIXct").

Otherwise for the "internal" method, a character vector of the filepaths extracted to, invisibly.

Note

The default internal method is a minimal implementation, principally designed for Windows’ users to be able to unpack Windows binary packages without external software. It does not (for example) support Unicode filenames as introduced in zip 3.0: for that use unzip = "unzip" with unzip 6.00 or later. It does have some support for bzip2 compression and > 2GB zip files (but not >= 4GB files pre-compression contained in a zip file: like many builds of unzip it may truncate these, in R’s case with a warning if possible).

If unzip specifies a program, the format of the dates listed with list = TRUE is unknown (on Windows it can even depend on the current locale) and the return values could be NA or expressed in the wrong time zone or misinterpreted (the latter being far less likely as from unzip 6.00).

File times in zip files are stored in the style of MS-DOS, as local times to an accuracy of 2 seconds. This is not very useful when transferring zip files between machines (even across continents), so we chose not to restore them by default.

Source

The internal C code uses zlib and is in particular based on the contributed 'minizip' application in the zlib sources (from https://zlib.net/) by Gilles Vollant.

See Also

unz to read a single component from a zip file.

zip for packing, i.e., the “inverse” of unzip(); further untar and tar, the corresponding pair for (un)packing tar archives (“tarballs”) such as R source packages.
update.packages

Compare Installed Packages with CRAN-like Repositories

Description

old.packages indicates packages which have a (suitable) later version on the repositories whereas update.packages offers to download and install such packages.

new.packages looks for (suitable) packages on the repositories that are not already installed, and optionally offers them for installation.

Usage

update.packages(lib.loc = NULL, repos = getOption("repos"),
    contriburl = contrib.url(repos, type),
    method, instlib = NULL,
    ask = TRUE, available = NULL,
    oldPkgs = NULL, ..., checkBuilt = FALSE,
    type = getOption("pkgType"))

old.packages(lib.loc = NULL, repos = getOption("repos"),
    contriburl = contrib.url(repos, type),
    instPkgs = installed.packages(lib.loc = lib.loc, ...),
    method, available = NULL, checkBuilt = FALSE, ...,
    type = getOption("pkgType"))

new.packages(lib.loc = NULL, repos = getOption("repos"),
    contriburl = contrib.url(repos, type),
    instPkgs = installed.packages(lib.loc = lib.loc, ...),
    method, available = NULL, ask = FALSE, ...,
    type = getOption("pkgType"))

Arguments

lib.loc character vector describing the location of R library trees to search through (and update packages therein), or NULL for all known trees (see .libPaths).
repos character vector, the base URL(s) of the repositories to use, e.g., the URL of a CRAN mirror such as "https://cloud.r-project.org".
contriburl URL(s) of the contrib sections of the repositories. Use this argument if your repository is incomplete. Overrides argument repos. Incompatible with type = "both".
method Download method, see download.file. Unused if a non-NULL available is supplied.
instlib character string giving the library directory where to install the packages.
ask logical indicating whether to ask the user to select packages before they are downloaded and installed, or the character string "graphics", which brings up a widget to allow the user to (de-)select from the list of packages which could be updated. The latter value only works on systems with a GUI version of select.list, and is otherwise equivalent to ask = TRUE. ask does not control questions asked before installing packages from source via type = "both" (see option "install.packages.compile.from.source").
update.packages

available an object as returned by available.packages listing packages available at the repositories, or NULL which makes an internal call to available.packages. Incompatible with type = "both".

checkBuilt If TRUE, a package built under an earlier major.minor version of R (e.g., 3.4) is considered to be ‘old’.

oldPkgs if specified as non-NULL, update.packages() only considers these packages for updating. This may be a character vector of package names or a matrix as returned by old.packages.

instPkgs by default all installed packages, installed.packages(lib.loc = lib.loc). A subset can be specified; currently this must be in the same (character matrix) format as returned by installed.packages().

... Arguments such as destdir and dependencies to be passed to install.packages and ignore_repo_cache, max_repo_cache_age and noCache to available.packages or installed.packages.

type character, indicating the type of package to download and install. See install.packages.

Details

diff.packages compares the information from available.packages with that from instPkgs (computed by installed.packages by default) and reports installed packages that have newer versions on the repositories or, if checkBuilt = TRUE, that were built under an earlier minor version of R (for example built under 3.3.x when running R 3.4.0). (For binary package types there is no check that the version on the repository was built under the current minor version of R, but it is advertised as being suitable for this version.)

diff.new.packages does the same comparison but reports uninstalled packages that are available at the repositories. If ask != FALSE it asks which packages should be installed in the first element of lib.loc.

The main function of the set is update.packages. First a list of all packages found in lib.loc is created and compared with those available at the repositories. If ask = TRUE (the default) packages with a newer version are reported and for each one the user can specify if it should be updated. If so the packages are downloaded from the repositories and installed in the respective library path (or instlib if specified).

For how the list of suitable available packages is determined see available.packages. available = NULL make a call to available.packages(contriburl = contriburl, method = method) and hence by default filters on R version, OS type and removes duplicates.

Value

update.packages returns NULL invisibly.

For old.packages, NULL or a matrix with one row per package, row names the package names and column names "Package", "LibPath", "Installed" (the version), "Built" (the version built under), "ReposVer" and "Repository".

For new.packages a character vector of package names, after any selected via ask have been installed.

Warning

Take care when using dependencies (passed to install.packages) with update.packages, for it is unclear where new dependencies should be installed. The current implementation will only allow it if all the packages to be updated are in a single library, when that library will be used.
### upgrade

**Upgrade**

### Description
Upgrade objects.

### Usage
```
upgrade(object, ...)  
```

### Arguments
- **object**: an R object.
- **...**: further arguments passed to or from other methods.

### Details
This is a generic function, with a method for "packageStatus" objects.

### url.show

**Display a Text URL**

### Description
Extension of `file.show` to display text files from a remote server.

### Usage
```
url.show(url, title = url, file = tempfile(), 
          delete.file = TRUE, method, ...)  
```

### Arguments
- **url**: The URL to read from.
- **title**: Title for the browser.
- **file**: File to copy to.
- **delete.file**: Delete the file afterwards?
- **method**: File transfer method: see `download.file`
- **...**: Arguments to pass to `file.show`.  

---

**See Also**

- `install.packages`, `available.packages`, `download.packages`, `installed.packages`, `contrib.url`

The options listed for `install.packages` under `options`.

See `download.file` for how to handle proxies and other options to monitor file transfers.

- `INSTALL`, `REMOVE`, `remove.packages`, `library`, `.packages`, `read.dcf`

The "R Installation and Administration" manual for how to set up a repository.
Note

Since this is for text files, it will convert to CRLF line endings on Windows.

See Also

url, file.show, download.file

Examples

## Not run: url.show("https://www.stats.ox.ac.uk/pub/datasets/csb/ch3a.txt")

---

**URLencode**

**Encode or Decode (partial) URLs**

**Description**

Functions to percent-encode or decode characters in URLs.

**Usage**

URLencode(URL, reserved = FALSE, repeated = FALSE)
URLdecode(URL)

**Arguments**

URL  a character vector.
reserved  logical: should ‘reserved’ characters be encoded? See ‘Details’.
repeated  logical: should apparently already-encoded URLs be encoded again?

**Details**

Characters in a URL other than the English alphanumeric characters and ‘- _ . ~’ should be encoded as % plus a two-digit hexadecimal representation, and any single-byte character can be so encoded. (Multi-byte characters are encoded byte-by-byte.) The standard refers to this as ‘percent-encoding’. In addition, ‘! $ & ’ ( ) * + , ; = : / ? @ # [ ]’ are reserved characters, and should be encoded unless used in their reserved sense, which is scheme specific. The default in `URLencode` is to leave them alone, which is appropriate for ‘file://’ URLs, but probably not for ‘http://’ ones.

An ‘apparently already-encoded URL’ is one containing %xx for two hexadecimal digits.

**Value**

A character vector.

**References**

Internet STD 66 (formerly RFC 3986), [https://www.rfc-editor.org/info/std66](https://www.rfc-editor.org/info/std66)
Examples

```r
(y <- URLencode("a url with spaces and / and @"))
URLdecode(y)
(y <- URLencode("a url with spaces and / and @", reserved = TRUE))
URLdecode(y)

URLdecode(z <- "ab%20cd")
c(URLencode(z), URLencode(z, repeated = TRUE)) # first is usually wanted

## both functions support character vectors of length > 1
y <- URLdecode(URLencode(c("url with space", "another one")))
```

### `utils-deprecated`

#### Deprecated Functions in Package `utils`

**Description**

(Currently none)

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as of the next release.

**See Also**

`Deprecated`, `Defunct`

---

#### `View`

**Invoke a Data Viewer**

**Description**

Invoke a spreadsheet-style data viewer on a matrix-like R object.

**Usage**

```r
View(x, title)
```

**Arguments**

- **x**: an R object which can be coerced to a data frame with non-zero numbers of rows and columns.
- **title**: title for viewer window. Defaults to name of `x` prefixed by `Data:`.
Details

Object x is coerced (if possible) to a data frame, then columns are converted to character using `format.data.frame`. The object is then viewed in a spreadsheet-like data viewer, a read-only version of `data.entry`.

If there are row names on the data frame that are not `1:nrow`, they are displayed in a separate first column called `row.names`.

Objects with zero columns or zero rows are not accepted.

**On Unix-alikes**, the array of cells can be navigated by the cursor keys and Home, End, Page Up and Page Down (where supported by X11) as well as Enter and Tab.

**On Windows**, the array of cells can be navigated via the scrollbars and by the cursor keys, Home, End, Page Up and Page Down.

On Windows, the initial size of the data viewer window is taken from the default dimensions of a pager (see `Rconsole`), but adjusted downwards to show a whole number of rows and columns.

Value

Invisible `NULL`. The functions puts up a window and returns immediately: the window can be closed via its controls or menus.

See Also

`edit.data.frame, data.entry`.

---

**vignette** View, List or Get R Source of Package Vignettes

Description

View a specified package vignette, or list the available ones; display it rendered in a viewer, and get or edit its R source file.

Usage

```r
vignette(topic, package = NULL, lib.loc = NULL, all = TRUE)
```

```r
## S3 method for class 'vignette'
print(x, ...)
## S3 method for class 'vignette'
edit(name, ...)
```

Arguments

- `topic` a character string giving the (base) name of the vignette to view. If omitted, all vignettes from all installed packages are listed.
- `package` a character vector with the names of packages to search through, or `NULL` in which ‘all’ packages (as defined by argument `all`) are searched.
vignette

lib.loc a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known.

all logical; if TRUE search all available packages in the library trees specified by lib.loc, and if FALSE, search only attached packages.

x, name object of class vignette.

... ignored by the print method, passed on to file.edit by the edit method.

Details

Function vignette returns an object of the same class, the print method opens a viewer for it.

On Unix-alikes, the program specified by the pdfviewer option is used for viewing PDF versions of vignettes.

If several vignettes have PDF/HTML versions with base name identical to topic, the first one found is used.

If no topics are given, all available vignettes are listed. The corresponding information is returned in an object of class "packageIQR".

See Also

browseVignettes for an HTML-based vignette browser; RShowDoc(<basename>, package = "<pkg>") displays a “rendered” vignette (pdf or html).

Examples

## List vignettes from all *attached* packages
vignette(all = FALSE)

## List vignettes from all *installed* packages (can take a long time!):
vignette(all = TRUE)

## The grid intro vignette -- open it
## Not run: vignette("grid") # calling print()
## The same (conditional on existence of the vignette).
## Note that 'package = *' is much faster in the case of many installed packages:
#(!!is.null(v1 <- vignette("grid", package="grid"))) {
## Not run: v1 # calling print(.)
  str(v1)
## Now let us have a closer look at the code

## Not run: edit(v1) # e.g., to send lines ...
## if( has vignette "installed")
## A package can have more than one vignette (package grid has several):
vignette(package = "grid")
if(interactive()) {
  ## vignette("rotated")
  ## The same, but without searching for it:
  vignette("rotated", package = "grid")
}
Collect and Summarize Errors From List

**Description**
Collect errors (class "error", typically from `tryCatch`) from a list `x` into a “summary warning”, by default produce a `warning` and keep that message as "warningMsg" attribute.

**Usage**
```r
warnErrList(x, warn = TRUE, errValue = NULL)
```

**Arguments**
- `x` a list, typically from applying models to a list of data (sub)sets, e.g., using `tryCatch(*, error = identity).
- `warn` logical indicating if `warning()` should be called.
- `errValue` the value with which errors should be replaced.

**Value**
a list of the same length and names as the `x` argument, with the error components replaced by `errValue`, `NULL` by default, and summarized in the "warningMsg" attribute.

**See Also**
The `warnErrList()` utility has been used in `lmList()` and `nlsList()` in recommended package `nlme` forever.

**Examples**
```r
## Regression for each Chick:
ChWtgrps <- split(ChickWeight, ChickWeight[,"Chick"])
sapply(ChWtgrps, nrow)# typically 12 obs.
nlis1 <- lapply(ChWtgrps, function(DAT) tryCatch(error = identity,
  lm(weight ~ (Time + I(Time^2)) * Diet, data = DAT))
nl1 <- warnErrList(nlis1) #-> warning :
## 50 times the same error (as Diet has only one level in each group)
stopifnot(sapply(nl1, is.null)) ## all errors --> all replaced by NULL
nlis2 <- lapply(ChWtgrps, function(DAT) tryCatch(error = identity,
  lm(weight ~ Time + I(Time^2), data = DAT))
nl2 <- warnErrList(nlis2)
stopifnot(identical(nl2, nlis2)) # because there was *no* error at all
nlis3 <- lapply(ChWtgrps, function(DAT) tryCatch(error = identity,
  lm(weight ~ poly(Time, 3), data = DAT))
nl3 <- warnErrList(nlis3) # 1 error caught:
stopifnot(inherits(nlis3[[1]], "error")
  , identical(nlis3[-1], nlis3[-1]))
  , is.null(nlis3[[1]])
)
```
```r
## With different error messages
if(requireNamespace("nlme")) { # almost always, as it is recommended
```
data(Soybean, package="nlme")
attr(Soybean, "formula") #-> weight ~ Time | Plot => split by "Plot":
L <- lapply(split(Soybean, Soybean[,"Plot"]),
    function(DD) tryCatch(error = identity,
        nls(weight ~ SSlogis(Time, Asym, xmid, scal), data = DD)))
Lw <- warnErrList(L)
) # if <nlme>

Description

On MS Windows only, put up a dialog box to communicate with the user. There are various types,
either for the user to select from a set of buttons or to edit a string.

Usage

winDialog(type = c("ok", "okcancel", "yesno", "yesnocancel"),
    message)

winDialogString(message, default)

Arguments

type character. The type of dialog box. It will have the buttons implied by its name.
message character. The information field of the dialog box. Limited to 255 chars (by
    Windows, checked by R).
default character. The default string.

Value

For winDialog a character string giving the name of the button pressed (in capitals) or NULL (invis-
ibly) if the user had no choice.
For winDialogString a string giving the contents of the text box when Ok was pressed, or NULL if
Cancel was pressed.

Note

The standard keyboard accelerators work with these dialog boxes: where appropriate Return ac-
cepts the default action, Esc cancels and the underlined initial letter (Y or N) can be used.
These functions are only available on Windows.

See Also

winMenuAdd
file.choose to select a file
package windlgs in the package source distribution for ways to program dialogs in C in the
GraphApp toolkit.

Examples

## Not run: winDialog("yesno", "Is it OK to delete file blah")
Get Windows Version

Description
Get the self-reported Microsoft Windows version number.

Usage
win.version()

Details
win.version is an auxiliary function for sessionInfo and bug.report.

Value
A character string describing the version of Windows reported to be in use.

Note
This function is only available on Microsoft Windows.
The result is based on the Windows GetVersionEx API function. It is not known how to detect
a version of Windows before it is released, and hence the textual information returned by R may
identify an older version than installed. The build number is more reliable. When running R in
compatibility mode, the reported version including the build number is the compatibility version,
not the installed version.

Examples
if(.Platform$OS.type == "windows")
  print(win.version())

User Menus under MS Windows (Rgui)

Description
Enables users to add, delete and program menus for the Rgui in MS Windows.

Usage
winMenuAdd(menuName)
winMenuAddItem(menuName, itemName, action)
winMenuDel(menuName)
winMenuDelItem(menuName, itemName)
winMenuNames()
winMenuItems(menuName)
Arguments

menuname a character string naming a menu.
itemname a character string naming a menu item on an existing menu.
action a character string describing the action when that menu is selected, or "enable" or "disable".

Details

User menus are added to the right of existing menus, and items are added at the bottom of the menu. By default the action character string is treated as R input, being echoed on the command line and parsed and executed as usual.

If the menuname parameter of winMenuAddItem does not already exist, it will be created automatically.

Normally new submenus and menu items are added to the main console menu. They may be added elsewhere using the following special names:

$ConsoleMain The console menu (the default)
$ConsolePopup The console popup menu
$Graph<n>Main The menu for graphics window <n>
$Graph<n>Popup The popup menu for graphics window <n>

Specifying an existing item in winMenuAddItem enables the action to be changed.

Submenus can be specified by separating the elements in menuname by slashes: as a consequence menu names may not contain slashes.

If the action is specified as "none" no action is taken: this can be useful to reserve items for future expansion.

The function winMenuNames can be used to find out what menus have been created by the user and returns a vector of the existing menu names.

The winMenuItems function will take the name of a menu and return the items that exist in that menu. The return value is a named vector where the names correspond to the names of the items and the values of the vector are the corresponding actions.

The winMenuDel function will delete a menu and all of its items and submenus. winMenuDelItem just deletes one menu item.

The total path to an item (menu string plus item string) cannot exceed 1000 bytes, and the menu string cannot exceed 500 bytes.

Value

NULL, invisibly. If an error occurs, an informative error message will be given.

Note

These functions are only available on Windows and only when using the Rgui, hence not in ESS nor RStudio.

See Also

winDialog
Examples

```r
## Not run:
winMenuAdd("Testit")
winMenuAddItem("Testit", "one", "aaaa")
winMenuAddItem("Testit", "two", "bbbb")
winMenuAdd("Testit/extras")
winMenuAddItem("Testit", "-", "")
winMenuAddItem("Testit", "two", "disable")
winMenuAddItem("Testit", "three", "cccc")
winMenuAddItem("Testit/extras", "one more", "ddd")
winMenuAddItem("Testit/extras", "and another", "eee")
winMenuAdd("$ConsolePopup/Testit")
winMenuAddItem("$ConsolePopup/Testit", "six", "fff")
winMenuNames()
winMenuItems("Testit")
## End(Not run)
```

### winProgressBar

**Progress Bars under MS Windows**

**Description**

Put up a Windows progress bar widget, update and access it.

**Usage**

```r
winProgressBar(title = "R progress bar", label = "", 
min = 0, max = 1, initial = 0, width = 300)
```

```r
getWinProgressBar(pb)
setWinProgressBar(pb, value, title = NULL, label = NULL)
```

## S3 method for class 'winProgressBar'

```r
close(con, ...)
```

**Arguments**

- `title`, `label` character strings, giving the window title and the label on the dialog box respectively.
- `min, max` (finite) numeric values for the extremes of the progress bar.
- `initial, value` initial or new value for the progress bar.
- `width` the width of the progress bar in pixels: the dialog box will be 40 pixels wider (plus frame).
- `pb, con` an object of class "winProgressBar".
- `...` for consistency with the generic.
write.table

Details

**winProgressBar** will display a progress bar centred on the screen. Space will be allocated for the label only if it is non-empty.

**setWinProgressBar** will update the value and for non-NULL values, the title and label (provided there was one when the widget was created). Missing (NA) and out-of-range values of value will be (silently) ignored.

The progress bar should be closed when finished with, but it will be garbage-collected once no R object refers to it.

Value

For **winProgressBar** an object of class "winProgressBar".

For **getWinProgressBar** and **setWinProgressBar**, a length-one numeric vector giving the previous value (invisibly for **setWinProgressBar**).

Note

These functions are only available on Windows.

See Also

On all platforms, **txtProgressBar**, **tkProgressbar**

---

write.table  Data Output

Description

write.table prints its required argument x (after converting it to a data frame if it is not one nor a matrix) to a file or connection.

Usage

```r
write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ",
eol = "\n", na = "NA", dec = ".", row.names = TRUE,
col.names = TRUE, qmethod = c("escape", "double"),
fileEncoding = "")
write.csv(...)
write.csv2(...)
```

Arguments

- **x**: the object to be written, preferably a matrix or data frame. If not, it is attempted to coerce x to a data frame.
- **file**: either a character string naming a file or a connection open for writing. "" indicates output to the console.
- **append**: logical. Only relevant if file is a character string. If TRUE, the output is appended to the file. If FALSE, any existing file of the name is destroyed.
write.table

quote a logical value (TRUE or FALSE) or a numeric vector. If TRUE, any character or factor columns will be surrounded by double quotes. If a numeric vector, its elements are taken as the indices of columns to quote. In both cases, row and column names are quoted if they are written. If FALSE, nothing is quoted.

sep the field separator string. Values within each row of \texttt{x} are separated by this string.

eol the character(s) to print at the end of each line (row). For example, \texttt{eol = \"\r\n\"} will produce Windows’ line endings on a Unix-alike OS, and \texttt{eol = \"\r\"} will produce files as expected by Excel:mac 2004.

na the string to use for missing values in the data.

dec the string to use for decimal points in numeric or complex columns: must be a single character.

row.names either a logical value indicating whether the row names of \texttt{x} are to be written along with \texttt{x}, or a character vector of row names to be written.

col.names either a logical value indicating whether the column names of \texttt{x} are to be written along with \texttt{x}, or a character vector of column names to be written. See the section on ‘CSV files’ for the meaning of \texttt{col.names = NA}.

qmethod a character string specifying how to deal with embedded double quote characters when quoting strings. Must be one of "escape" (default for \texttt{write.table}), in which case the quote character is escaped in C style by a backslash, or "double" (default for \texttt{write.csv} and \texttt{write.csv2}), in which case it is doubled. You can specify just the initial letter.

fileEncoding character string: if non-empty declares the encoding to be used on a file (not a connection) so the character data can be re-encoded as they are written. See \texttt{file}.

... arguments to \texttt{write.table}: \texttt{append, col.names, sep, dec} and \texttt{qmethod} cannot be altered.

Details

If the table has no columns the rownames will be written only if \texttt{row.names = TRUE}, and \texttt{vice versa}.

Real and complex numbers are written to the maximal possible precision.

If a data frame has matrix-like columns these will be converted to multiple columns in the result (\texttt{via \texttt{as.matrix}}) and so a character \texttt{col.names} or a numeric \texttt{quote} should refer to the columns in the result, not the input. Such matrix-like columns are unquoted by default.

Any columns in a data frame which are lists or have a class (e.g., dates) will be converted by the appropriate \texttt{as.character} method: such columns are unquoted by default. On the other hand, any class information for a matrix is discarded and non-atomic (e.g., list) matrices are coerced to character.

Only columns which have been converted to character will be quoted if specified by \texttt{quote}.

The \texttt{dec} argument only applies to columns that are not subject to conversion to character because they have a class or are part of a matrix-like column (or matrix), in particular to columns protected by \texttt{I()}. Use \texttt{options("OutDec"}) to control such conversions.

In almost all cases the conversion of numeric quantities is governed by the option "scipen" (see \texttt{options}), but with the internal equivalent of \texttt{digits = 15}. For finer control, use \texttt{format} to make a character matrix/data frame, and call \texttt{write.table} on that.

These functions check for a user interrupt every 1000 lines of output.
If file is a non-open connection, an attempt is made to open it and then close it after use.

To write a Unix-style file on Windows, use a binary connection e.g. file = file("filename", "wb").

**CSV files**

By default there is no column name for a column of row names. If col.names = NA and row.names = TRUE a blank column name is added, which is the convention used for CSV files to be read by spreadsheets. Note that such CSV files can be read in R by

```r
read.csv(file = "<filename>", row.names = 1)
```

write.csv and write.csv2 provide convenience wrappers for writing CSV files. They set sep and dec (see below), qmethod = "double", and col.names to NA if row.names = TRUE (the default) and to TRUE otherwise.

write.csv uses "," for the decimal point and a comma for the separator.
write.csv2 uses a comma for the decimal point and a semicolon for the separator, the Excel convention for CSV files in some Western European locales.

These wrappers are deliberately inflexible: they are designed to ensure that the correct conventions are used to write a valid file. Attempts to change append, col.names, sep, dec or qmethod are ignored, with a warning.

CSV files do not record an encoding, and this causes problems if they are not ASCII for many other applications. Windows Excel 2007/10 will open files (e.g., by the file association mechanism) correctly if they are ASCII or UTF-16 (use fileEncoding = "UTF-16LE") or perhaps in the current Windows codepage (e.g., "CP1252"), but the ‘Text Import Wizard’ (from the ‘Data’ tab) allows far more choice of encodings. Excel:mac 2004/8 can import only ‘Macintosh’ (which seems to mean Mac Roman), ‘Windows’ (perhaps Latin-1) and ‘PC-8’ files. OpenOffice 3.x asks for the character set when opening the file.

There is an IETF RFC4180 (https://www.rfc-editor.org/rfc/rfc4180) for CSV files, which mandates comma as the separator and CRLF line endings. write.csv writes compliant files on Windows: use eol = "\r\n" on other platforms.

**Note**

write.table can be slow for data frames with large numbers (hundreds or more) of columns: this is inevitable as each column could be of a different class and so must be handled separately. If they are all of the same class, consider using a matrix instead.

**See Also**

The ‘R Data Import/Export’ manual.

```r
read.table, write.
write.matrix in package MASS.
```

**Examples**

```r
x <- data.frame(a = I("a \" quote""), b = pi)
```
```
tf <- tempfile(fileext = ".csv")
```

```r
## To write a CSV file for input to Excel one might use
write.table(x, file = tf, sep = ",", col.names = NA,
```
qmethod = "double")

file.show(tf)
## and to read this file back into R one needs
read.table(tf, header = TRUE, sep = ",", row.names = 1)
## NB: you do need to specify a separator if qmethod = "double".

### Alternatively
write.csv(x, file = tf)
read.csv(tf, row.names = 1)
## or without row names
write.csv(x, file = tf, row.names = FALSE)
read.csv(tf)

## Not run:
## To write a file in Mac Roman for simple use in Mac Excel 2004/8
write.csv(x, file = "foo.csv", fileEncoding = "macroman")
## or for Windows Excel 2007/10
write.csv(x, file = "foo.csv", fileEncoding = "UTF-16LE")

## End(Not run)

---

### Description

A wrapper for an external zip command to create zip archives.

### Usage

```r
zip(zipfile, files, flags = "-r9X", extras = ",",
    zip = Sys.getenv("R_ZIPCMD", "zip"))
```

### Arguments

- **zipfile**: The pathname of the zip file: tilde expansion (see `path.expand`) will be performed.
- **files**: A character vector of recorded filepaths to be included.
- **flags**: A character string of flags to be passed to the command: see `Details`.
- **extras**: An optional character vector: see `Details`.
- **zip**: A character string specifying the external command to be used.

### Details

On a Unix-alike, the default for zip will use the value of `R_ZIPCMD`, whose default is set in ‘`etc/Renviron`’ to the zip command found during configuration. On Windows, the default relies on a zip program (for example that from Rtools) being in the path.

The default for `flags` is that appropriate for zipping up a directory tree in a portable way: see `Details` for the zip command for other possibilities.

Argument `extras` can be used to specify `-x` or `-i` followed by a list of filepaths to exclude or include. Since `extras` will be treated as if passed to `system`, if the filepaths contain spaces they must be quoted e.g. by `shQuote`. 

### Create Zip Archives

A wrapper for an external zip command to create zip archives.
Value

The status value returned by the external command, invisibly.

See Also

unzip, unz; further, tar and untar for (un)packing tar archives.
Part II
Chapter 15

The KernSmooth package

bkde  Compute a Binned Kernel Density Estimate

Description
Returns x and y coordinates of the binned kernel density estimate of the probability density of the data.

Usage
bkde(x, kernel = "normal", canonical = FALSE, bandwidth, gridsize = 401L, range.x, truncate = TRUE)

Arguments
x  numeric vector of observations from the distribution whose density is to be estimated. Missing values are not allowed.
bandwidth  the kernel bandwidth smoothing parameter. Larger values of bandwidth make smoother estimates, smaller values of bandwidth make less smooth estimates. The default is a bandwidth computed from the variance of x, specifically the 'oversmoothed bandwidth selector' of Wand and Jones (1995, page 61).
kernel  character string which determines the smoothing kernel. kernel can be: "normal" - the Gaussian density function (the default). "box" - a rectangular box. "epanech" - the centred beta(2,2) density. "biweight" - the centred beta(3,3) density. "triweight" - the centred beta(4,4) density. This can be abbreviated to any unique abbreviation.
canonical  length-one logical vector: if TRUE, canonically scaled kernels are used.
gridsize  the number of equally spaced points at which to estimate the density.
range.x  vector containing the minimum and maximum values of x at which to compute the estimate. The default is the minimum and maximum data values, extended by the support of the kernel.
truncate  logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.
**Details**

This is the binned approximation to the ordinary kernel density estimate. Linear binning is used to obtain the bin counts. For each \( x \) value in the sample, the kernel is centered on that \( x \) and the heights of the kernel at each datapoint are summed. This sum, after a normalization, is the corresponding \( y \) value in the output.

**Value**

A list containing the following components:

- **x**: vector of sorted \( x \) values at which the estimate was computed.
- **y**: vector of density estimates at the corresponding \( x \).

**Background**

Density estimation is a smoothing operation. Inevitably there is a trade-off between bias in the estimate and the estimate’s variability: large bandwidths will produce smooth estimates that may hide local features of the density; small bandwidths may introduce spurious bumps into the estimate.

**References**


**See Also**

- `density`, `dpik`, `hist`, `ksmooth`.

**Examples**

```r
data(geyser, package="MASS")
x <- geyser$duration
est <- bkde(x, bandwidth=0.25)
plot(est, type="l")
```

---

**bkde2D**

*Compute a 2D Binned Kernel Density Estimate*

**Description**

Returns the set of grid points in each coordinate direction, and the matrix of density estimates over the mesh induced by the grid points. The kernel is the standard bivariate normal density.

**Usage**

```r
bkde2D(x, bandwidth, gridsize = c(51L, 51L), range.x, truncate = TRUE)
```
Arguments

- **x**: a two-column numeric matrix containing the observations from the distribution whose density is to be estimated. Missing values are not allowed.
- **bandwidth**: numeric vector of length 2, containing the bandwidth to be used in each coordinate direction.
- **gridsize**: vector containing the number of equally spaced points in each direction over which the density is to be estimated.
- **range.x**: a list containing two vectors, where each vector contains the minimum and maximum values of `x` at which to compute the estimate for each direction. The default minimum in each direction is minimum data value minus 1.5 times the bandwidth for that direction. The default maximum is the maximum data value plus 1.5 times the bandwidth for that direction.
- **truncate**: logical flag: if TRUE, data with `x` values outside the range specified by `range.x` are ignored.

Value

A list containing the following components:

- **x1**: vector of values of the grid points in the first coordinate direction at which the estimate was computed.
- **x2**: vector of values of the grid points in the second coordinate direction at which the estimate was computed.
- **fhat**: matrix of density estimates over the mesh induced by `x1` and `x2`.

Details

This is the binned approximation to the 2D kernel density estimate. Linear binning is used to obtain the bin counts and the Fast Fourier Transform is used to perform the discrete convolutions. For each `x1`, `x2` pair the bivariate Gaussian kernel is centered on that location and the heights of the kernel, scaled by the bandwidths, at each datapoint are summed. This sum, after a normalization, is the corresponding `fhat` value in the output.

References


See Also

- `bkde`, `density`, `hist`.

Examples

```r
data(geyser, package="MASS")
x <- cbind(geyser$sduration, geyser$swaiting)
est <- bkde2D(x, bandwidth=c(0.7, 7))
contour(est$x1, est$x2, est$fhat)
persp(est$fhat)
```
Compute a Binned Kernel Functional Estimate

**Description**

Returns an estimate of a binned approximation to the kernel estimate of the specified density functional. The kernel is the standard normal density.

**Usage**

```r
bkfe(x, drv, bandwidth, gridsize = 401L, range.x, binned = FALSE, truncate = TRUE)
```

**Arguments**

- `x`: numeric vector of observations from the distribution whose density is to be estimated. Missing values are not allowed.
- `drv`: order of derivative in the density functional. Must be a non-negative even integer.
- `bandwidth`: the kernel bandwidth smoothing parameter. Must be supplied.
- `gridsize`: the number of equally-spaced points over which binning is performed.
- `range.x`: vector containing the minimum and maximum values of `x` at which to compute the estimate. The default is the minimum and maximum data values, extended by the support of the kernel.
- `binned`: logical flag: if TRUE, then `x` and `y` are taken to be grid counts rather than raw data.
- `truncate`: logical flag: if TRUE, data with `x` values outside the range specified by `range.x` are ignored.

**Details**

The density functional of order `drv` is the integral of the product of the density and its `drv`th derivative. The kernel estimates of such quantities are computed using a binned implementation, and the kernel is the standard normal density.

**Value**

the (scalar) estimated functional.

**Background**

Estimates of this type were proposed by Sheather and Jones (1991).

**References**


Examples

```r
data(geyser, package="MASS")
x <- geyser$duration
est <- bkfe(x, drv=4, bandwidth=0.3)
```

dpih  
Select a Histogram Bin Width

Description

Uses direct plug-in methodology to select the bin width of a histogram.

Usage

```r
dpih(x, scalest = "minim", level = 2L, gridsize = 401L, range.x = range(x), truncate = TRUE)
```

Arguments

- `x`: numeric vector containing the sample on which the histogram is to be constructed.
- `scalest`: estimate of scale.
  - "stdev": standard deviation is used.
  - "iqr": inter-quartile range divided by 1.349 is used.
  - "minim": minimum of "stdev" and "iqr" is used.
- `level`: number of levels of functional estimation used in the plug-in rule.
- `gridsize`: number of grid points used in the binned approximations to functional estimates.
- `range.x`: range over which functional estimates are obtained. The default is the minimum and maximum data values.
- `truncate`: if `truncate` is TRUE then observations outside of the interval specified by `range.x` are omitted. Otherwise, they are used to weight the extreme grid points.

Details

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bin width and bandwidths are replaced by kernel estimates, is used. The normal distribution is used to provide an initial estimate.

Value

the selected bin width.

Background

This method for selecting the bin width of a histogram is described in Wand (1995). It is an extension of the normal scale rule of Scott (1979) and uses plug-in ideas from bandwidth selection for kernel density estimation (e.g. Sheather and Jones, 1991).
References

See Also
hist

Examples
```r
data(geyser, package="MASS")
x <- geyser$duration
h <- dpih(x)
bins <- seq(min(x)-h, max(x)+h, by=h)
hist(x, breaks=bins)
```

dpik

Select a Bandwidth for Kernel Density Estimation

Description
Use direct plug-in methodology to select the bandwidth of a kernel density estimate.

Usage
```r
dpik(x, scalest = "minim", level = 2L, kernel = "normal",
    canonical = FALSE, gridsize = 401L, range.x = range(x),
    truncate = TRUE)
```

Arguments
- `x` numeric vector containing the sample on which the kernel density estimate is to be constructed.
- `scalest` estimate of scale.
  - "stdev" - standard deviation is used.
  - "iqr" - inter-quartile range divided by 1.349 is used.
  - "minim" - minimum of "stdev" and "iqr" is used.
- `level` number of levels of functional estimation used in the plug-in rule.
- `kernel` character string which determines the smoothing kernel. kernel can be:
  - "normal" - the Gaussian density function (the default).
  - "box" - a rectangular box.
  - "epanech" - the centred beta(2,2) density.
  - "biweight" - the centred beta(3,3) density.
  - "triweight" - the centred beta(4,4) density. This can be abbreviated to any unique abbreviation.
- `canonical` logical flag: if TRUE, canonically scaled kernels are used
- `gridsize` the number of equally-spaced points over which binning is performed to obtain kernel functional approximation.
dpill

range.x vector containing the minimum and maximum values of x at which to compute the estimate. The default is the minimum and maximum data values.
trunc vector logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.

Details
The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bandwidths are replaced by kernel estimates, is used. The normal distribution is used to provide an initial estimate.

Value
the selected bandwidth.

Background
This method for selecting the bandwidth of a kernel density estimate was proposed by Sheather and Jones (1991) and is described in Section 3.6 of Wand and Jones (1995).

References

See Also
bkde, density, ksmooth

Examples

data(geyser, package="MASS")
x <- geyser$duration
h <- dpik(x)
est <- bkde(x, bandwidth=h)
plot(est,type="l")
Arguments

- **x**: numeric vector of x data. Missing values are not accepted.
- **y**: numeric vector of y data. This must be same length as x, and missing values are not accepted.
- **blockmax**: the maximum number of blocks of the data for construction of an initial parametric estimate.
- **divisor**: the value that the sample size is divided by to determine a lower limit on the number of blocks of the data for construction of an initial parametric estimate.
- **trim**: the proportion of the sample trimmed from each end in the x direction before application of the plug-in methodology.
- **proptrun**: the proportion of the range of x at each end truncated in the functional estimates.
- **gridsize**: number of equally-spaced grid points over which the function is to be estimated.
- **range.x**: vector containing the minimum and maximum values of x at which to compute the estimate. For density estimation the default is the minimum and maximum data values with 5% of the range added to each end. For regression estimation the default is the minimum and maximum data values.
- **truncate**: logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.

Details

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bandwidths are replaced by kernel estimates, is used. The kernel is the standard normal density. Least squares quartic fits over blocks of data are used to obtain an initial estimate. Mallow’s $C_p$ is used to select the number of blocks.

Value

the selected bandwidth.

Warning

If there are severe irregularities (i.e. outliers, sparse regions) in the x values then the local polynomial smooths required for the bandwidth selection algorithm may become degenerate and the function will crash. Outliers in the y direction may lead to deterioration of the quality of the selected bandwidth.

References


See Also

- ksmooth, locpoly.
Examples

data(geyser, package = "MASS")
x <- geyser$duration
y <- geyser$waiting
plot(x, y)
h <- dpill(x, y)
fit <- locpoly(x, y, bandwidth = h)
lines(fit)

locpoly

Estimate Functions Using Local Polynomials

Description

Estimates a probability density function, regression function or their derivatives using local polynomials. A fast binned implementation over an equally-spaced grid is used.

Usage

locpoly(x, y, drv = 0L, degree, kernel = "normal",
        bandwidth, gridsize = 401L, bwdisc = 25,
        range.x, binned = FALSE, truncate = TRUE)

Arguments

x numeric vector of x data. Missing values are not accepted.
bandwidth the kernel bandwidth smoothing parameter. It may be a single number or an array having length gridsize, representing a bandwidth that varies according to the location of estimation.
y vector of y data. This must be same length as x, and missing values are not accepted.
drv order of derivative to be estimated.
degree degree of local polynomial used. Its value must be greater than or equal to the value of drv. The default value is of degree is drv + 1.
kernnel "normal" - the Gaussian density function. Currently ignored.
gridsize number of equally-spaced grid points over which the function is to be estimated.
bwdisc number of logarithmically-equally-spaced bandwidths on which bandwidth is discretised, to speed up computation.
range.x vector containing the minimum and maximum values of x at which to compute the estimate.
binned logical flag: if TRUE, then x and y are taken to be grid counts rather than raw data.
truncate logical flag: if TRUE, data with x values outside the range specified by range.x are ignored.
if \( y \) is specified, a local polynomial regression estimate of \( \text{E}[Y|X] \) (or its derivative) is computed. If \( y \) is missing, a local polynomial estimate of the density of \( x \) (or its derivative) is computed. A list containing the following components:

- **x**: vector of sorted \( x \) values at which the estimate was computed.
- **y**: vector of smoothed estimates for either the density or the regression at the corresponding \( x \).

**Details**

Local polynomial fitting with a kernel weight is used to estimate either a density, regression function or their derivatives. In the case of density estimation, the data are binned and the local fitting procedure is applied to the bin counts. In either case, binned approximations over an equally-spaced grid is used for fast computation. The bandwidth may be either scalar or a vector of length gridsize.

**References**


**See Also**

- `bkde`
- `density`
- `dpill`
- `ksmooth`
- `loess`
- `smooth`
- `supsmu`

**Examples**

```r
data(geyser, package = "MASS")
# local linear density estimate
x <- geyser$duration
est <- locpoly(x, bandwidth = 0.25)
plot(est, type = "l")

# local linear regression estimate
y <- geyser$waiting
plot(x, y)
fit <- locpoly(x, y, bandwidth = 0.25)
lines(fit)
```
Chapter 16

The MASS package

---

**abbey**

*Determinations of Nickel Content*

**Description**

A numeric vector of 31 determinations of nickel content (ppm) in a Canadian syenite rock.

**Usage**

abbey

**Source**


**References**


---

**accdeaths**

*Accidental Deaths in the US 1973-1978*

**Description**

A regular time series giving the monthly totals of accidental deaths in the USA.

**Usage**

accdeaths

**Details**

The values for first six months of 1979 (p. 326) were 7798 7406 8363 8460 9217 9316.
addterm

Try All One-Term Additions to a Model

Description

Try fitting all models that differ from the current model by adding a single term from those supplied, maintaining marginality.

This function is generic; there exist methods for classes `lm` and `glm` and the default method will work for many other classes.

Usage

```
addterm(object, ...)  
```

## Default S3 method:
addterm(object, scope, scale = 0, test = c("none", "Chisq"),
        k = 2, sorted = FALSE, trace = FALSE, ...)

## S3 method for class 'lm'
addterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, ...)

## S3 method for class 'glm'
addterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, trace = FALSE, ...)

Arguments

object    An object fitted by some model-fitting function.

scope     A formula specifying a maximal model which should include the current one. All additional terms in the maximal model with all marginal terms in the original model are tried.

scale     Used in the definition of the AIC statistic for selecting the models, currently only for `lm`, `aov` and `glm` models. Specifying `scale` asserts that the residual standard error or dispersion is known.

test      Should the results include a test statistic relative to the original model? The F test is only appropriate for `lm` and `aov` models, and perhaps for some over-dispersed `glm` models. The Chisq test can be an exact test (`lm` models with known scale) or a likelihood-ratio test depending on the method.

k         The multiple of the number of degrees of freedom used for the penalty. Only k=2 gives the genuine AIC: k = log(n) is sometimes referred to as BIC or SBC.

sorted    Should the results be sorted on the value of AIC?

trace     If TRUE additional information may be given on the fits as they are tried.

...       Arguments passed to or from other methods.
**Details**

The definition of AIC is only up to an additive constant: when appropriate (in models with specified scale) the constant is taken to be that used in Mallows’ Cp statistic and the results are labelled accordingly.

**Value**

A table of class "anova" containing at least columns for the change in degrees of freedom and AIC (or Cp) for the models. Some methods will give further information, for example sums of squares, deviances, log-likelihoods and test statistics.

**References**


**See Also**

`dropterm`, `stepAIC`

**Examples**

```r
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.lo <- aov(log(Days+2.5) ~ 1, quine)
addterm(quine.lo, quine.hi, test="F")

house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family=poisson,
data=housing)
addterm(house.glm0, ~. + Sat:(Infl+Type+Cont), test="Chisq")
house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
addterm(house.glm1, ~. + Sat:(Infl+Type+Cont)^2, test = "Chisq")
```

---

**Description**

Data on patients diagnosed with AIDS in Australia before 1 July 1991.

**Usage**

Aids2

**Format**

This data frame contains 2843 rows and the following columns:

- **state**  Grouped state of origin: "NSW" includes ACT and "other" is WA, SA, NT and TAS.
- **sex**  Sex of patient.
- **diag** (Julian) date of diagnosis.
- **death** (Julian) date of death or end of observation.
- **status**  "A" (alive) or "D" (dead) at end of observation.
- **T.categ**  Reported transmission category.
- **age**  Age (years) at diagnosis.
Note

This data set has been slightly jittered as a condition of its release, to ensure patient confidentiality.

Source

Dr P. J. Solomon and the Australian National Centre in HIV Epidemiology and Clinical Research.

References


---

<table>
<thead>
<tr>
<th>Animals</th>
<th>Brain and Body Weights for 28 Species</th>
</tr>
</thead>
</table>

Description

Average brain and body weights for 28 species of land animals.

Usage

Animals

Format

- body  body weight in kg.
- brain  brain weight in g.

Note

The name Animals avoided conflicts with a system dataset animals in S-PLUS 4.5 and later.

Source


References

Description

The anorexia data frame has 72 rows and 3 columns. Weight change data for young female anorexia patients.

Usage

anorexia

Format

This data frame contains the following columns:

- **Treat**: Factor of three levels: "Cont" (control), "CBT" (Cognitive Behavioural treatment) and "FT" (family treatment).
- **Prewt**: Weight of patient before study period, in lbs.
- **Postwt**: Weight of patient after study period, in lbs.

Source


(Note that the original source mistakenly says that weights are in kg.)

References


Description

Method function to perform sequential likelihood ratio tests for Negative Binomial generalized linear models.

Usage

## S3 method for class 'negbin'
anova(object, ..., test = "Chisq")
Arguments

object  Fitted model object of class "negbin", inheriting from classes "glm" and "lm", specifying a Negative Binomial fitted GLM. Typically the output of glm.nb().

...  Zero or more additional fitted model objects of class "negbin". They should form a nested sequence of models, but need not be specified in any particular order.

test  Argument to match the test argument of anova.glm. Ignored (with a warning if changed) if a sequence of two or more Negative Binomial fitted model objects is specified, but possibly used if only one object is specified.

Details

This function is a method for the generic function anova() for class "negbin". It can be invoked by calling anova(x) for an object x of the appropriate class, or directly by calling anova.negbin(x) regardless of the class of the object.

Note

If only one fitted model object is specified, a sequential analysis of deviance table is given for the fitted model. The theta parameter is kept fixed. If more than one fitted model object is specified they must all be of class "negbin" and likelihood ratio tests are done of each model within the next. In this case theta is assumed to have been re-estimated for each model.

References


See Also

glm.nb, negative.binomial, summary.negbin

Examples

m1 <- glm.nb(Days ~ Eth*Age*Lrn*Sex, quine, link = log)
m2 <- update(m1, . ~ . - Eth:Age:Lrn:Sex)
anova(m2, m1)
anova(m2)

area

Adaptive Numerical Integration

Description

Integrate a function of one variable over a finite range using a recursive adaptive method. This function is mainly for demonstration purposes.

Usage

area(f, a, b, ..., fa = f(a, ...), fb = f(b, ...), limit = 10, eps = 1e-05)
Arguments

\( f \) The integrand as an S function object. The variable of integration must be the first argument.

\( a \) Lower limit of integration.

\( b \) Upper limit of integration.

\( ... \) Additional arguments needed by the integrand.

\( fa \) Function value at the lower limit.

\( fb \) Function value at the upper limit.

\( \text{limit} \) Limit on the depth to which recursion is allowed to go.

\( \text{eps} \) Error tolerance to control the process.

Details

The method divides the interval in two and compares the values given by Simpson’s rule and the trapezium rule. If these are within \( \text{eps} \) of each other the Simpson’s rule result is given, otherwise the process is applied separately to each half of the interval and the results added together.

Value

The integral from \( a \) to \( b \) of \( f(x) \).

References


Examples

\[
\text{area(sin, 0, pi)} \quad \# \text{ integrate the sin function from 0 to pi.}
\]

bacteria

**Presence of Bacteria after Drug Treatments**

Description

Tests of the presence of the bacteria *H. influenzae* in children with otitis media in the Northern Territory of Australia.

Usage

bacteria

Format

This data frame has 220 rows and the following columns:

- **y** presence or absence: a factor with levels n and y.
- **ap** active/placebo: a factor with levels a and p.
- **hilo** hi/low compliance: a factor with levels hi and lo.
- **week** numeric: week of test.
- **ID** subject ID: a factor.
- **trt** a factor with levels placebo, drug and drug+, a re-coding of ap and hilo.
Dr A. Leach tested the effects of a drug on 50 children with a history of otitis media in the Northern Territory of Australia. The children were randomized to the drug or the a placebo, and also to receive active encouragement to comply with taking the drug. 

The presence of *H. influenzae* was checked at weeks 0, 2, 4, 6 and 11: 30 of the checks were missing and are not included in this data frame.

**Source**

Dr Amanda Leach via Mr James McBroom.

**References**


**Examples**

```r
contrasts(bacteria$trt) <- structure(contr.sdif(3),
  dimnames = list(NULL, c("drug", "encourage")))

## fixed effects analyses
## IGNORE_RDIFF_BEGIN
summary(glm(y ~ trt * week, binomial, data = bacteria))
summary(glm(y ~ trt + week, binomial, data = bacteria))
summary(glm(y ~ trt + I(week > 2), binomial, data = bacteria))
## IGNORE_RDIFF_END

# conditional random-effects analysis
library(survival)
bacteria$Time <- rep(1, nrow(bacteria))
coxph(Surv(Time, unclass(y)) ~ week + strata(ID),
  data = bacteria, method = "exact")
coxph(Surv(Time, unclass(y)) ~ factor(week) + strata(ID),
  data = bacteria, method = "exact")
coxph(Surv(Time, unclass(y)) ~ I(week > 2) + strata(ID),
  data = bacteria, method = "exact")

# PQL glmm analysis
library(nlme)
## IGNORE_RDIFF_BEGIN
summary(glmmPQL(y ~ trt + I(week > 2), random = ~ 1 | ID, family = binomial, data = bacteria))
## IGNORE_RDIFF_END
```

**Description**

A well-supported rule-of-thumb for choosing the bandwidth of a Gaussian kernel density estimator.
Usage

bandwidth.nrd(x)

Arguments

x
A data vector.

Value

A bandwidth on a scale suitable for the width argument of density.

References


Examples

# The function is currently defined as
function(x)
{
  r <- quantile(x, c(0.25, 0.75))
  h <- (r[2] - r[1])/1.34
  4 * 1.06 * min(sqrt(var(x)), h) * length(x)^(-1/5)
}

bcv

Biased Cross-Validation for Bandwidth Selection

Description

Uses biased cross-validation to select the bandwidth of a Gaussian kernel density estimator.

Usage

bcv(x, nb = 1000, lower, upper)

Arguments

x
a numeric vector

nb
number of bins to use.

lower, upper
Range over which to minimize. The default is almost always satisfactory.

Value

a bandwidth

References

See Also

ucv, width.SJ, density

Examples

bcv(geyser$duration)

beav1

See Also

ucv, width.SJ, density

Examples

bcv(geyser$duration)

---

**Description**

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

**Usage**

beav1

**Format**

The beav1 data frame has 114 rows and 4 columns. This data frame contains the following columns:

- **day**: Day of observation (in days since the beginning of 1990), December 12–13.
- **time**: Time of observation, in the form 0330 for 3.30am.
- **temp**: Measured body temperature in degrees Celsius.
- **activ**: Indicator of activity outside the retreat.

**Note**

The observation at 22:20 is missing.

**Source**


**References**


**See Also**

beav2
beav2

Body Temperature Series of Beaver 2

Description

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

Usage

beav2

Format

The beav2 data frame has 100 rows and 4 columns. This data frame contains the following columns:

- day  Day of observation (in days since the beginning of 1990), November 3–4.
- time  Time of observation, in the form 0330 for 3.30am.
- temp  Measured body temperature in degrees Celsius.
- activ  Indicator of activity outside the retreat.

Source

Belgian-phones

References


See Also

beav1

Examples

```r
attach(beav2)
beav2$hours <- 24*(day-307) + trunc(time/100) + (time%%100)/60
plot(beav2$hours, beav2$temp, type = "l", xlab = "time",
     ylab = "temperature", main = "Beaver 2")
usr <- par("usr"); usr[3:4] <- c(-0.2, 8); par(usr = usr)
lines(beav2$hours, beav2$activ, type = "s", lty = 2)

temp <- ts(temp, start = 8+2/3, frequency = 6)
activ <- ts(activ, start = 8+2/3, frequency = 6)
acf(temp[activ == 0]); acf(temp[activ == 1]) # also look at PACFs
ar(temp[activ == 0]); ar(temp[activ == 1])

arima(temp[activ == 0], order = c(1,0,0), xreg = activ)
arima(temp[activ == 1], order = c(1,0,0), xreg = cbind(active=activ, dreg))
```

```
library(nlme) # for gls and corAR1
beav2.gls <- gls(temp ~ activ, data = beav2, correlation = corAR1(0.8),
          method = "ML")
summary(beav2.gls)
summary(update(beav2.gls, subset = 6:100))
detach("beav2.gls"); rm(temp, activ)
```

Belgian-phones

**Belgium Phone Calls 1950-1973**

Description

A list object with the annual numbers of telephone calls, in Belgium. The components are:

- **year** last two digits of the year.
- **calls** number of telephone calls made (in millions of calls).

Usage

phones

Source


References

Biopsy Data on Breast Cancer Patients

Description

This breast cancer database was obtained from the University of Wisconsin Hospitals, Madison from Dr. William H. Wolberg. He assessed biopsies of breast tumours for 699 patients up to 15 July 1992; each of nine attributes has been scored on a scale of 1 to 10, and the outcome is also known. There are 699 rows and 11 columns.

Usage

biopsy

Format

This data frame contains the following columns:

ID  sample code number (not unique).
V1  clump thickness.
V2  uniformity of cell size.
V3  uniformity of cell shape.
V4  marginal adhesion.
V5  single epithelial cell size.
V6  bare nuclei (16 values are missing).
V7  bland chromatin.
V8  normal nucleoli.
V9  mitoses.
class "benign" or "malignant".

Source


References


---

**birthwt**

*Risk Factors Associated with Low Infant Birth Weight*

**Description**

The *birthwt* data frame has 189 rows and 10 columns. The data were collected at Baystate Medical Center, Springfield, Mass during 1986.

**Usage**

`birthwt`

**Format**

This data frame contains the following columns:

- `low` indicator of birth weight less than 2.5 kg.
- `age` mother’s age in years.
- `lwt` mother’s weight in pounds at last menstrual period.
- `race` mother’s race (1 = white, 2 = black, 3 = other).
- `smoke` smoking status during pregnancy.
- `ptl` number of previous premature labours.
- `ht` history of hypertension.
- `ui` presence of uterine irritability.
- `ftv` number of physician visits during the first trimester.
- `bwt` birth weight in grams.

**Source**


**References**


**Examples**

```r
bwt <- with(birthwt, {
  race <- factor(race, labels = c("white", "black", "other"))
  ptd <- factor(ptl > 0)
  ftv <- factor(ftv)
  levels(ftv)[c(1,2)] <- "2+
  data.frame(low = factor(low), age, lwt, race, smoke = (smoke > 0),
             ptd, ht = (ht > 0), ui = (ui > 0), ftv)
})
options(contrasts = c("contr.treatment", "contr.poly"))
glm(low ~ ., binomial, bwt)
```
Description

The Boston data frame has 506 rows and 14 columns.

Usage

Boston

Format

This data frame contains the following columns:

- crim  per capita crime rate by town.
- zn    proportion of residential land zoned for lots over 25,000 sq.ft.
- indus proportion of non-retail business acres per town.
- chas  Charles River dummy variable (= 1 if tract bounds river; 0 otherwise).
- nox   nitrogen oxides concentration (parts per 10 million).
- rm    average number of rooms per dwelling.
- age   proportion of owner-occupied units built prior to 1940.
- dis   weighted mean of distances to five Boston employment centres.
- rad   index of accessibility to radial highways.
- tax   full-value property-tax rate per $10,000.
- ptratio pupil-teacher ratio by town.
- black 1000 \((Bk - 0.63)^2\) where \(Bk\) is the proportion of blacks by town.
- lstat  lower status of the population (percent).
- medv  median value of owner-occupied homes in $1000s.

Source


Box-Cox Transformations for Linear Models

Description

Computes and optionally plots profile log-likelihoods for the parameter of the Box-Cox power transformation.

Usage

boxcox(object, ...)  
## Default S3 method:  
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,  
       interp, eps = 1/50, xlab = expression(lambda),  
       ylab = "log-Likelihood", ...)  
## S3 method for class 'formula'  
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,  
       interp, eps = 1/50, xlab = expression(lambda),  
       ylab = "log-Likelihood", ...)  
## S3 method for class 'lm'  
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,  
       interp, eps = 1/50, xlab = expression(lambda),  
       ylab = "log-Likelihood", ...)  

Arguments

object a formula or fitted model object. Currently only lm and aov objects are handled.
lambda vector of values of lambda – default (-2, 2) in steps of 0.1.
plotit logical which controls whether the result should be plotted.
interp logical which controls whether spline interpolation is used. Default to TRUE if plotting with lambda of length less than 100.
eps Tolerance for lambda = 0; defaults to 0.02.
xlab defaults to "lambda".
ylab defaults to "log-Likelihood".
... additional parameters to be used in the model fitting.

Value

A list of the lambda vector and the computed profile log-likelihood vector, invisibly if the result is plotted.

Side Effects

If plotit = TRUE plots log-likelihood vs lambda and indicates a 95% confidence interval about the maximum observed value of lambda. If interp = TRUE, spline interpolation is used to give a smoother plot.
cabbages

References


Examples

```
boxcox(Volume ~ log(Height) + log(Girth), data = trees,  
lambda = seq(-0.25, 0.25, length.out = 10))

boxcox(Days+1 ~ Eth*Sex*Age*Lrn, data = quine,  
lambda = seq(-0.05, 0.45, length.out = 20))
```

---

**Data from a cabbage field trial**

**Description**

The cabbages data set has 60 observations and 4 variables

**Usage**

cabbages

**Format**

This data frame contains the following columns:

- **Cult** Factor giving the cultivar of the cabbage, two levels: c39 and c52.
- **Date** Factor specifying one of three planting dates: d16, d20 or d21.
- **HeadWt** Weight of the cabbage head, presumably in kg.
- **VitC** Ascorbic acid content, in undefined units.

**Source**


**References**

caith  

Colours of Eyes and Hair of People in Caithness

Description

Data on the cross-classification of people in Caithness, Scotland, by eye and hair colour. The region of the UK is particularly interesting as there is a mixture of people of Nordic, Celtic and Anglo-Saxon origin.

Usage

craith

Format

A 4 by 5 table with rows the eye colours (blue, light, medium, dark) and columns the hair colours (fair, red, medium, dark, black).

Source


References


Examples

```r
## IGNORE_RDIFF_BEGIN
## The signs can vary by platform
corresp(caith)
## IGNORE_RDIFF_END
dimnames(caith)[[2]] <- c("F", "R", "M", "D", "B")
par(mfcol=c(1,3))
plot(corresp(caith, nf=2)); title("symmetric")
plot(corresp(caith, nf=2), type="rows"); title("rows")
plot(corresp(caith, nf=2), type="col"); title("columns")
par(mfrow=c(1,1))
```

Cars93  

Data from 93 Cars on Sale in the USA in 1993

Description

The Cars93 data frame has 93 rows and 27 columns.

Usage

Cars93
Format

This data frame contains the following columns:

- **Manufacturer**
- **Model**
- **Type**
- **Min.Price** Minimum Price (in $1,000): price for a basic version.
- **Price** Midrange Price (in $1,000): average of Min.Price and Max.Price.
- **Max.Price** Maximum Price (in $1,000): price for “a premium version”.
- **MPG.city** City MPG (miles per US gallon by EPA rating).
- **MPG.highway** Highway MPG.
- **AirBags** Air Bags standard. Factor: none, driver only, or driver & passenger.
- **DriveTrain** Drive train type: rear wheel, front wheel or 4WD; (factor).
- **Cylinders** Number of cylinders (missing for Mazda RX-7, which has a rotary engine).
- **EngineSize** Engine size (litres).
- **Horsepower** Horsepower (maximum).
- **RPM** RPM (revs per minute at maximum horsepower).
- **Rev.per.mile** Engine revolutions per mile (in highest gear).
- **Man.transavail** Is a manual transmission version available? (yes or no, Factor).
- **Fuel.tank.capacity** Fuel tank capacity (US gallons).
- **Passengers** Passenger capacity (persons)
- **Length** Length (inches).
- **Wheelbase** Wheelbase (inches).
- **Width** Width (inches).
- **Turn.circle** U-turn space (feet).
- **Rear.seat.room** Rear seat room (inches) (missing for 2-seater vehicles).
- **Luggage.room** Luggage capacity (cubic feet) (missing for vans).
- **Weight** Weight (pounds).
- **Origin** Of non-USA or USA company origins? (factor).
- **Make** Combination of Manufacturer and Model (character).

Details

Cars were selected at random from among 1993 passenger car models that were listed in both the *Consumer Reports* issue and the *PACE Buying Guide*. Pickup trucks and Sport/Utility vehicles were eliminated due to incomplete information in the *Consumer Reports* source. Duplicate models (e.g., Dodge Shadow and Plymouth Sundance) were listed at most once.

Further description can be found in Lock (1993).

Source


References

cats

Anatomical Data from Domestic Cats

Description

The heart and body weights of samples of male and female cats used for digitalis experiments. The cats were all adult, over 2 kg body weight.

Usage
cats

Format

This data frame contains the following columns:

- Sex  sex: Factor with levels "F" and "M".
- Bwt  body weight in kg.
- Hwt  heart weight in g.

Source


References


cement

Heat Evolved by Setting Cements

Description

Experiment on the heat evolved in the setting of each of 13 cements.

Usage
cement

Format

- x1, x2, x3, x4  Proportions (%) of active ingredients.
- y  heat evolved in cals/gm.

Details

Thirteen samples of Portland cement were set. For each sample, the percentages of the four main chemical ingredients was accurately measured. While the cement was setting the amount of heat evolved was also measured.
Source


References


Examples

```r
lm(y ~ x1 + x2 + x3 + x4, cement)
```

---

### chem

**Copper in Wholemeal Flour**

**Description**

A numeric vector of 24 determinations of copper in wholemeal flour, in parts per million.

**Usage**

```r
chem
```

**Source**


**References**


---

### con2tr

**Convert Lists to Data Frames for use by lattice**

**Description**

Convert lists to data frames for use by lattice.

**Usage**

```r
con2tr(obj)
```

**Arguments**

- `obj` A list of components `x`, `y` and `z` as passed to `contour`.

**Details**

`con2tr` repeats the `x` and `y` components suitably to match the vector `z`. 
Value

A data frame suitable for passing to lattice (formerly trellis) functions.

References


---

confint-MASS

Confidence Intervals for Model Parameters

Description

Computes confidence intervals for one or more parameters in a fitted model. Package MASS adds methods for glm and nls fits.

Usage

```r
## S3 method for class 'glm'
confint(object, parm, level = 0.95, trace = FALSE, ...)

## S3 method for class 'nls'
confint(object, parm, level = 0.95, ...)
```

Arguments

- **object**: a fitted model object. Methods currently exist for the classes "glm", "nls" and for profile objects from these classes.
- **parm**: a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
- **level**: the confidence level required.
- **trace**: logical. Should profiling be traced?
- **...**: additional argument(s) for methods.

Details

confint is a generic function in package stats.

These confint methods call the appropriate profile method, then find the confidence intervals by interpolation in the profile traces. If the profile object is already available it should be used as the main argument rather than the fitted model object itself.

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1 - level)/2 and 1 - (1 - level)/2 in % (by default 2.5% and 97.5%).

References

See Also

`confint` (the generic and "lm" method), `profile`

Examples

```r
expn1 <- deriv(y ~ b0 + b1 * 2^(-x/th), c("b0", "b1", "th"),
function(b0, b1, th, x) ())
wtloss.gr <- nls(Weight ~ expn1(b0, b1, th, Days),
data = wtloss, start = c(b0=90, b1=95, th=120))
expn2 <- deriv(-b0 + b1*((w0 - b0)/b1)^(x/d0),
c("b0","b1","d0"), function(b0, b1, d0, x, w0) ())
wtloss.init <- function(obj, w0) {
p <- coef(obj)
d0 <- - log((w0 - p["b0"]/p["b1"])/log(2) * p["th"]
c[p[c("b0", "b1")], d0 = as.vector(d0))
}
out <- NULL
w0s <- c(110, 100, 90)
for(w0 in w0s) {
  fm <- nls(Weight ~ expn2(b0, b1, d0, Days, w0),
             wtloss, start = wtloss.init(wtloss.gr, w0))
  out <- rbind(out, c(coef(fm)["d0"], confint(fm, "d0")))
}
dimnames(out) <- list(paste(w0s, "kg:"), c("d0", "low", "high"))
out
```

```r
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
budworm.lg0 <- glm(SF ~ sex + ldose - 1, family = binomial)
confint(budworm.lg0)
confint(budworm.lg0, "ldose")
```

---

**contr.sdif**

### Successive Differences Contrast Coding

#### Description

A coding for factors based on successive differences.

#### Usage

```r
contr.sdif(n, contrasts = TRUE, sparse = FALSE)
```

#### Arguments

- `n` The number of levels required.
- `contrasts` logical: Should there be `n - 1` columns orthogonal to the mean (the default) or `n` columns spanning the space?
sparse logical. If true and the result would be sparse (only true for contrasts = FALSE), return a sparse matrix.

Details
The contrast coefficients are chosen so that the coded coefficients in a one-way layout are the differences between the means of the second and first levels, the third and second levels, and so on. This makes most sense for ordered factors, but does not assume that the levels are equally spaced.

Value
If contrasts is TRUE, a matrix with n rows and n - 1 columns, and the n by n identity matrix if contrasts is FALSE.

References

See Also
contr.treatment, contr.sum, contr.helmert.

Examples
(A <- contr.sdif(6))
zapsmall(ginv(A))

---

coop Co-operative Trial in Analytical Chemistry

Description
Seven specimens were sent to 6 laboratories in 3 separate batches and each analysed for Analyte. Each analysis was duplicated.

Usage
coop

Format
This data frame contains the following columns:

Lab Laboratory, L1, L2, ..., L6.
Spc Specimen, S1, S2, ..., S7.
Bat Batch, B1, B2, B3 (nested within Spc/Lab),
Conc Concentration of Analyte in g/kg.

Source
corresp

References

See Also
chem, abbey.

corresp Simple Correspondence Analysis

Description
Find the principal canonical correlation and corresponding row- and column-scores from a correspondence analysis of a two-way contingency table.

Usage
corresp(x, ...)  
## S3 method for class 'matrix'
corresp(x, nf = 1, ...)  
## S3 method for class 'factor'
corresp(x, y, ...)  
## S3 method for class 'data.frame'
corresp(x, ...)  
## S3 method for class 'xtabs'
corresp(x, ...)  
## S3 method for class 'formula'
corresp(formula, data, ...)

Arguments
  x, formula The function is generic, accepting various forms of the principal argument for specifying a two-way frequency table. Currently accepted forms are matrices, data frames (coerced to frequency tables), objects of class "xtabs" and formulae of the form ~ F1 + F2, where F1 and F2 are factors.
  nf The number of factors to be computed. Note that although 1 is the most usual, one school of thought takes the first two singular vectors for a sort of biplot.
  y a second factor for a cross-classification.
  data an optional data frame, list or environment against which to preferentially resolve variables in the formula.
  ... If the principal argument is a formula, a data frame may be specified as well from which variables in the formula are preferentially satisfied.
Details

See Venables & Ripley (2002). The plot method produces a graphical representation of the table if nf=1, with the areas of circles representing the numbers of points. If nf is two or more the biplot method is called, which plots the second and third columns of the matrices \( A = D r^{-1/2} U L \) and \( B = D c^{-1/2} V L \) where the singular value decomposition is \( U L V \). Thus the x-axis is the canonical correlation times the row and column scores. Although this is called a biplot, it does not have any useful inner product relationship between the row and column scores. Think of this as an equally-scaled plot with two unrelated sets of labels. The origin is marked on the plot with a cross. (For other versions of this plot see the book.)

Value

An list object of class "correspondence" for which print, plot and biplot methods are supplied. The main components are the canonical correlation(s) and the row and column scores.

References


See Also

svd, princomp.

Examples

```r
## IGNORE_RDIFF_BEGIN
## The signs can vary by platform
(ct <- corresp(~ Age + Eth, data = quine))
plot(ct)

corresp(caith)
biplot(corresp(caith, nf = 2))
## IGNORE_RDIFF_END
```

Description

Compute a multivariate location and scale estimate with a high breakdown point – this can be thought of as estimating the mean and covariance of the good part of the data. cov.mve and cov.mcd are compatibility wrappers.

Usage

```r
cov.rob(x, cor = FALSE, quantile.used = floor((n + p + 1)/2),
       method = c("mve", "mcd", "classical"),
       nsamp = "best", seed)

cov.mve(...)
cov.mcd(...)
```
Arguments

- **x**  
a matrix or data frame.
- **cor**  
should the returned result include a correlation matrix?
- **quantile.used**  
the minimum number of the data points regarded as good points.
- **method**  
the method to be used – minimum volume ellipsoid, minimum covariance determinant or classical product-moment. Using cov.mve or cov.mcd forces mve or mcd respectively.
- **nsamp**  
the number of samples or "best" or "exact" or "sample". The limit If "sample" the number chosen is \( \min(5p, 3000) \), taken from Rousseeuw and Hubert (1997). If "best" exhaustive enumeration is done up to 5000 samples: if "exact" exhaustive enumeration will be attempted.
- **seed**  
the seed to be used for random sampling: see RNGkind. The current value of .Random.seed will be preserved if it is set.
- **...**  
arguments to cov.rob other than method.

Details

For method "mve", an approximate search is made of a subset of size quantile.used with an enclosing ellipsoid of smallest volume; in method "mcd" it is the volume of the Gaussian confidence ellipsoid, equivalently the determinant of the classical covariance matrix, that is minimized. The mean of the subset provides a first estimate of the location, and the rescaled covariance matrix a first estimate of scatter. The Mahalanobis distances of all the points from the location estimate for this covariance matrix are calculated, and those points within the 97.5% point under Gaussian assumptions are declared to be good. The final estimates are the mean and rescaled covariance of the good points.

The rescaling is by the appropriate percentile under Gaussian data; in addition the first covariance matrix has an \textit{ad hoc} finite-sample correction given by Marazzi.

For method "mve" the search is made over ellipsoids determined by the covariance matrix of \( p \) of the data points. For method "mcd" an additional improvement step suggested by Rousseeuw and van Driessen (1999) is used, in which once a subset of size quantile.used is selected, an ellipsoid based on its covariance is tested (as this will have no larger a determinant, and may be smaller).

There is a hard limit on the allowed number of samples, \( 2^{31} - 1 \). However, practical limits are likely to be much lower and one might check the number of samples used for exhaustive enumeration, \( \text{combn(NROW(x), NCOL(x) + 1)} \), before attempting it.

Value

A list with components

- **center**  
the final estimate of location.
- **cov**  
the final estimate of scatter.
- **cor**  
(only is cor = TRUE) the estimate of the correlation matrix.
- **sing**  
message giving number of singular samples out of total
- **crit**  
the value of the criterion on log scale. For MCD this is the determinant, and for MVE it is proportional to the volume.
- **best**  
the subset used. For MVE the best sample, for MCD the best set of size quantile.used.
- **n.obs**  
total number of observations.
References


See Also

lqs

Examples

```r
set.seed(123)
cov.rob(stackloss)
cov.rob(stack.x, method = "mcd", nsamp = "exact")
```

description

Estimates a covariance or correlation matrix assuming the data came from a multivariate t distribution: this provides some degree of robustness to outlier without giving a high breakdown point.

Usage

```r
cov.trob(x, wt = rep(1, n), cor = FALSE, center = TRUE, nu = 5,
        maxit = 25, tol = 0.01)
```

Arguments

- `x`: data matrix. Missing values (NAs) are not allowed.
- `wt`: A vector of weights for each case: these are treated as if the case i actually occurred wt[i] times.
- `cor`: Flag to choose between returning the correlation (cor = TRUE) or covariance (cor = FALSE) matrix.
- `center`: a logical value or a numeric vector providing the location about which the covariance is to be taken. If center = FALSE, no centering is done; if center = TRUE the MLE of the location vector is used.
- `nu`: ‘degrees of freedom’ for the multivariate t distribution. Must exceed 2 (so that the covariance matrix is finite).
- `maxit`: Maximum number of iterations in fitting.
- `tol`: Convergence tolerance for fitting.
Value

A list with the following components:

- `cov`: the fitted covariance matrix.
- `center`: the estimated or specified location vector.
- `wt`: the specified weights: only returned if the `wt` argument was given.
- `n.obs`: the number of cases used in the fitting.
- `cor`: the fitted correlation matrix: only returned if `cor = TRUE`.
- `call`: The matched call.
- `iter`: The number of iterations used.

References


See Also

cov, cov.wt, cov.mve

Examples

cov.trob(stackloss)
Source


References


crabs

*Morphological Measurements on Leptograpsus Crabs*

Description

The crabs data frame has 200 rows and 8 columns, describing 5 morphological measurements on 50 crabs each of two colour forms and both sexes, of the species *Leptograpsus variegatus* collected at Fremantle, W. Australia.

Usage

`crabs`

Format

This data frame contains the following columns:

- `sp` species: "B" or "O" for blue or orange.
- `sex` as it says.
- `index` index 1:50 within each of the four groups.
- `FL` frontal lobe size (mm).
- `RW` rear width (mm).
- `CL` carapace length (mm).
- `CW` carapace width (mm).
- `BD` body depth (mm).

Source


References

**Cushings**  

*Diagnostic Tests on Patients with Cushing’s Syndrome*

**Description**

Cushing’s syndrome is a hypertensive disorder associated with over-secretion of cortisol by the adrenal gland. The observations are urinary excretion rates of two steroid metabolites.

**Usage**

Cushings

**Format**

The Cushings data frame has 27 rows and 3 columns:

- Tetrahydrocortisone urinary excretion rate (mg/24hr) of Tetrahydrocortisone.
- Pregnanetriol urinary excretion rate (mg/24hr) of Pregnanetriol.
- Type underlying type of syndrome, coded a (adenoma), b (bilateral hyperplasia), c (carcinoma) or u for unknown.

**Source**


**References**


---

**DDT**  

*DDT in Kale*

**Description**

A numeric vector of 15 measurements by different laboratories of the pesticide DDT in kale, in ppm (parts per million) using the multiple pesticide residue measurement.

**Usage**

DDT

**Source**


denumerate

Description

A time series giving the monthly deaths from bronchitis, emphysema and asthma in the UK, 1974-1979, both sexes (deaths).

Usage
deaths

Source


References


See Also

This the same as dataset `ideaths` in R’s `datasets` package.

denumerate

Transform an Allowable Formula for `loglm` into one for `terms`

Description

`loglm` allows dimension numbers to be used in place of names in the formula. `denumerate` modifies such a formula into one that `terms` can process.

Usage
denumerate(x)

Arguments

x A formula conforming to the conventions of `loglm`, that is, it may allow dimension numbers to stand in for names when specifying a log-linear model.

Details

The model fitting function `loglm` fits log-linear models to frequency data using iterative proportional scaling. To specify the model the user must nominate the margins in the data that remain fixed under the log-linear model. It is convenient to allow the user to use dimension numbers, 1, 2, 3, ... for the first, second, third, ..., margins in a similar way to variable names. As the model formula has to be parsed by `terms`, which treats 1 in a special way and requires parseable variable names, these formulae have to be modified by giving genuine names for these margin, or dimension numbers. `denumerate` replaces these numbers with names of a special form, namely n is replaced by .vn. This allows `terms` to parse the formula in the usual way.
dose.p

Value

A linear model formula like that presented, except that where dimension numbers, say \( n \), have been used to specify fixed margins these are replaced by names of the form \(.v_n\) which may be processed by terms.

See Also

renumerate

Examples

denumerator(~(1+2+3)^3 + a/b)
## which gives ~ (.v1 + .v2 + .v3)^3 + a/b

dose.p

Predict Doses for Binomial Assay model

Description

Calibrate binomial assays, generalizing the calculation of LD50.

Usage

dose.p(obj, cf = 1:2, p = 0.5)

Arguments

obj
A fitted model object of class inheriting from "glm".

cf
The terms in the coefficient vector giving the intercept and coefficient of (log-)dose

p
Probabilities at which to predict the dose needed.

Value

An object of class "glm.dose" giving the prediction (attribute "p" and standard error (attribute "SE") at each response probability.

References


Examples

ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
budworm.lg0 <- glm(SF ~ sex + ldose - 1, family = binomial)
dose.p(budworm.lg0, cf = c(1,3), p = 1:3/4)
dose.p(update(budworm.lg0, family = binomial(link=probit)),
    cf = c(1,3), p = 1:3/4)
Deaths of Car Drivers in Great Britain 1969-84

Description

A regular time series giving the monthly totals of car drivers in Great Britain killed or seriously injured Jan 1969 to Dec 1984. Compulsory wearing of seat belts was introduced on 31 Jan 1983.

Usage

drivers

Source


References


dropterm

Try All One-Term Deletions from a Model

Description

Try fitting all models that differ from the current model by dropping a single term, maintaining marginality.

This function is generic; there exist methods for classes lm and glm and the default method will work for many other classes.

Usage

dropterm(object, ...)  

## Default S3 method:
dropterm(object, scope, scale = 0, test = c("none", "Chisq"),
        k = 2, sorted = FALSE, trace = FALSE, ...)

## S3 method for class 'lm'
dropterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, ...)

## S3 method for class 'glm'
dropterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, trace = FALSE, ...)
Arguments

object A object fitted by some model-fitting function.

scope a formula giving terms which might be dropped. By default, the model formula. Only terms that can be dropped and maintain marginality are actually tried.

scale used in the definition of the AIC statistic for selecting the models, currently only for \texttt{lm}, \texttt{aov} and \texttt{glm} models. Specifying \texttt{scale} asserts that the residual standard error or dispersion is known.

test should the results include a test statistic relative to the original model? The F test is only appropriate for \texttt{lm} and \texttt{aov} models, and perhaps for some over-dispersed \texttt{glm} models. The Chisq test can be an exact test (\texttt{lm} models with known scale) or a likelihood-ratio test depending on the method.

k the multiple of the number of degrees of freedom used for the penalty. Only \( k = 2 \) gives the genuine AIC: \( k = \log(n) \) is sometimes referred to as BIC or SBC.

sorted should the results be sorted on the value of AIC?

trace if \texttt{TRUE} additional information may be given on the fits as they are tried.

... arguments passed to or from other methods.

Details

The definition of AIC is only up to an additive constant: when appropriate (\texttt{lm} models with specified scale) the constant is taken to be that used in Mallows’ \texttt{Cp} statistic and the results are labelled accordingly.

Value

A table of class "\texttt{anova}" containing at least columns for the change in degrees of freedom and AIC (or \texttt{Cp}) for the models. Some methods will give further information, for example sums of squares, deviances, log-likelihoods and test statistics.

References


See Also

\texttt{addterm}, \texttt{stepAIC}

Examples

\begin{verbatim}
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.nxt <- update(quine.hi, . ~ . - Eth:Sex:Age:Lrn)
dropterm(quine.nxt, test= "F")
quine.stp <- stepAIC(quine.nxt, scope = list(upper = ~Eth*Sex*Age*Lrn, lower = ~1), trace = FALSE)
dropterm(quine.stp, test = "F")
quine.3 <- update(quine.stp, . ~ . - Eth:Age:Lrn)
dropterm(quine.3, test = "F")
quine.4 <- update(quine.3, . ~ . - Eth:Age)
dropterm(quine.4, test = "F")
quine.5 <- update(quine.4, . ~ . - Age:Lrn)
dropterm(quine.5, test = "F")
\end{verbatim}
eagles <- glm(Freq ~ Infl*Type*Cont + Sat, family=poisson, data = housing)
house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
dropterm(house.glm1, test = "Chisq")

---

**Foraging Ecology of Bald Eagles**

**Description**

Knight and Skagen collected during a field study on the foraging behaviour of wintering Bald Eagles in Washington State, USA data concerning 160 attempts by one (pirating) Bald Eagle to steal a chum salmon from another (feeding) Bald Eagle.

**Usage**

eagles

**Format**

The `eagles` data frame has 8 rows and 5 columns.

- `y` Number of successful attempts.
- `n` Total number of attempts.
- `P` Size of pirating eagle (L = large, S = small).
- `A` Age of pirating eagle (I = immature, A = adult).
- `V` Size of victim eagle (L = large, S = small).

**Source**


**References**


**Examples**

eagles.glm <- glm(cbind(y, n - y) ~ P*A + V, data = eagles, family = binomial)
dropterm(eagles.glm)
prof <- profile(eagles.glm)
plot(prof)
pairs(prof)
Description

Thall and Vail (1990) give a data set on two-week seizure counts for 59 epileptics. The number of seizures was recorded for a baseline period of 8 weeks, and then patients were randomly assigned to a treatment group or a control group. Counts were then recorded for four successive two-week periods. The subject’s age is the only covariate.

Usage

epil

Format

This data frame has 236 rows and the following 9 columns:

- **y**: the count for the 2-week period.
- **trt**: treatment, “placebo” or “progabide”.
- **base**: the counts in the baseline 8-week period.
- **age**: subject’s age, in years.
- **V4**: 0/1 indicator variable of period 4.
- **subject**: subject number, 1 to 59.
- **period**: period, 1 to 4.
- **lbase**: log-counts for the baseline period, centred to have zero mean.
- **lage**: log-ages, centred to have zero mean.

Source


References


Examples

```r
### IGNORE_RODIFF_BEGIN
summary(glm(y ~ lbase*trt + lage + V4, family = poisson, data = epil), correlation = FALSE)
### IGNORE_RODIFF_END

epil2 <- epil[epil$period == 1, ]
epil2["period"] <- rep(0, 59); epil2["y"] <- epil2["base"]
epil2["time"] <- 1; epil2["time"] <- 4
epil2 <- rbind(epil, epil2)
epil2$pred <- unclass(epil2$trt) * (epil2$period > 0)
epil2$subject <- factor(epil2$subject)
```
eqscplot

Plots with Geometrically Equal Scales

description

Version of a scatterplot with scales chosen to be equal on both axes, that is 1 cm represents the same units on each

usage

eqscplot(x, y, ratio = 1, tol = 0.04, uin, ...)

arguments

x vector of x values, or a 2-column matrix, or a list with components x and y
y vector of y values
ratio desired ratio of units on the axes. Units on the y axis are drawn at ratio times the size of units on the x axis. Ignored if uin is specified and of length 2.
tol proportion of white space at the margins of plot
uin desired values for the units-per-inch parameter. If of length 1, the desired units per inch on the x axis.
... further arguments for plot and graphical parameters. Note that par(xaxs="i", yaxs="i") is enforced, and xlim and ylim will be adjusted accordingly.

details

Limits for the x and y axes are chosen so that they include the data. One of the sets of limits is then stretched from the midpoint to make the units in the ratio given by ratio. Finally both are stretched by 1 + tol to move points away from the axes, and the points plotted.

value

invisibly, the values of uin used for the plot.
farms

Side Effects

performs the plot.

Note

Arguments ratio and uin were suggested by Bill Dunlap.

References


See Also

plot, par

farms

Ecological Factors in Farm Management

Description

The farms data frame has 20 rows and 4 columns. The rows are farms on the Dutch island of Terschelling and the columns are factors describing the management of grassland.

Usage

farms

Format

This data frame contains the following columns:

Mois Five levels of soil moisture – level 3 does not occur at these 20 farms.

Manag Grassland management type (SF = standard, BF = biological, HF = hobby farming, NM = nature conservation).

Use Grassland use (U1 = hay production, U2 = intermediate, U3 = grazing).

Manure Manure usage – classes C0 to C4.

Source


Quoted as from:


References

Examples

```r
defarms <- mca(farms, abbrev = TRUE)  # Use levels as names
eqscplot(farms.mca$cs, type = "n")
text(farms.mca$rs, cex = 0.7)
text(farms.mca$cs, labels = dimnames(farms.mca$cs)[[1]], cex = 0.7)
```

---

**fgl Measurements of Forensic Glass Fragments**

**Description**

The `fgl` data frame has 214 rows and 10 columns. It was collected by B. German on fragments of glass collected in forensic work.

**Usage**

`fgl`

**Format**

This data frame contains the following columns:

**RI** refractive index; more precisely the refractive index is 1.518xxxx.

The next 8 measurements are percentages by weight of oxides.

- **Na** sodium.
- **Mg** manganese.
- **Al** aluminium.
- **Si** silicon.
- **K** potassium.
- **Ca** calcium.
- **Ba** barium.
- **Fe** iron.

**type** The fragments were originally classed into seven types, one of which was absent in this dataset. The categories which occur are window float glass (WinF: 70), window non-float glass (WinNF: 76), vehicle window glass (Veh: 17), containers (Con: 13), tableware (Tabl: 9) and vehicle headlamps (Head: 29).

**References**

Maximum-likelihood Fitting of Univariate Distributions

Description
Maximum-likelihood fitting of univariate distributions, allowing parameters to be held fixed if desired.

Usage
fitdistr(x, densfun, start, ...)

Arguments
x
A numeric vector of length at least one containing only finite values.
densfun
Either a character string or a function returning a density evaluated at its first argument. Distributions "beta", "cauchy", "chi-squared", "exponential", "gamma", "geometric", "log-normal", "lognormal", "logistic", "negative binomial", "normal", "Poisson", "t" and "weibull" are recognised, case being ignored.
start
A named list giving the parameters to be optimized with initial values. This can be omitted for some of the named distributions and must be for others (see Details).
...
Additional parameters, either for densfun or for optim. In particular, it can be used to specify bounds via lower or upper or both. If arguments of densfun (or the density function corresponding to a character-string specification) are included they will be held fixed.

Details
For the Normal, log-Normal, geometric, exponential and Poisson distributions the closed-form MLEs (and exact standard errors) are used, and start should not be supplied.
For all other distributions, direct optimization of the log-likelihood is performed using optim. The estimated standard errors are taken from the observed information matrix, calculated by a numerical approximation. For one-dimensional problems the Nelder-Mead method is used and for multi-dimensional problems the BFGS method, unless arguments named lower or upper are supplied (when L-BFGS-B is used) or method is supplied explicitly.
For the "t" named distribution the density is taken to be the location-scale family with location m and scale s.
For the following named distributions, reasonable starting values will be computed if start is omitted or only partially specified: "cauchy", "gamma", "logistic", "negative binomial" (parametrized by mu and size), "t" and "weibull". Note that these starting values may not be good enough if the fit is poor: in particular they are not resistant to outliers unless the fitted distribution is long-tailed.
There are print, coef, vcov and logLik methods for class "fitdistr".
Value

An object of class "fitdistr", a list with four components,

- `estimate`: the parameter estimates,
- `sd`: the estimated standard errors,
- `vcov`: the estimated variance-covariance matrix, and
- `loglik`: the log-likelihood.

Note

Numerical optimization cannot work miracles: please note the comments in `optim` on scaling data. If the fitted parameters are far away from one, consider re-fitting specifying the control parameter `parscale`.

References


Examples

```r
## avoid spurious accuracy
op <- options(digits = 3)
set.seed(123)
x <- rgamma(100, shape = 5, rate = 0.1)
fitdistr(x, "gamma")
## now do this directly with more control.
fitdistr(x, dgamma, list(shape = 1, rate = 0.1), lower = 0.001)

set.seed(123)
x2 <- rt(250, df = 9)
fitdistr(x2, "t", df = 9)
## allow df to vary: not a very good idea!
fitdistr(x2, "t")
## now do fixed-df fit directly with more control.
mydt <- function(x, m, s, df) dt((x-m)/s, df)/s
fitdistr(x2, mydt, list(m = 0, s = 1), df = 9, lower = c(-Inf, 0))

set.seed(123)
x3 <- rweibull(100, shape = 4, scale = 100)
fitdistr(x3, "weibull")

set.seed(123)
x4 <- rnegbin(500, mu = 5, theta = 4)
fitdistr(x4, "Negative Binomial")
options(op)
```

forbes

Forbes’ Data on Boiling Points in the Alps

Description

A data frame with 17 observations on boiling point of water and barometric pressure in inches of mercury.
fractions

Usage

forbes

Format

bp  boiling point (degrees Farenheit).
pres barometric pressure in inches of mercury.

Source


fractions  Rational Approximation

Description

Find rational approximations to the components of a real numeric object using a standard continued fraction method.

Usage

fractions(x, cycles = 10, max.denominator = 2000, ...)

as.fractions(x)

is.fractions(f)

Arguments

x  Any object of mode numeric. Missing values are now allowed.
cycles  The maximum number of steps to be used in the continued fraction approximation process.
max.denominator  An early termination criterion. If any partial denominator exceeds max.denominator the continued fraction stops at that point.
...  arguments passed to or from other methods.
f  an R object.

Details

Each component is first expanded in a continued fraction of the form

\[ x = \text{floor}(x) + 1/(p_1 + 1/(p_2 + \ldots)) \]

where \( p_1, p_2, \ldots \) are positive integers, terminating either at cycles terms or when a \( p_j \) exceeds max.denominator. The continued fraction is then re-arranged to retrieve the numerator and denominator as integers.

The numerators and denominators are then combined into a character vector that becomes the "fracs" attribute and used in printed representations.

Arithmetic operations on "fractions" objects have full floating point accuracy, but the character representation printed out may not.
Value

An object of class "fractions". A structure with .Data component the same as the input numeric 
x, but with the rational approximations held as a character vector attribute, "fracs". Arithmetic 
operations on "fractions" objects are possible.

References

Springer.

See Also

rational

Examples

X <- matrix(runif(25), 5, 5)
zapsmall(solve(X, X/5)) # print near-zeroes as zero 
fractions(solve(X, X/5))

Source

Mrs Susan Prosser, Paediatrics Department, University of Oxford, via Department of Statistics 
Consulting Service.

References

galaxies

Description
A numeric vector of velocities in km/sec of 82 galaxies from 6 well-separated conic sections of an unfilled survey of the Corona Borealis region. Multimodality in such surveys is evidence for voids and superclusters in the far universe.

Usage
galaxies

Note
There is an 83rd measurement of 5607 km/sec in the Postman et al. paper which is omitted in Roeder (1990) and from the dataset here.
There is also a typo: this dataset has 78th observation 26690 which should be 26960.

Source

References

Examples
gal <- galaxies/1000
c(width.SJ(gal, method = "dpi"), width.SJ(gal))
plot(x = c(0, 40), y = c(0, 0.3), type = "n", xlab = "velocity of galaxy (1000km/s)", ylab = "density")
rug(gal)
lines(density(gal, width = 3.25, n = 200), lty = 1)
lines(density(gal, width = 2.56, n = 200), lty = 3)

gamma.dispersion

Description
A front end to gamma.shape for convenience. Finds the reciprocal of the estimate of the shape parameter only.

Usage
gamma.dispersion(object, ...)

Arguments

- **object**: Fitted model object giving the gamma fit.
- **...**: Additional arguments passed on to `gamma.shape`.

Value

The MLE of the dispersion parameter of the gamma distribution.

References


See Also

`gamma.shape.glm`, including the example on its help page.

---

**Description**

Find the maximum likelihood estimate of the shape parameter of the gamma distribution after fitting a Gamma generalized linear model.

**Usage**

`gamma.shape(object, ...)`

```r
## S3 method for class 'glm'
gamma.shape(object, it.lim = 10,
             eps.max = .Machine$double.eps^0.25, verbose = FALSE, ...)
```

**Arguments**

- **object**: Fitted model object from a Gamma family or quasi family with `variance = "mu^2"`.
- **it.lim**: Upper limit on the number of iterations.
- **eps.max**: Maximum discrepancy between approximations for the iteration process to continue.
- **verbose**: If `TRUE`, causes successive iterations to be printed out. The initial estimate is taken from the deviance.
- **...**: further arguments passed to or from other methods.

**Details**

A glm fit for a Gamma family correctly calculates the maximum likelihood estimate of the mean parameters but provides only a crude estimate of the dispersion parameter. This function takes the results of the glm fit and solves the maximum likelihood equation for the reciprocal of the dispersion parameter, which is usually called the shape (or exponent) parameter.
Description

A data frame from a trial of 42 leukaemia patients. Some were treated with the drug 6-mercaptopurine and the rest are controls. The trial was designed as matched pairs, both withdrawn from the trial when either came out of remission.

Usage

gehan

Format

This data frame contains the following columns:

- pair label for pair.
- time remission time in weeks.
- cens censoring, 0/1.
- treat treatment, control or 6-MP.
Source


References


Examples

```r
library(survival)
gehan.surv <- survfit(Surv(time, cens) ~ treat, data = gehan,
                      conf.type = "log-log")
survreg(Surv(time, cens) ~ factor(pair) + treat, gehan, dist = "exponential")
survreg(Surv(time, cens) ~ treat, gehan, dist = "exponential")
gehan.cox <- coxph(Surv(time, cens) ~ treat, gehan)
survreg(Surv(time, cens) ~ treat, gehan)
survreg(Surv(time, cens) ~ treat, gehan)
summary(gehan.surv)
summary(survreg(Surv(time, cens) ~ treat, gehan))
summary(survreg(Surv(time, cens) ~ pair + treat, gehan))
summary(gehan.cox)
```

description

**Rat Genotype Data**

Data from a foster feeding experiment with rat mothers and litters of four different genotypes: A, B, I and J. Rat litters were separated from their natural mothers at birth and given to foster mothers to rear.

Usage

`genotype`

Format

The data frame has the following components:

- **Litter**: genotype of the litter.
- **Mother**: genotype of the foster mother.
- **Wt**: Litter average weight gain of the litter, in grams at age 28 days. (The source states that the within-litter variability is negligible.)

Source


References

Description

A version of the eruptions data from the ‘Old Faithful’ geyser in Yellowstone National Park, Wyoming. This version comes from Azzalini and Bowman (1990) and is of continuous measurement from August 1 to August 15, 1985.

Some nocturnal duration measurements were coded as 2, 3 or 4 minutes, having originally been described as ‘short’, ‘medium’ or ‘long’.

Usage

geyer

Format

A data frame with 299 observations on 2 variables.

| duration | numeric | Eruption time in mins |
| waiting  | numeric | Waiting time for this eruption |

Note

The waiting time was incorrectly described as the time to the next eruption in the original files, and corrected for MASS version 7.3-30.

References


See Also

faithful.

CRAN package sm.
Description

This dataset was collected on a line transect survey in gilgai territory in New South Wales, Australia. Gilgais are natural gentle depressions in otherwise flat land, and sometimes seem to be regularly distributed. The data collection was stimulated by the question: are these patterns reflected in soil properties? At each of 365 sampling locations on a linear grid of 4 meters spacing, samples were taken at depths 0-10 cm, 30-40 cm and 80-90 cm below the surface. pH, electrical conductivity and chloride content were measured on a 1:5 soil:water extract from each sample.

Usage

gilgais

Format

This data frame contains the following columns:

- pH00  pH at depth 0–10 cm.
- pH30  pH at depth 30–40 cm.
- pH80  pH at depth 80–90 cm.
- e00  electrical conductivity in mS/cm (0–10 cm).
- e30  electrical conductivity in mS/cm (30–40 cm).
- e80  electrical conductivity in mS/cm (80–90 cm).
- c00  chloride content in ppm (0–10 cm).
- c30  chloride content in ppm (30–40 cm).
- c80  chloride content in ppm (80–90 cm).

Source


References

ginv  Generalized Inverse of a Matrix

Description
Calculates the Moore-Penrose generalized inverse of a matrix X.

Usage
ginv(X, tol = sqrt(.Machine$double.eps))

Arguments
X Matrix for which the Moore-Penrose inverse is required.
tol A relative tolerance to detect zero singular values.

Value
A MP generalized inverse matrix for X.

References

See Also
solve, svd, eigen

glm.convert  Change a Negative Binomial fit to a GLM fit

Description
This function modifies an output object from glm.nb() to one that looks like the output from glm() with a negative binomial family. This allows it to be updated keeping the theta parameter fixed.

Usage
glm.convert(object)

Arguments
object An object of class "negbin", typically the output from glm.nb().

Details
Convenience function needed to effect some low level changes to the structure of the fitted model object.
Value

An object of class "glm" with negative binomial family. The theta parameter is then fixed at its present estimate.

See Also

 glm.nb, negative.binomial, glm

Examples

 quine.nb1 <- glm.nb(Days ~ Sex/(Age + Eth*Lrn), data = quine)
 quine.nbA <- glm.convert(quine.nb1)
 quine.nbB <- update(quine.nb1, . ~ . + Sex:Age:Lrn)
 anova(quine.nbA, quine.nbB)

glm.nb

Fit a Negative Binomial Generalized Linear Model

Description

A modification of the system function glm() to include estimation of the additional parameter, theta, for a Negative Binomial generalized linear model.

Usage

 glm.nb(formula, data, weights, subset, na.action, start = NULL, etastart, mustart, control = glm.control(...), method = "glm.fit", model = TRUE, x = FALSE, y = TRUE, contrasts = NULL, ...,
 init.theta, link = log)

Arguments

 formula, data, weights, subset, na.action, start, etastart, mustart, control = glm.control(...), method = "glm.fit", model = TRUE, x = FALSE, y = TRUE, contrasts = NULL, ...
 init.theta Optional initial value for the theta parameter. If omitted a moment estimator after an initial fit using a Poisson GLM is used.
 link The link function. Currently must be one of log, sqrt or identity.

Details

An alternating iteration process is used. For given theta the GLM is fitted using the same process as used by glm(). For fixed means the theta parameter is estimated using score and information iterations. The two are alternated until convergence of both. (The number of alternations and the number of iterations when estimating theta are controlled by the maxit parameter of glm.control.)

Setting trace > 0 traces the alternating iteration process. Setting trace > 1 traces the glm fit, and setting trace > 2 traces the estimation of theta.
Value

A fitted model object of class `negbin` inheriting from `glm` and `lm`. The object is like the output of `glm` but contains three additional components, namely `theta` for the ML estimate of theta, `SE.theta` for its approximate standard error (using observed rather than expected information), and `twologlik` for twice the log-likelihood function.

References


See Also

glm, negative.binomial, anova.negbin, summary.negbin, theta.md

There is a `simulate` method.

Examples

```r
quine.nb1 <- glm.nb(Days ~ Sex/(Age + Eth*Lrn), data = quine)
quine.nb2 <- update(quine.nb1, . ~ . + Sex:Age:Lrn)
quine.nb3 <- update(quine.nb2, Days ~ .^4)
anova(quine.nb1, quine.nb2, quine.nb3)
```

---

**glmmPQL**

**Fit Generalized Linear Mixed Models via PQL**

Description

Fit a GLMM model with multivariate normal random effects, using Penalized Quasi-Likelihood.

Usage

```r
glmmPQL(fixed, random, family, data, correlation, weights,
        control, niter = 10, verbose = TRUE, ...)
```

Arguments

- `fixed` a two-sided linear formula giving fixed-effects part of the model.
- `random` a formula or list of formulae describing the random effects.
- `family` a GLM family.
- `data` an optional data frame, list or environment used as the first place to find variables in the formulae, weights and if present in `. . .` subset.
- `correlation` an optional correlation structure.
- `weights` optional case weights as in `glm`.
- `control` an optional argument to be passed to `lme`.
- `niter` maximum number of iterations.
- `verbose` logical: print out record of iterations?
- `...` Further arguments for `lme`. 
Details

`glmmPQL` works by repeated calls to `lme`, so namespace `nlme` will be loaded at first use. (Before 2015 it used to attach `nlme` but nowadays only loads the namespace.)

Unlike `lme`, `offset` terms are allowed in `fixed` – this is done by pre- and post-processing the calls to `lme`.

Note that the returned object inherits from class "lme" and that most generics will use the method for that class. As from version 3.1-158, the fitted values have any offset included, as do the results of calling `predict`.

Value

A object of class `c("glmmPQL", "lme")`: see `lmeObject`.

References


See Also

lme

Examples

```r
summary(glmmPQL(y ~ trt + I(week > 2), random = ~ 1 | ID,
family = binomial, data = bacteria))
## an example of an offset: the coefficient of 'week' changes by one.
summary(glmmPQL(y ~ trt + week, random = ~ 1 | ID,
family = binomial, data = bacteria))
summary(glmmPQL(y ~ trt + week + offset(week), random = ~ 1 | ID,
family = binomial, data = bacteria))
```

---

**hills**

*Record Times in Scottish Hill Races*

Description

The record times in 1984 for 35 Scottish hill races.

Usage

hills
Format

The components are:

- `dist` distance in miles (on the map).
- `climb` total height gained during the route, in feet.
- `time` record time in minutes.

Source


[A.C. Atkinson (1988) Transformations unmasked. *Technometrics* 30, 311–318 “corrects” the time for Knock Hill from 78.65 to 18.65. It is unclear if this based on the original records.]

References


hist.scott

*Plot a Histogram with Automatic Bin Width Selection*

Description

Plot a histogram with automatic bin width selection, using the Scott or Freedman–Diaconis formulae.

Usage

```r
hist.scott(x, prob = TRUE, xlab = deparse(substitute(x)), ...)
hist.FD(x, prob = TRUE, xlab = deparse(substitute(x)), ...)
```

Arguments

- `x` A data vector
- `prob` Should the plot have unit area, so be a density estimate?
- `xlab, ...` Further arguments to `hist`.

Value

For the `nclass.*` functions, the suggested number of classes.

Side Effects

Plot a histogram.

References


See Also

`hist`
Frequency Table from a Copenhagen Housing Conditions Survey

Description

The housing data frame has 72 rows and 5 variables.

Usage

housing

Format

Sat  Satisfaction of householders with their present housing circumstances, (High, Medium or Low, ordered factor).
Infl  Perceived degree of influence householders have on the management of the property (High, Medium, Low).
Type  Type of rental accommodation, (Tower, Atrium, Apartment, Terrace).
Cont  Contact residents are afforded with other residents, (Low, High).
Freq  Frequencies: the numbers of residents in each class.

Source


References


Examples

options(contrasts = c("contr.treatment", "contr.poly"))

# Surrogate Poisson models
house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family = poisson, data = housing)
## IGNORE_RDIFF_BEGIN
summary(house.glm0, correlation = FALSE)
## IGNORE_RDIFF_END
addterm(house.glm0, . ~ . + Sat:(Infl+Type+Cont), test = "Chisq")

house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
## IGNORE_RDIFF_BEGIN
summary(house.glm1, correlation = FALSE)
## IGNORE_RDIFF_END

1 - pchisq(deviance(house.glm1), house.glm1$df.residual)
dropterm(house.glm1, test = "Chisq")
addterm(house.glm1, ~. + Sat:(Infl+Type+Cont)^2, test = "Chisq")

hnames <- lapply(housing[, -5], levels) # omit Freq
newData <- expand.grid(hnames)
newData$Sat <- ordered(newData$Sat)

house.pm <- predict(house.glm1, newData,
    type = "response") # poisson means

house.pr <- house.pm/drop(house.pm %*% rep(1, 3))
cbind(expand.grid(hnames[-1]), round(house.pr, 2))

# Iterative proportional scaling
loglm(Freq ~ Infl*Type*Cont + Sat*(Infl+Type+Cont), data = housing)

# multinomial model
library(nnet)
(house.mult <- multinom(Sat ~ Infl + Type + Cont, weights = Freq,
    data = housing))
(house.mult2 <- multinom(Sat ~ Infl*Type*Cont, weights = Freq,
    data = housing))
anova(house.mult, house.mult2)

house.pm <- predict(house.mult, expand.grid(hnames[-1]), type = "probs")
cbind(expand.grid(hnames[-1]), round(house.pm, 2))

# proportional odds model
house.cpr <- apply(house.pr, 1, cumsum)
logit <- function(x) log(x/(1-x))
house.ld <- logit(house.cpr[2, ]) - logit(house.cpr[1, ])
(ratio <- sort(drop(house.ld)))
mean(ratio)

(house.plr <- polr(Sat ~ Infl + Type + Cont,
    data = housing, weights = Freq))

house.pr1 <- predict(house.plr, expand.grid(hnames[-1]), type = "probs")
cbind(expand.grid(hnames[-1]), round(house.pr1, 2))

Fr <- matrix(housing$Freq, ncol = 3, byrow = TRUE)
2*sum(Fr*log(house.pr/house.pr1))

house.plr2 <- stepAIC(house.plr, ~.^2)
house.plr2$anova

---

**huber**

*Huber M-estimator of Location with MAD Scale*

**Description**

Finds the Huber M-estimator of location with MAD scale.
hubers

Usage

huber(y, k = 1.5, tol = 1e-06)

Arguments

y  vector of data values
k  Winsorizes at k standard deviations
tol convergence tolerance

Value

list of location and scale parameters

mu  location estimate
s  MAD scale estimate

References


See Also

hubers, mad

Examples

huber(chem)

---

hubers  *Huber Proposal 2 Robust Estimator of Location and/or Scale*

Description

Finds the Huber M-estimator for location with scale specified, scale with location specified, or both if neither is specified.

Usage

hubers(y, k = 1.5, mu, s, initmu = median(y), tol = 1e-06)

Arguments

y  vector of data values
k  Winsorizes at k standard deviations
mu  specified location
s  specified scale
initmu initial value of mu
tol convergence tolerance
The `immer` data frame has 30 rows and 4 columns. Five varieties of barley were grown in six locations in each of 1931 and 1932.

Usage

```r
immer
```

Format

This data frame contains the following columns:

- `Loc` The location.
- `Var` The variety of barley ("manchuria", "svansota", "velvet", "trebi" and "peatland").
- `Y1` Yield in 1931.
- `Y2` Yield in 1932.

Source


References

Examples

```r
immer.aov <- aov(cbind(Y1,Y2) ~ Loc + Var, data = immer)
summary(immer.aov)

immer.aov <- aov((Y1+Y2)/2 ~ Var + Loc, data = immer)
summary(immer.aov)
model.tables(immer.aov, type = "means", se = TRUE, cterms = "Var")
```

**Description**

The data given in data frame `Insurance` consist of the numbers of policyholders of an insurance company who were exposed to risk, and the numbers of car insurance claims made by those policyholders in the third quarter of 1973.

**Usage**

`Insurance`

**Format**

This data frame contains the following columns:

- **District**: factor: district of residence of policyholder (1 to 4): 4 is major cities.
- **Group**: an ordered factor: group of car with levels <1 litre, 1–1.5 litre, 1.5–2 litre, >2 litre.
- **Age**: an ordered factor: the age of the insured in 4 groups labelled <25, 25–29, 30–35, >35.
- **Holders**: numbers of policyholders.
- **Claims**: numbers of claims.

**Source**


**References**


**Examples**

```r
## main-effects fit as Poisson GLM with offset
glm(Claims ~ District + Group + Age + offset(log(Holders)),
    data = Insurance, family = poisson)

# same via loglm
loglm(Claims ~ District + Group + Age + offset(log(Holders)),
     data = Insurance)
```
Kruskal’s Non-metric Multidimensional Scaling

Description
One form of non-metric multidimensional scaling

Usage
isoMDS(d, y = cmdscale(d, k), k = 2, maxit = 50, trace = TRUE, 
tol = 1e-3, p = 2)
Shepard(d, x, p = 2)

Arguments
d distance structure of the form returned by dist, or a full, symmetric matrix. Data are assumed to be dissimilarities or relative distances, but must be positive except for self-distance. Both missing and infinite values are allowed.
y An initial configuration. If none is supplied, cmdscale is used to provide the classical solution, unless there are missing or infinite dissimilarities.
k The desired dimension for the solution, passed to cmdscale.
maxit The maximum number of iterations.
trace Logical for tracing optimization. Default TRUE.
tol convergence tolerance.
p Power for Minkowski distance in the configuration space.
x A final configuration.

Details
This chooses a k-dimensional (default k = 2) configuration to minimize the stress, the square root of the ratio of the sum of squared differences between the input distances and those of the configuration to the sum of configuration distances squared. However, the input distances are allowed a monotonic transformation.

An iterative algorithm is used, which will usually converge in around 10 iterations. As this is necessarily an $O(n^2)$ calculation, it is slow for large datasets. Further, since for the default $p = 2$ the configuration is only determined up to rotations and reflections (by convention the centroid is at the origin), the result can vary considerably from machine to machine.

Value
Two components:

points A k-column vector of the fitted configuration.
stress The final stress achieved (in percent).

Side Effects
If trace is true, the initial stress and the current stress are printed out every 5 iterations.
kde2d

Two-Dimensional Kernel Density Estimation

Description

Two-dimensional kernel density estimation with an axis-aligned bivariate normal kernel, evaluated on a square grid.

Usage

kde2d(x, y, h, n = 25, lims = c(range(x), range(y)))

Arguments

x  x coordinate of data
y  y coordinate of data
h  vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (see bandwidth.nrd). A scalar value will be taken to apply to both directions.
n  Number of grid points in each direction. Can be scalar or a length-2 integer vector.
lims  The limits of the rectangle covered by the grid as c(xl, xu, yl, yu).

Value

A list of three components.

x, y  The x and y coordinates of the grid points, vectors of length n.

Examples

attach(geyser)
plot(duration, waiting, xlim = c(0.5, 6), ylim = c(40, 100))
f1 <- kde2d(duration, waiting, n = 50, lims = c(0.5, 6, 40, 100))
image(f1, zlim = c(0, 0.05))
f2 <- kde2d(duration, waiting, n = 50, lims = c(0.5, 6, 40, 100),
  h = c(width.SJ(duration), width.SJ(waiting)) )
image(f2, zlim = c(0, 0.05))
persp(f2, phi = 30, theta = 20, d = 5)

plot(duration[-272], duration[-1], xlim = c(0.5, 6),
  ylim = c(1, 6), xlab = "previous duration", ylab = "duration")
f1 <- kde2d(duration[-272], duration[-1],
  h = rep(1.5, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
  ylab = "duration", levels = c(0.05, 0.1, 0.2, 0.4))
f1 <- kde2d(duration[-272], duration[-1],
  h = rep(0.6, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
  ylab = "duration", levels = c(0.05, 0.1, 0.2, 0.4))
f1 <- kde2d(duration[-272], duration[-1],
  h = rep(0.4, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
  ylab = "duration", levels = c(0.05, 0.1, 0.2, 0.4))
detach("geyser")

---

**lda**  
*Linear Discriminant Analysis*

**Description**

Linear discriminant analysis.

**Usage**

```r
lda(x, ...)
```

## S3 method for class 'formula'
```r
lda(formula, data, ..., subset, na.action)
```

### Default S3 method:
```r
lda(x, grouping, prior = proportions, tol = 1.0e-4,
    method, CV = FALSE, nu, ...)
```

### S3 method for class 'data.frame'
```r
lda(x, ...)
```

### S3 method for class 'matrix'
```r
lda(x, grouping, ..., subset, na.action)
```
Arguments

formula
A formula of the form \( groups \sim x_1 + x_2 + \ldots \). That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.

data
An optional data frame, list or environment from which variables specified in \texttt{formula} are preferentially to be taken.

x
(required if no formula is given as the principal argument.) a matrix or data frame or Matrix containing the explanatory variables.

grouping
(required if no formula principal argument is given.) a factor specifying the class for each observation.

prior
the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If present, the probabilities should be specified in the order of the factor levels.

tol
A tolerance to decide if a matrix is singular; it will reject variables and linear combinations of unit-variance variables whose variance is less than \( tol^2 \).

subset
An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)

na.action
A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is \texttt{na.omit}, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)

method
"moment" for standard estimators of the mean and variance, "mle" for MLEs, "mve" to use \texttt{cov.mve}, or "t" for robust estimates based on a \( t \) distribution.

CV
If true, returns results (classes and posterior probabilities) for leave-one-out cross-validation. Note that if the prior is estimated, the proportions in the whole dataset are used.

nu
degrees of freedom for method = "t".

...
arguments passed to or from other methods.

Details

The function tries hard to detect if the within-class covariance matrix is singular. If any variable has within-group variance less than \( tol^2 \) it will stop and report the variable as constant. This could result from poor scaling of the problem, but is more likely to result from constant variables.

Specifying the prior will affect the classification unless over-ridden in \texttt{predict.lda}. Unlike in most statistical packages, it will also affect the rotation of the linear discriminants within their space, as a weighted between-groups covariance matrix is used. Thus the first few linear discriminants emphasize the differences between groups with the weights given by the prior, which may differ from their prevalence in the dataset.

If one or more groups is missing in the supplied data, they are dropped with a warning, but the classifications produced are with respect to the original set of levels.

Value

If CV = TRUE the return value is a list with components \texttt{class}, the MAP classification (a factor), and \texttt{posterior}, posterior probabilities for the classes.

Otherwise it is an object of class "lda" containing the following components:

prior
the prior probabilities used.
means  the group means.
scaling a matrix which transforms observations to discriminant functions, normalized so that within groups covariance matrix is spherical.
svd  the singular values, which give the ratio of the between- and within-group standard deviations on the linear discriminant variables. Their squares are the canonical F-statistics.
N  The number of observations used.
call The (matched) function call.

Note
This function may be called giving either a formula and optional data frame, or a matrix and grouping factor as the first two arguments. All other arguments are optional, but subset= and na.action=, if required, must be fully named.
If a formula is given as the principal argument the object may be modified using update() in the usual way.

References

See Also
`predict.lda`, `qda`, `predict.qda`

Examples
```r
Iris <- data.frame(rbind(iris3[,1], iris3[,2], iris3[,3]),
                   Sp = rep(c("s","c","v"), rep(50,3)))
train <- sample(1:150, 75)
table(Iris$Sp[train])
## your answer may differ
## c s v
## 22 23 30
z <- lda(Sp ~ ., Iris, prior = c(1,1,1)/3, subset = train)
predict(z, Iris[-train,])$class
## [1] s s s s s s s s s s s s s s s s s s s s c c c
## [31] c c c c c c c c c c c c c c c c c c c c c c v v v v
## [61] v v v v v v v v v v v v v v v v
(z1 <- update(z, . ~ . - Petal.W.))
```

---

**ldahist**  
*Histograms or Density Plots of Multiple Groups*

**Description**
Plot histograms or density plots of data on a single Fisher linear discriminant.
Idahist

Usage

Idahist(data, g, nbins = 25, h, x0 = - h/1000, breaks,
    xlim = range(breaks), ymax = 0, width,
    type = c("histogram", "density", "both"),
    sep = (type != "density"),
    col = 5, xlab = deparse(substitute(data)), bty = "n", ...)

Arguments

data vector of data. Missing values (NAs) are allowed and omitted.
g factor or vector giving groups, of the same length as data.
nbins Suggested number of bins to cover the whole range of the data.
h The bin width (takes precedence over nbins).
x0 Shift for the bins - the breaks are at x0 + h * (... -1, 0, 1, ...)
breaks The set of breakpoints to be used. (Usually omitted, takes precedence over h
    and nbins).
xlim The limits for the x-axis.
ymax The upper limit for the y-axis.
width Bandwidth for density estimates. If missing, the Sheather-Jones selector is used
    for each group separately.
type Type of plot.
sep Whether there is a separate plot for each group, or one combined plot.
col The colour number for the bar fill.
xlab label for the plot x-axis. By default, this will be the name of data.
bty The box type for the plot - defaults to none.
... additional arguments to polygon.

Side Effects

Histogram and/or density plots are plotted on the current device.

References


See Also

plot.lda.
Description

A data frame of data from 33 leukaemia patients.

Usage

leuk

Format

A data frame with columns:

- `wbc` white blood count.
- `ag` a test result, "present" or "absent".
- `time` survival time in weeks.

Details

Survival times are given for 33 patients who died from acute myelogenous leukaemia. Also measured was the patient’s white blood cell count at the time of diagnosis. The patients were also factored into 2 groups according to the presence or absence of a morphologic characteristic of white blood cells. Patients termed AG positive were identified by the presence of Auer rods and/or significant granulation of the leukaemic cells in the bone marrow at the time of diagnosis.

Source


Taken from


References


Examples

```r
library(survival)
plot(survfit(Surv(time) ~ ag, data = leuk), lty = 2:3, col = 2:3)
# now Cox models
leuk.cox <- coxph(Surv(time) ~ ag + log(wbc), leuk)
summary(leuk.cox)
```
Fit Linear Models by Generalized Least Squares

Description

Fit linear models by Generalized Least Squares

Usage

lm.gls(formula, data, W, subset, na.action, inverse = FALSE, 
method = "qr", model = FALSE, x = FALSE, y = FALSE, 
contrasts = NULL, ...)

Arguments

formula a formula expression as for regression models, of the form response ~ 
predictors. See the documentation of formula for other details.
data an optional data frame, list or environment in which to interpret the variables 
occuring in formula.
W a weight matrix.
subset expression saying which subset of the rows of the data should be used in the fit. 
All observations are included by default.
na.action a function to filter missing data.
inverse logical: if true W specifies the inverse of the weight matrix: this is appropriate if 
a variance matrix is used.
method method to be used by lm.fit.
model should the model frame be returned?
x should the design matrix be returned?
y should the response be returned?
contrasts a list of contrasts to be used for some or all of 
... additional arguments to lm.fit.

Details

The problem is transformed to uncorrelated form and passed to lm.fit.

Value

An object of class "lm.gls", which is similar to an "lm" object. There is no "weights" component, 
and only a few "lm" methods will work correctly. As from version 7.1-22 the residuals and fitted 
values refer to the untransformed problem.

See Also

gls, lm, lm.ridge
lm.ridge

Ridge Regression

Description

Fit a linear model by ridge regression.

Usage

`lm.ridge(formula, data, subset, na.action, lambda = 0, model = FALSE, x = FALSE, y = FALSE, contrasts = NULL, ...)`

Arguments

- `formula`: a formula expression as for regression models, of the form `response ~ predictors`. See the documentation of `formula` for other details.
- `data`: an optional data frame, list or environment in which to interpret the variables occurring in `formula`.
- `subset`: expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
- `na.action`: a function to filter missing data.
- `lambda`: A scalar or vector of ridge constants.
- `model`: should the model frame be returned? Not implemented.
- `x`: should the design matrix be returned? Not implemented.
- `y`: should the response be returned? Not implemented.
- `contrasts`: a list of contrasts to be used for some or all of factor terms in the formula. See the `contrasts.arg` of `model.matrix.default`.
- `...`: additional arguments to `lm.fit`.
- `obj`: an R object, such as an "lm.ridge" fit.

Details

If an intercept is present in the model, its coefficient is not penalized. (If you want to penalize an intercept, put in your own constant term and remove the intercept.)

Value

A list with components

- `coef`: matrix of coefficients, one row for each value of `lambda`. Note that these are not on the original scale and are for use by the `coef` method.
- `scales`: scalings used on the X matrix.
- `Inter`: was intercept included?
- `lambda`: vector of lambda values
- `ym`: mean of y
loglm

xm column means of x matrix
GCV vector of GCV values
kHKB HKB estimate of the ridge constant.
kLW L-W estimate of the ridge constant.

References


See Also

lm

Examples

longley # not the same as the S-PLUS dataset
names(longley)[1] <- "y"
lm.ridge(y ~ ., longley)
plot(lm.ridge(y ~ ., longley,
lambda = seq(0,0.1,0.001)))
select(lm.ridge(y ~ ., longley,
lambda = seq(0,0.1,0.0001)))

loglm

Fit Log-Linear Models by Iterative Proportional Scaling

Description

This function provides a front-end to the standard function, loglin, to allow log-linear models to be specified and fitted in a manner similar to that of other fitting functions, such as glm.

Usage

loglm(formula, data, subset, na.action, ...)

Arguments

formula A linear model formula specifying the log-linear model.
If the left-hand side is empty, the data argument is required and must be a (complete) array of frequencies. In this case the variables on the right-hand side may be the names of the dimnames attribute of the frequency array, or may be the positive integers: 1, 2, 3, ... used as alternative names for the 1st, 2nd, 3rd, ... dimension (classifying factor). If the left-hand side is not empty it specifies a vector of frequencies. In this case the data argument, if present, must be a data frame from which the left-hand side vector and the classifying factors on the right-hand side are (preferentially) obtained. The usual abbreviation of a . to stand for ‘all other variables in the data frame’ is allowed. Any non-factors on the right-hand side of the formula are coerced to factor.

data Numeric array or data frame (or list or environment). In the first case it specifies the array of frequencies; in the second it provides the data frame from which the variables occurring in the formula are preferentially obtained in the usual way. This argument may be the result of a call to xtabs.
subset: Specifies a subset of the rows in the data frame to be used. The default is to take all rows.

aa.action: Specifies a method for handling missing observations. The default is to fail if missing values are present.

...: May supply other arguments to the function `loglm`.

Details

If the left-hand side of the formula is empty the `data` argument supplies the frequency array and the right-hand side of the formula is used to construct the list of fixed faces as required by `loglin`. Structural zeros may be specified by giving a `start` argument with those entries set to zero, as described in the help information for `loglin`.

If the left-hand side is not empty, all variables on the right-hand side are regarded as classifying factors and an array of frequencies is constructed. If some cells in the complete array are not specified they are treated as structural zeros. The right-hand side of the formula is again used to construct the list of faces on which the observed and fitted totals must agree, as required by `loglin`. Hence terms such as `a:b`, `a*b` and `a/b` are all equivalent.

Value

An object of class "loglm" conveying the results of the fitted log-linear model. Methods exist for the generic functions `print`, `summary`, `deviance`, `fitted`, `coef`, `resid`, `anova` and `update`, which perform the expected tasks. Only log-likelihood ratio tests are allowed using `anova`.

The deviance is simply an alternative name for the log-likelihood ratio statistic for testing the current model within a saturated model, in accordance with standard usage in generalized linear models.

Warning

If structural zeros are present, the calculation of degrees of freedom may not be correct. `loglin` itself takes no action to allow for structural zeros. `loglm` deducts one degree of freedom for each structural zero, but cannot make allowance for gains in error degrees of freedom due to loss of dimension in the model space. (This would require checking the rank of the model matrix, but since iterative proportional scaling methods are developed largely to avoid constructing the model matrix explicitly, the computation is at least difficult.)

When structural zeros (or zero fitted values) are present the estimated coefficients will not be available due to infinite estimates. The deviances will normally continue to be correct, though.

References


See Also

`loglm1`, `loglin`

Examples

```
# The data frames Cars93, minn38 and quine are available
# in the MASS package.

# Case 1: frequencies specified as an array.
sapply(minn38, function(x) length(levels(x)))
## hs phs fol sex f
```
logtrans

## 3 4 7 2 0
## minn38a <- array(0, c(3,4,7,2), lapply(minn38[, -5], levels))
## minn38a[data.matrix(minn38[, -5])] <- minn38$f

## or more simply
minn38a <- xtabs(f ~ ., minn38)

fm <- loglm(~ 1 + 2 + 3 + 4, minn38a)  # numerals as names.
deviance(fm)
## [1] 3711.9
fm1 <- update(fm, .~.^2)
fm2 <- update(fm, .~.^3, print = TRUE)
## 5 iterations: deviation 0.075
anova(fm, fm1, fm2)

# Case 1. An array generated with xtabs.

loglm(~ Type + Origin, xtabs(~ Type + Origin, Cars93))

# Case 2. Frequencies given as a vector in a data frame
names(quine)
## [1] "Eth" "Sex" "Age" "Lrn" "Days"
fm <- loglm(Days ~ .^2, quine)
gm <- glm(Days ~ .^2, poisson, quine)  # check glm.
c(deviance(fm), deviance(gm))  # deviances agree
## [1] 1368.7 1368.7
c(fm$df, gm$df)  # resid df do not!
c(fm$df, gm$df.residual)  # resid df do not!
## [1] 127 128

# The loglm residual degrees of freedom is wrong because of
# a non-detectable redundancy in the model matrix.

---

### Description

Find and optionally plot the marginal (profile) likelihood for alpha for a transformation model of
the form log(y + alpha) ~ x1 + x2 + ....

### Usage

logtrans(object, ...)

## Default S3 method:
logtrans(object, ..., alpha = seq(0.5, 6, by = 0.25) - min(y),
plotit = TRUE, interp =, xlab = "alpha",
ylab = "log Likelihood")

## S3 method for class 'formula'
logtrans(object, data, ...)

## S3 method for class 'lm'
logtrans(object, ...)
Arguments

object Fitted linear model object, or formula defining the untransformed model that is \( y \sim x_1 + x_2 + \ldots \). The function is generic.

... If object is a formula, this argument may specify a data frame as for \( \text{lm} \).

alpha Set of values for the transformation parameter, alpha.

plotit Should plotting be done?

interp Should the marginal log-likelihood be interpolated with a spline approximation? (Default is \( \text{TRUE} \) if plotting is to be done and the number of real points is less than 100.)

xlab as for \( \text{plot} \).

ylab as for \( \text{plot} \).

data optional data argument for \( \text{lm} \) fit.

Value

List with components \( x \) (for alpha) and \( y \) (for the marginal log-likelihood values).

Side Effects

A plot of the marginal log-likelihood is produced, if requested, together with an approximate mle and 95% confidence interval.

References


See Also

boxcox

Examples

logtrans(Days ~ Age*Sex*Eth*Lrn, data = quine, alpha = seq(0.75, 6.5, length.out = 20))

Description

Fit a regression to the good points in the dataset, thereby achieving a regression estimator with a high breakdown point. \( \text{lmsreg} \) and \( \text{ltsreg} \) are compatibility wrappers.
Usage

lqs(x, ...)

## S3 method for class 'formula'

lqs(formula, data, ...,
    method = c("lts", "lqs", "lms", "S", "model.frame"),
    subset, na.action, model = TRUE,
    x.ret = FALSE, y.ret = FALSE, contrasts = NULL)

## Default S3 method:
lqs(x, y, intercept = TRUE, method = c("lts", "lqs", "lms", "S"),
    quantile, control = lqs.control(...), k0 = 1.548, seed, ...)

lmsreg(...)
ltsreg(...)

Arguments

formula a formula of the form y ~ x1 + x2 + ....
data an optional data frame, list or environment from which variables specified in
formula are preferentially to be taken.
subset an index vector specifying the cases to be used in fitting. (NOTE: If given, this
argument must be named exactly.)
na.action function to specify the action to be taken if NAs are found. The default action is
for the procedure to fail. Alternatives include na.omit and na.exclude, which
lead to omission of cases with missing values on any required variable. (NOTE:
If given, this argument must be named exactly.)
model, x.ret, y.ret logical. If TRUE the model frame, the model matrix and the response are re-
turned, respectively.
contrasts an optional list. See the contrasts.arg of model.matrix.default.
x a matrix or data frame containing the explanatory variables.
y the response: a vector of length the number of rows of x.
intercept should the model include an intercept?
method the method to be used. model.frame returns the model frame: for the others
see the Details section. Using lmsreg or ltsreg forces "lms" and "lts" respectively.
quantile the quantile to be used: see Details. This is over-ridden if method = "lms".
control additional control items: see Details.
k0 the cutoff/tuning constant used for χ() and ψ() functions when method = "S",
currently corresponding to Tukey’s ‘biweight’.
seed the seed to be used for random sampling: see .Random.seed. The current value of
(Random.seed will be preserved if it is set.
... arguments to be passed to lqs.default or lqs.control, see control above
and Details.
Details

Suppose there are \( n \) data points and \( p \) regressors, including any intercept.

The first three methods minimize some function of the sorted squared residuals. For methods "lqs" and "lms" is the quantile squared residual, and for "lts" it is the sum of the quantile smallest squared residuals. "lqs" and "lms" differ in the defaults for quantile, which are \( \text{floor}((n+p+1)/2) \) and \( \text{floor}((n+1)/2) \) respectively. For "lts" the default is \( \text{floor}(n/2) + \text{floor}(p/2) \).

The "S" estimation method solves for the scale \( s \) such that the average of a function \( \chi \) of the residuals divided by \( s \) is equal to a given constant.

The control argument is a list with components

- \( \text{psamp} \): the size of each sample. Defaults to \( p \).
- \( \text{nsamp} \): the number of samples or "best" (the default) or "exact" or "sample". If "sample" the number chosen is \( \min(5*p, 3000) \), taken from Rousseeuw and Hubert (1997). If "best" exhaustive enumeration is done up to 5000 samples; if "exact" exhaustive enumeration will be attempted however many samples are needed.
- \( \text{adjust} \): should the intercept be optimized for each sample? Defaults to TRUE.

Value

An object of class "lqs". This is a list with components

- \( \text{crit} \): the value of the criterion for the best solution found, in the case of method == "S" before IWLS refinement.
- \( \text{sing} \): character. A message about the number of samples which resulted in singular fits.
- \( \text{coefficients} \): of the fitted linear model
- \( \text{bestone} \): the indices of those points fitted by the best sample found (prior to adjustment of the intercept, if requested).
- \( \text{fitted.values} \): the fitted values.
- \( \text{residuals} \): the residuals.
- \( \text{scale} \): estimate(s) of the scale of the error. The first is based on the fit criterion. The second (not present for method == "S") is based on the variance of those residuals whose absolute value is less than 2.5 times the initial estimate.

Note

There seems no reason other than historical to use the lms and lqs options. LMS estimation is of low efficiency (converging at rate \( n^{-1/3} \)) whereas LTS has the same asymptotic efficiency as an M estimator with trimming at the quartiles (Marazzi, 1993, p.201). LQS and LTS have the same maximal breakdown value of \( (\text{floor}((n-p)/2) + 1)/n \) attained if \( \text{floor}((n+p)/2) \leq \text{quantile} \leq \text{floor}((n+p+1)/2) \). The only drawback mentioned of LTS is greater computation, as a sort was thought to be required (Marazzi, 1993, p.201) but this is not true as a partial sort can be used (and is used in this implementation).

Adjusting the intercept for each trial fit does need the residuals to be sorted, and may be significant extra computation if \( n \) is large and \( p \) small.

Opinions differ over the choice of \( \text{psamp} \). Rousseeuw and Hubert (1997) only consider \( p \); Marazzi (1993) recommends \( p+1 \) and suggests that more samples are better than adjustment for a given computational limit.
The computations are exact for a model with just an intercept and adjustment, and for LQS for a model with an intercept plus one regressor and exhaustive search with adjustment. For all other cases the minimization is only known to be approximate.

References


See Also

predict.lqs

Examples

```r
## IGNORE_RDIFF_BEGIN
set.seed(123) # make reproducible
lqs(stack.loss ~ ., data = stackloss)
lqs(stack.loss ~ ., data = stackloss, method = "S", nsamp = "exact")
## IGNORE_RDIFF_END
```

mammals

Brain and Body Weights for 62 Species of Land Mammals

Description

A data frame with average brain and body weights for 62 species of land mammals.

Usage

mammals

Format

- **body**: body weight in kg.
- **brain**: brain weight in g.
- **name**: Common name of species. (Rock hyrax-a = *Heterohyrax brucci*, Rock hyrax-b = *Procavia habessinic*..)

Source


References

Description
Computes a multiple correspondence analysis of a set of factors.

Usage
mca(df, nf = 2, abbrev = FALSE)

Arguments
df A data frame containing only factors
nf The number of dimensions for the MCA. Rarely 3 might be useful.
abbrev Should the vertex names be abbreviated? By default these are of the form ‘factor.level’ but if abbrev = TRUE they are just ‘level’ which will suffice if the factors have distinct levels.

Value
An object of class "mca", with components
rs The coordinates of the rows, in nf dimensions.
cs The coordinates of the column vertices, one for each level of each factor.
fs Weights for each row, used to interpolate additional factors in predict.mca.
p The number of factors
d The singular values for the nf dimensions.
call The matched call.

References

See Also
predict.mca, plot.mca, corresp

Examples
farms.mca <- mca(farms, abbrev=TRUE)
farms.mca
plot(farms.mca)
Melanoma

Data from a Simulated Motorcycle Accident

Description
A data frame giving a series of measurements of head acceleration in a simulated motorcycle accident, used to test crash helmets.

Usage
mcycle

Format
- `times`: in milliseconds after impact.
- `accel`: in g.

Source

References

Survival from Malignant Melanoma

Description
The Melanoma data frame has data on 205 patients in Denmark with malignant melanoma.

Usage
Melanoma

Format
This data frame contains the following columns:
- `time`: survival time in days, possibly censored.
- `status`: 1 died from melanoma, 2 alive, 3 dead from other causes.
- `sex`: 1 = male, 0 = female.
- `age`: age in years.
- `year`: of operation.
- `thickness`: tumour thickness in mm.
- `ulcer`: 1 = presence, 0 = absence.
menarche

Source


---

<table>
<thead>
<tr>
<th>menarche</th>
<th>Age of Menarche in Warsaw</th>
</tr>
</thead>
</table>

Description

Proportions of female children at various ages during adolescence who have reached menarche.

Usage

menarche

Format

This data frame contains the following columns:

- **Age**: Average age of the group. (The groups are reasonably age homogeneous.)
- **Total**: Total number of children in the group.
- **Menarche**: Number who have reached menarche.

Source


The data are also given in

References


Examples

```r
mprob <- glm(cbind(Menarche, Total - Menarche) ~ Age,
             binomial(link = probit), data = menarche)
```
Michelson’s Speed of Light Data

Description

Measurements of the speed of light in air, made between 5th June and 2nd July, 1879. The data consists of five experiments, each consisting of 20 consecutive runs. The response is the speed of light in km/s, less 299000. The currently accepted value, on this scale of measurement, is 734.5.

Usage

michelson

Format

The data frame contains the following components:

- Expt  The experiment number, from 1 to 5.
- Run   The run number within each experiment.
- Speed Speed-of-light measurement.

Source


References


Minnesota High School Graduates of 1938

Description

The Minnesota high school graduates of 1938 were classified according to four factors, described below. The minn38 data frame has 168 rows and 5 columns.

Usage

minn38

Format

This data frame contains the following columns:

- hs  high school rank: "L", "M" and "U" for lower, middle and upper third.
- phs post high school status: Enrolled in college, ("C"), enrolled in non-collegiate school, ("N"), employed full-time, ("E") and other, ("O").
- fol father’s occupational level, (seven levels, "F1", "F2", . . . , "F7").
- sex sex: factor with levels "F" or "M".
- f  frequency.
motors

Source

who quotes the data from

---

motors

**Accelerated Life Testing of Motorettes**

Description

The *motors* data frame has 40 rows and 3 columns. It describes an accelerated life test at each of four temperatures of 10 motorettes, and has rather discrete times.

Usage

`motors`

Format

This data frame contains the following columns:

- `temp`: the temperature (degrees C) of the test.
- `time`: the time in hours to failure or censoring at 8064 hours (= 336 days).
- `cens`: an indicator variable for death.

Source

taken from

References


Examples

```r
library(survival)
plot(survfit(Surv(time, cens) ~ factor(temp), motors), conf.int = FALSE)
# fit Weibull model
motor.wei <- survreg(Surv(time, cens) ~ temp, motors)
summary(motor.wei)
# and predict at 130C
unlist(predict(motor.wei, data.frame(temp=130), se.fit = TRUE))

motor.cox <- coxph(Surv(time, cens) ~ temp, motors)
summary(motor.cox)
# predict at temperature 200
```
plot(survfit(motor.cox, newdata = data.frame(temp=200),
conf.type = "log-log")
summary( survfit(motor.cox, newdata = data.frame(temp=130)) )

<table>
<thead>
<tr>
<th>muscle</th>
<th>Effect of Calcium Chloride on Muscle Contraction in Rat Hearts</th>
</tr>
</thead>
</table>

**Description**

The purpose of this experiment was to assess the influence of calcium in solution on the contraction of heart muscle in rats. The left auricle of 21 rat hearts was isolated and on several occasions a constant-length strip of tissue was electrically stimulated and dipped into various concentrations of calcium chloride solution, after which the shortening of the strip was accurately measured as the response.

**Usage**

`muscle`

**Format**

This data frame contains the following columns:

- **Strip** which heart muscle strip was used?
- **Conc** concentration of calcium chloride solution, in multiples of 2.2 mM.
- **Length** the change in length (shortening) of the strip, (allegedly) in mm.

**Source**


**References**


**Examples**

```r
## IGNORE_RDIFF_BEGIN
A <- model.matrix(~ Strip - 1, data=muscle)
rats.nls1 <- nls(log(Length) ~ cbind(A, rho^Conc),
data = muscle, start = c(rho=0.1), algorithm="plinear")
(B <- coef(rats.nls1))

st <- list(alpha = B[2:22], beta = B[23], rho = B[1])
(rats.nls2 <- nls(log(Length) ~ alpha[Strip] + beta*rho^Conc,
data = muscle, start = st))
## IGNORE_RDIFF_END

Muscle <- with(muscle, {
Muscle <- expand.grid(Conc = sort(unique(Conc)), Strip = levels(Strip))
```

Muscle$Yhat <- predict(rats.nls2, Muscle)
Muscle <- cbind(Muscle, logLength = rep(as.numeric(NA), 126))
ind <- match(paste(Strip, Conc),
             paste(Muscle$Strip, Muscle$Conc))
Muscle$logLength[ind] <- log(Length)
}

lattice::xyplot(Yhat ~ Conc | Strip, Muscle, as.table = TRUE,
                ylim = range(c(Muscle$Yhat, Muscle$logLength), na.rm = TRUE),
                subscripts = TRUE, xlab = "Calcium Chloride concentration (mM)",
                ylab = "log(Length in mm)", panel =
                function(x, y, subscripts, ...) {
                    panel.xyplot(x, Muscle$logLength[subscripts], ...)
                    llines(spline(x, y))
                })

---

**mvrnorm**

_Simulate from a Multivariate Normal Distribution_

### Description

Produces one or more samples from the specified multivariate normal distribution.

### Usage

```r
mvrnorm(n = 1, mu, Sigma, tol = 1e-6, empirical = FALSE, EISPACK = FALSE)
```

### Arguments

- **n**: the number of samples required.
- **mu**: a vector giving the means of the variables.
- **Sigma**: a positive-definite symmetric matrix specifying the covariance matrix of the variables.
- **tol**: tolerance (relative to largest variance) for numerical lack of positive-definiteness in Sigma.
- **empirical**: logical. If true, mu and Sigma specify the empirical not population mean and covariance matrix.
- **EISPACK**: logical: values other than FALSE are an error.

### Details

The matrix decomposition is done via `eigen`; although a Choleski decomposition might be faster, the eigendecomposition is stabler.

### Value

If n = 1 a vector of the same length as mu, otherwise an n by `length(mu)` matrix with one sample in each row.

### Side Effects

Causes creation of the dataset .Random.seed if it does not already exist, otherwise its value is updated.
negative.binomial

Family function for Negative Binomial GLMs

Description

Specifies the information required to fit a Negative Binomial generalized linear model, with known theta parameter, using glm().

Usage

negative.binomial(theta = stop("'theta' must be specified"), link = "log")

Arguments

theta          The known value of the additional parameter, theta.
link           The link function, as a character string, name or one-element character vector specifying one of log, sqrt or identity, or an object of class "link-glm".

Value

An object of class "family", a list of functions and expressions needed by glm() to fit a Negative Binomial generalized linear model.

References


See Also

glm.nb, anova.negbin, summary.negbin

Examples

# Fitting a Negative Binomial model to the quine data
# with theta = 2 assumed known.
#
glm(Days ~ .^4, family = negative.binomial(2), data = quine)
**newcomb**

*Newcomb’s Measurements of the Passage Time of Light*

**Description**

A numeric vector giving the ‘Third Series’ of measurements of the passage time of light recorded by Newcomb in 1882. The given values divided by 1000 plus 24.8 give the time in millionths of a second for light to traverse a known distance. The ‘true’ value is now considered to be 33.02.

The dataset is given in the order in Staudte and Sheather. Stigler (1977, Table 5) gives the dataset as

```
28 26 33 24 34 -44 27 16 40 -2 29 22 24 21 25 30 23 29 31 19
24 20 36 32 36 28 25 21 28 29 37 25 28 26 30 32 36 26 30 22
36 23 27 27 28 27 31 27 26 33 26 32 32 24 39 28 24 25 32 25
29 27 28 29 16 23
```

However, order is not relevant to its use as an example of robust estimation. (Thanks to Anthony Unwin for bringing this difference to our attention.)

**Usage**

newcomb

**Source**


---

**nlschools**

*Eighth-Grade Pupils in the Netherlands*

**Description**

Snijders and Bosker (1999) use as a running example a study of 2287 eighth-grade pupils (aged about 11) in 132 classes in 131 schools in the Netherlands. Only the variables used in our examples are supplied.

**Usage**

nlschools
Format

This data frame contains 2287 rows and the following columns:

- lang  language test score.
- IQ    verbal IQ.
- class class ID.
- GS    class size: number of eighth-grade pupils recorded in the class (there may be others: see COMB, and some may have been omitted with missing values).
- SES   social-economic status of pupil’s family.
- COMB  were the pupils taught in a multi-grade class (0/1)? Classes which contained pupils from grades 7 and 8 are coded 1, but only eighth-graders were tested.

Source


References


Examples

```r
nl1 <- within(nlschools, {
  IQave <- tapply(IQ, class, mean)[as.character(class)]
  IQ <- IQ - IQave
})
cen <- c("IQ", "IQave", "SES")
nl1[cen] <- scale(nl1[cen], center = TRUE, scale = FALSE)
nl.lme <- nlme::lme(lang ~ IQ*COMB + IQave + SES, 
                      random = ~ IQ | class, data = nl1)
## IGNORE_RDIFF_BEGIN
summary(nl.lme)
## IGNORE_RDIFF_END
```

Description

A classical N, P, K (nitrogen, phosphate, potassium) factorial experiment on the growth of peas conducted on 6 blocks. Each half of a fractional factorial design confounding the NPK interaction was used on 3 of the plots.

Usage

npk

npk  

Classical N, P, K Factorial Experiment
**Format**

The npk data frame has 24 rows and 5 columns:

- `block` which block (label 1 to 6).
- `N` indicator (0/1) for the application of nitrogen.
- `P` indicator (0/1) for the application of phosphate.
- `K` indicator (0/1) for the application of potassium.
- `yield` Yield of peas, in pounds/plot (the plots were 1/70 acre).

**Note**

This dataset is also contained in R 3.0.2 and later.

**Source**


**References**


**Examples**

```r
options(contrasts = c("contr.sum", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
## IGNORE_RDIFF_BEGIN
npk.aov
summary(npk.aov)
alias(npk.aov)
coef(npk.aov)
options(contrasts = c("contr.treatment", "contr.poly"))
npk.aov1 <- aov(yield ~ block + N + K, data = npk)
summary.lm(npk.aov1)
se.contrast(npk.aov1, list(N=="0", N=="1"), data = npk)
model.tables(npk.aov1, type = "means", se = TRUE)
## IGNORE_RDIFF_END
```

---

**npr1**

*US Naval Petroleum Reserve No. 1 data*

**Description**

Data on the locations, porosity and permeability (a measure of oil flow) on 104 oil wells in the US Naval Petroleum Reserve No. 1 in California.

**Usage**

npr1
Format

This data frame contains the following columns:

- x: x coordinates, in miles (origin unspecified).
- y: y coordinates, in miles.
- perm: permeability in milli-Darcies.
- por: porosity (%).

Source


References


---

**Null**

**Null Spaces of Matrices**

Description

Given a matrix, $M$, find a matrix $N$ giving a basis for the (left) null space. That is, $\text{crossprod}(N, M) = \text{t}(N) \times M$ is an all-zero matrix and $N$ has the maximum number of linearly independent columns.

Usage

```
Null(M)
```

Arguments

- `M`: Input matrix. A vector is coerced to a 1-column matrix.

Details

For a basis for the (right) null space $\{x : Mx = 0\}$, use `Null(t(M))`.

Value

The matrix $N$ with the basis for the (left) null space, or a matrix with zero columns if the matrix $M$ is square and of maximal rank.

References


See Also

- `qr`, `qr.Q`
Examples

The function is currently defined as

```r
function(M)
{
  tmp <- qr(M)
  set <- if(tmp$rank == 0L) seq_len(ncol(M)) else -seq_len(tmp$rank)
  qr.Q(tmp, complete = TRUE)[, set, drop = FALSE]
}
```

---

**oats**

Data from an Oats Field Trial

**Description**

The yield of oats from a split-plot field trial using three varieties and four levels of manurial treatment. The experiment was laid out in 6 blocks of 3 main plots, each split into 4 sub-plots. The varieties were applied to the main plots and the manurial treatments to the sub-plots.

**Usage**

`oats`

**Format**

This data frame contains the following columns:

- **B** Blocks, levels I, II, III, IV, V and VI.
- **V** Varieties, 3 levels.
- **N** Nitrogen (manurial) treatment, levels 0.0cwt, 0.2cwt, 0.4cwt and 0.6cwt, showing the application in cwt/acre.
- **Y** Yields in 1/4lbs per sub-plot, each of area 1/80 acre.

**Source**


**References**


**Examples**

```r
oats$Nf <- ordered(oats$N, levels = sort(levels(oats$N))
oats.aov <- aov(Y ~ Nf*V + Error(B/V), data = oats, qr = TRUE)
## IGNORE_RDIFF_BEGIN
summary(oats.aov)
summary(oats.aov, split = list(Nf=list(L=1, Dev=2:3)))
## IGNORE_RDIFF_END
par(mfrow = c(1,2), pty = "s")
plot(fitted(oats.aov[[4]]), studres(oats.aov[[4]]))
```
Tests of Auditory Perception in Children with OME

Description

Experiments were performed on children on their ability to differentiate a signal in broad-band noise. The noise was played from a pair of speakers and a signal was added to just one channel; the subject had to turn his/her head to the channel with the added signal. The signal was either coherent (the amplitude of the noise was increased for a period) or incoherent (independent noise was added for the same period to form the same increase in power).

The threshold used in the original analysis was the stimulus loudness needs to get 75% correct responses. Some of the children had suffered from otitis media with effusion (OME).

Usage

OME

Format

The OME data frame has 1129 rows and 7 columns:

ID  Subject ID (1 to 99, with some IDs missing). A few subjects were measured at different ages.
OME "low" or "high" or "N/A" (at ages other than 30 and 60 months).
Age  Age of the subject (months).
Loud  Loudness of stimulus, in decibels.
Noise  Whether the signal in the stimulus was "coherent" or "incoherent".
Correct  Number of correct responses from Trials trials.
Trials  Number of trials performed.

Background

The experiment was to study otitis media with effusion (OME), a very common childhood condition where the middle ear space, which is normally air-filled, becomes congested by a fluid. There is a concomitant fluctuating, conductive hearing loss which can result in various language, cognitive and social deficits. The term ‘binaural hearing’ is used to describe the listening conditions in which the brain is processing information from both ears at the same time. The brain computes differences in the intensity and/or timing of signals arriving at each ear which contributes to sound localisation and also to our ability to hear in background noise.

Some years ago, it was found that children of 7–8 years with a history of significant OME had significantly worse binaural hearing than children without such a history, despite having equivalent sensitivity. The question remained as to whether it was the timing, the duration, or the degree of
severity of the otitis media episodes during critical periods, which affected later binaural hearing. In an attempt to begin to answer this question, 95 children were monitored for the presence of effusion every month since birth. On the basis of OME experience in their first two years, the test population was split into one group of high OME prevalence and one of low prevalence.

Source

Sarah Hogan, Dept of Physiology, University of Oxford, via Dept of Statistics Consulting Service

Examples

# Fit logistic curve from p = 0.5 to p = 1.0
fp1 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/scal)), c("L75", "scal"),
    function(x,L75,scal)NULL)
nls(Correct/Trials ~ fp1(Loud, L75, scal), data = OME,
    start = c(L75=45, scal=3))
nls(Correct/Trials ~ fp1(Loud, L75, scal),
    data = OME[OME$Noise == "coherent",],
    start=c(L75=45, scal=3))
nls(Correct/Trials ~ fp1(Loud, L75, scal),
    data = OME[OME$Noise == "incoherent",],
    start = c(L75=45, scal=3))

# individual fits for each experiment
aa <- factor(OME$Age)
ab <- 10*OME$ID + unclass(aa)
ac <- unclass(factor(ab))
OME$UID <- as.vector(ac)
OME$UIDn <- OME$UID + 0.1*(OME$Noise == "incoherent")
rm(aa, ab, ac)
OMEi <- OME
library(nlme)
fp2 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/2)),
    "L75", function(x,L75) NULL)
dec <- getOption("OutDec")
options(show.error.messages = FALSE, OutDec=".")
OMEi.nls <- nlsList(Correct/Trials ~ fp2(Loud, L75) | UIDn,
    data = OMEi, start = list(L75=45), control = list(maxiter=100))
options(show.error.messages = TRUE, OutDec=dec)
tmp <- sapply(OMEi.nls, function(X)
    {if(is.null(X)) NA else as.vector(coef(X))})
OMEif <- data.frame(UID = round(as.numeric(names(tmp))),
    Noise = rep(c("coherent", "incoherent"), 110),
    L75 = as.vector(tmp), stringsAsFactors = TRUE)
OMEif$Age <- OMEif$Age[match(OMEif$UID, OME$UID)]
OMEif$OME <- OMEif$OME[match(OMEif$UID, OME$UID)]
OMEif <- OMEif[OMEif$L75 > 30,]
summary(lm(L75 ~ Noise/Age, data = OMEif, na.action = na.omit))
summary(lm(L75 ~ Noise/(Age + OME), data = OMEif,
    subset = (Age >= 30 & Age <= 60),
    na.action = na.omit), correlation = FALSE)

# Or fit by weighted least squares
fpl75 <- deriv(~ sqrt(n)*(r/n - 0.5 - 0.5/(1 + exp(-(x-L75)/scal))),
    function(x,L75,scal)NULL)
nls(Correct/Trials ~ fpl75(Loud, L75, scal), data = OME,
    start = c(L75=45, scal=3))

The Painter’s Data of de Piles

c("L75", "scal"),
function(r,n,x,L75,scal) NULL)
nls(0 ~ fp75(Correct, Trials, Loud, L75, scal),
data = OME[OME$Noise == "coherent",],
start = c(L75=45, scal=3))
nls(0 ~ fp75(Correct, Trials, Loud, L75, scal),
data = OME[OME$Noise == "incoherent",],
start = c(L75=45, scal=3))

# Test to see if the curves shift with age
fp75age <- deriv(~sqrt(n)*(r/n - 0.5 - 0.5/(1 +
exp(-(x-L75-slope*age)/scal))),
c("L75", "slope", "scal"),
function(r,n,x,age,L75,slope,scal) NULL)
OME.nls1 <-
nls(0 ~ fp75age(Correct, Trials, Loud, Age, L75, slope, scal),
data = OME[OME$Noise == "coherent",],
start = c(L75=45, slope=0, scal=2))
sqrt(diag(vcov(OME.nls1))))
OME.nls2 <-
nls(0 ~ fp75age(Correct, Trials, Loud, Age, L75, slope, scal),
data = OME[OME$Noise == "incoherent",],
start = c(L75=45, slope=0, scal=2))
sqrt(diag(vcov(OME.nls2))))

# Now allow random effects by using NLME
OMEf <- OME[rep(1:nrow(OME), OME$Trials),]
OMEf$Resp <- with(OME, rep(rep(c(1,0), length(Trials)),
t(cbind(Correct, Trials-Correct))))
OMEf <- OME[, -match(c("Correct", "Trials"), names(OMEf))]

## Not run: ## these fail in R on most platforms
fp2 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/exp(lsc))),
c("L75", "lsc"),
function(x, L75, lsc) NULL)
try(summary(nlme(Resp ~ fp2(Loud, L75, lsc),
fixed = list(L75 ~ Age, lsc ~ 1),
random = L75 + lsc ~ 1 | UID,
data = OMEf$Noise == "coherent",], method = "ML",
start = list(fixed=c(L75=c(48.7, -0.03), lsc=0.24)), verbose = TRUE)))

try(summary(nlme(Resp ~ fp2(Loud, L75, lsc),
fixed = list(L75 ~ Age, lsc ~ 1),
random = L75 + lsc ~ 1 | UID,
data = OMEf$Noise == "incoherent",], method = "ML",
start = list(fixed=c(L75=c(41.5, -0.1), lsc=0)), verbose = TRUE)))

## End(Not run)
Description

The subjective assessment, on a 0 to 20 integer scale, of 54 classical painters. The painters were assessed on four characteristics: composition, drawing, colour and expression. The data is due to the Eighteenth century art critic, de Piles.

Usage

painters

Format

The row names of the data frame are the painters. The components are:

- Composition: Composition score.
- Drawing: Drawing score.
- Colour: Colour score.
- Expression: Expression score.
- School: The school to which a painter belongs, as indicated by a factor level code as follows: "A": Renaissance; "B": Mannerist; "C": Seicento; "D": Venetian; "E": Lombard; "F": Sixteenth Century; "G": Seventeenth Century; "H": French.

Source


References


pairs.lda  
Produce Pairwise Scatterplots from an 'lda' Fit

Description

Pairwise scatterplot of the data on the linear discriminants.

Usage

```R
## S3 method for class 'lda'
pairs(x, labels = colnames(x), panel = panel.lda,
     dimen, abbrev = FALSE, ..., cex=0.7, type = c("std", "trellis"))
```
Arguments

- **x**: Object of class "lda".
- **labels**: vector of character strings for labelling the variables.
- **panel**: panel function to plot the data in each panel.
- **dimen**: The number of linear discriminants to be used for the plot; if this exceeds the number determined by x the smaller value is used.
- **abbrev**: whether the group labels are abbreviated on the plots. If abbrev > 0 this gives minlength in the call to abbreviate.
- **...**: additional arguments for pairs.default.
- **cex**: graphics parameter cex for labels on plots.
- **type**: type of plot. The default is in the style of pairs.default; the style "trellis" uses the Trellis function splom.

Details

This function is a method for the generic function pairs() for class "lda". It can be invoked by calling pairs(x) for an object x of the appropriate class, or directly by calling pairs.lda(x) regardless of the class of the object.

References


See Also

pairs

parcoord

Parallel Coordinates Plot

Description

Parallel coordinates plot

Usage

parcoord(x, col = 1, lty = 1, var.label = FALSE, ...)

Arguments

- **x**: a matrix or data frame who columns represent variables. Missing values are allowed.
- **col**: A vector of colours, recycled as necessary for each observation.
- **lty**: A vector of line types, recycled as necessary for each observation.
- **var.label**: If TRUE, each variable's axis is labelled with maximum and minimum values.
- **...**: Further graphics parameters which are passed to matplot.

Examples

The variables are as follows

No crude oil sample identification label. (Factor.)
SG specific gravity, degrees API. (Constant within sample.)
VP vapour pressure in pounds per square inch. (Constant within sample.)
V10 volatility of crude; ASTM 10% point. (Constant within sample.)
EP desired volatility of gasoline. (The end point. Varies within sample.)
Y yield as a percentage of crude.

Source

This dataset is also given in D. J. Hand, F. Daly, K. McConway, D. Lunn and E. Ostrowski (eds) (1994) A Handbook of Small Data Sets. Chapman & Hall.
References


Examples

```r
library(nlme)
Petrol <- petrol
Petrol[, 2:5] <- scale(as.matrix(Petrol[, 2:5]), scale = FALSE)
pet3.lme <- lme(Y ~ SG + VP + V10 + EP,
    random = ~ 1 | No, data = Petrol)
pet3.lme <- update(pet3.lme, method = "ML")
anova(pet4.lme, pet3.lme)
```

Description

A population of women who were at least 21 years old, of Pima Indian heritage and living near Phoenix, Arizona, was tested for diabetes according to World Health Organization criteria. The data were collected by the US National Institute of Diabetes and Digestive and Kidney Diseases. We used the 532 complete records after dropping the (mainly missing) data on serum insulin.

Usage

- `Pima.tr`
- `Pima.tr2`
- `Pima.te`

Format

These data frames contain the following columns:

- `npreg` number of pregnancies.
- `glu` plasma glucose concentration in an oral glucose tolerance test.
- `bp` diastolic blood pressure (mm Hg).
- `skin` triceps skin fold thickness (mm).
- `bmi` body mass index (weight in kg/(height in m)^2).
- `ped` diabetes pedigree function.
- `age` age in years.
- `type` Yes or No, for diabetic according to WHO criteria.

Details

The training set `Pima.tr` contains a randomly selected set of 200 subjects, and `Pima.te` contains the remaining 332 subjects. `Pima.tr2` contains `Pima.tr` plus 100 subjects with missing values in the explanatory variables.
plot.lda

Source

plot.lda  Plot Method for Class 'lda'

Description
Plots a set of data on one, two or more linear discriminants.

Usage
## S3 method for class 'lda'
plot(x, panel = panel.lda, ..., cex = 0.7, dimen,
abbrev = FALSE, xlab = "LD1", ylab = "LD2")

Arguments
x An object of class "lda".
panel the panel function used to plot the data.
... additional arguments to pairs.lda or eqscplot.
cex graphics parameter cex for labels on plots.
dimen The number of linear discriminants to be used for the plot; if this exceeds the number determined by x the smaller value is used.
abbrev whether the group labels are abbreviated on the plots. If abbrev > 0 this gives minlength in the call to abbreviate.
xlab label for the x axis
ylab label for the y axis

dimen

Details
This function is a method for the generic function plot() for class "lda". It can be invoked by calling plot(x) for an object x of the appropriate class, or directly by calling plot.lda(x) regardless of the class of the object.
The behaviour is determined by the value of dimen. For dimen > 2, a pairs plot is used. For dimen = 2, an equiscaled scatter plot is drawn. For dimen = 1, a set of histograms or density plots are drawn. Use argument type to match "histogram" or "density" or "both".

References

See Also
pairs.lda, ldahist, lda, predict.lda
plot.mca  

*Plot Method for Objects of Class 'mca'*

**Description**

Plot a multiple correspondence analysis.

**Usage**

```r
## S3 method for class 'mca'
plot(x, rows = TRUE, col, cex = par("cex"), ...)
```

**Arguments**

- **x**: An object of class "mca".
- **rows**: Should the coordinates for the rows be plotted, or just the vertices for the levels?
- **col, cex**: The colours and cex to be used for the row points and level vertices respectively.
- **...**: Additional parameters to plot.

**References**


**See Also**

`mca`, `predict.mca`

**Examples**

```r
plot(mca(farms, abbrev = TRUE))
```

---

plot.profile  

*Plotting Functions for 'profile' Objects*

**Description**

`plot` and `pairs` methods for objects of class "profile".

**Usage**

```r
## S3 method for class 'profile'
plot(x, ...)
## S3 method for class 'profile'
pairs(x, colours = 2:3, ...)```

**Arguments**

- **x**: an object inheriting from class "profile".
- **colours**: Colours to be used for the mean curves conditional on x and y respectively.
- **...**: arguments passed to or from other methods.
polr

Ordered Logistic or Probit Regression

Description

Fits a logistic or probit regression model to an ordered factor response. The default logistic case is proportional odds logistic regression, after which the function is named.

Usage

polr(formula, data, weights, start, ..., subset, na.action,
     contrasts = NULL, Hess = FALSE, model = TRUE,
     method = c("logistic", "probit", "loglog", "cloglog", "cauchit"))
Arguments

- **formula**: a formula expression as for regression models, of the form `response ~ predictors`. The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response, with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and be ignored. An offset may be used. See the documentation of `formula` for other details.

- **data**: an optional data frame, list or environment in which to interpret the variables occurring in formula.

- **weights**: optional case weights in fitting. Default to 1.

- **start**: initial values for the parameters. This is in the format `c(coefficients, zeta)`: see the Values section.

- **...**: additional arguments to be passed to `optim`, most often a control argument.

- **subset**: expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.

- **na.action**: a function to filter missing data.

- **contrasts**: a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.

- **Hess**: logical for whether the Hessian (the observed information matrix) should be returned. Use this if you intend to call `summary` or `vcov` on the fit.

- **model**: logical for whether the model matrix should be returned.

- **method**: logistic or probit or (complementary) log-log or cauchit (corresponding to a Cauchy latent variable).

Details

This model is what Agresti (2002) calls a *cumulative link* model. The basic interpretation is as a *coarsened* version of a latent variable $Y_i$ which has a logistic or normal or extreme-value or Cauchy distribution with scale parameter one and a linear model for the mean. The ordered factor which is observed is which bin $Y_i$ falls into with breakpoints

$$\zeta_0 = -\infty < \zeta_1 < \cdots < \zeta_K = \infty$$

This leads to the model

$$\text{logit}P(Y \leq k|x) = \zeta_k - \eta$$

with `logit` replaced by `probit` for a normal latent variable, and $\eta$ being the linear predictor, a linear function of the explanatory variables (with no intercept). Note that it is quite common for other software to use the opposite sign for $\eta$ (and hence the coefficients `beta`).

In the logistic case, the left-hand side of the last display is the log odds of category $k$ or less, and since these are log odds which differ only by a constant for different $k$, the odds are proportional. Hence the term *proportional odds logistic regression*.

The log-log and complementary log-log links are the increasing functions $F^{-1}(p) = -\log(-\log(p))$ and $F^{-1}(p) = \log(\log(1-p))$; some call the first the ‘negative log-log’ link. These correspond to a latent variable with the extreme-value distribution for the maximum and minimum respectively.

A *proportional hazards* model for grouped survival times can be obtained by using the complementary log-log link with grouping ordered by increasing times.

`predict`, `summary`, `vcov`, `anova`, `model.frame` and an `extractAIC` method for use with `stepAIC` (and `step`). There are also `profile` and `confint` methods.
Value

A object of class "polr". This has components

- **coefficients**: the coefficients of the linear predictor, which has no intercept.
- **zeta**: the intercepts for the class boundaries.
- **deviance**: the residual deviance.
- **fitted.values**: a matrix, with a column for each level of the response.
- **lev**: the names of the response levels.
- **terms**: the terms structure describing the model.
- **df.residual**: the number of residual degrees of freedoms, calculated using the weights.
- **edf**: the (effective) number of degrees of freedom used by the model.
- **n.obs**: the (effective) number of observations, calculated using the weights. (nobs is for use by stepAIC.
- **call**: the matched call.
- **method**: the matched method used.
- **convergence**: the convergence code returned by optim.
- **niter**: the number of function and gradient evaluations used by optim.
- **lp**: the linear predictor (including any offset).
- **Hessian**: (if Hess is true). Note that this is a numerical approximation derived from the optimization process.
- **model**: (if model is true).

Note

The vcov method uses the approximate Hessian: for reliable results the model matrix should be sensibly scaled with all columns having range the order of one.

Prior to version 7.3-32, method = "cloglog" confusingly gave the log-log link, implicitly assuming the first response level was the ‘best’.

References


See Also

optim, glm, multinom.

Examples

```r
options(contrasts = c("contr.treatment", "contr.poly"))
house.plr <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
house.plr
summary(house.plr, digits = 3)
## slightly worse fit from
summary(update(house.plr, method = "probit", Hess = TRUE), digits = 3)
## although it is not really appropriate, can fit
summary(update(house.plr, method = "loglog", Hess = TRUE), digits = 3)
```
predict.glmmPQL

Predict Method for glmmPQL Fits

Description
Obtains predictions from a fitted generalized linear model with random effects.

Usage

## S3 method for class 'glmmPQL'
predict(object, newdata = NULL, type = c("link", "response"),
         level, na.action = na.pass, ...)

Arguments

object a fitted object of class inheriting from "glmmPQL".
newdata optionally, a data frame in which to look for variables with which to predict.
type the type of prediction required. The default is on the scale of the linear predictors; the alternative "response" is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and type = "response" gives the predicted probabilities.
level an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping.
na.action function determining what should be done with missing values in newdata. The default is to predict NA.
...

Value
If level is a single integer, a vector otherwise a data frame.

See Also

glmmPQL, predict.lme.
Examples

```r
fit <- glmmPQL(y ~ trt + I(week > 2), random = ~1 | ID,
              family = binomial, data = bacteria)
predict(fit, bacteria, level = 0, type="response")
predict(fit, bacteria, level = 1, type="response")
```

**predict.lda**

*Classify Multivariate Observations by Linear Discrimination*

**Description**

Classify multivariate observations in conjunction with lda, and also project data onto the linear discriminants.

**Usage**

```
## S3 method for class 'lda'
predict(object, newdata, prior = object$prior, dimen,
         method = c("plug-in", "predictive", "debiased"), ...)
```

**Arguments**

- `object`: object of class "lda"
- `newdata`: data frame of cases to be classified or, if `object` has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If `newdata` is missing, an attempt will be made to retrieve the data used to fit the `lda` object.
- `prior`: The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to `lda`.
- `dimen`: the dimension of the space to be used. If this is less than \(\min(p, n_g-1)\), only the first `dimen` discriminant components are used (except for `method="predictive"`), and only those dimensions are returned in `x`.
- `method`: This determines how the parameter estimation is handled. With "plug-in" (the default) the usual unbiased parameter estimates are used and assumed to be correct. With "debiased" an unbiased estimator of the log posterior probabilities is used, and with "predictive" the parameter estimates are integrated out using a vague prior.
- `...`: arguments based from or to other methods

**Details**

This function is a method for the generic function `predict()` for class "lda". It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.lda(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the linear discriminants cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

This version centres the linear discriminants so that the weighted mean (weighted by `prior`) of the group centroids is at the origin.
Value

a list with components

- **class**: The MAP classification (a factor)
- **posterior**: posterior probabilities for the classes
- **x**: the scores of test cases on up to dimen discriminant variables

References


See Also

`lda`, `qda`, `predict.qda`

Examples

```r
tr <- sample(1:50, 25)
train <- rbind(iris3[,tr,1], iris3[,tr,2], iris3[,tr,3])
test <- rbind(iris3[-tr,1], iris3[-tr,2], iris3[-tr,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
z <- lda(train, cl)
predict(z, test)$class
```

### predict.lqs

**Predict from an lqs Fit**

**Description**

Predict from an resistant regression fitted by lqs.

**Usage**

```r
## S3 method for class 'lqs'
predict(object, newdata, na.action = na.pass, ...)
```

**Arguments**

- **object**: object inheriting from class "lqs"
- **newdata**: matrix or data frame of cases to be predicted or, if object has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If newdata is missing, an attempt will be made to retrieve the data used to fit the lqs object.
- **na.action**: function determining what should be done with missing values in newdata. The default is to predict NA.
- **...**: arguments to be passed from or to other methods.
**Details**

This function is a method for the generic function `predict()` for class `lqs`. It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.lqs(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the linear fit cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

**Value**

A vector of predictions.

**Author(s)**

B.D. Ripley

**See Also**

`lqs`

**Examples**

```r
set.seed(123)
fm <- lqs(stack.loss ~ ., data = stackloss, method = "S", nsamp = "exact")
predict(fm, stackloss)
```

---

**predict.mca**

*Predict Method for Class 'mca'*

**Description**

Used to compute coordinates for additional rows or additional factors in a multiple correspondence analysis.

**Usage**

```r
## S3 method for class 'mca'
predict(object, newdata, type = c("row", "factor"), ...)
```

**Arguments**

- `object`: An object of class "mca", usually the result of a call to `mca`.
- `newdata`: A data frame containing either additional rows of the factors used to fit `object` or additional factors for the cases used in the original fit.
- `type`: Are predictions required for further rows or for new factors?
- `...`: Additional arguments from `predict`: unused.

**Value**

If `type = "row"`, the coordinates for the additional rows.

If `type = "factor"`, the coordinates of the column vertices for the levels of the new factors.
predict.qda

References

See Also
mca, plot.mca

**predict.qda**

*Classify from Quadratic Discriminant Analysis*

**Description**

Classify multivariate observations in conjunction with qda

**Usage**

```r
## S3 method for class 'qda'
predict(object, newdata, prior = object$prior,
          method = c("plug-in", "predictive", "debiased", "looCV"), ...)
```

**Arguments**

- `object`: object of class "qda"
- `newdata`: data frame of cases to be classified or, if `object` has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If `newdata` is missing, an attempt will be made to retrieve the data used to fit the `qda` object.
- `prior`: The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to `qda`.
- `method`: This determines how the parameter estimation is handled. With "plug-in" (the default) the usual unbiased parameter estimates are used and assumed to be correct. With "debiased" an unbiased estimator of the log posterior probabilities is used, and with "predictive" the parameter estimates are integrated out using a vague prior. With "looCV" the leave-one-out cross-validation fits to the original dataset are computed and returned.
- ...: arguments based from or to other methods

**Details**

This function is a method for the generic function `predict()` for class "qda". It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.qda(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the quadratic discriminants cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.
profile.glm

Value

a list with components

class
The MAP classification (a factor)
posterior
posterior probabilities for the classes

References


See Also

qda, lda, predict.lda

Examples

tr <- sample(1:50, 25)
train <- rbind(iris3[,tr,,1], iris3[,tr,,2], iris3[,tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
qz <- qda(train, cl)
predict(qz, test)$class

profile.glm

Method for Profiling glm Objects

Description

Investigates the profile log-likelihood function for a fitted model of class "glm".

Usage

## S3 method for class 'glm'
profile(fitted, which = 1:p, alpha = 0.01, maxsteps = 10,
       del = zmax/5, trace = FALSE, ...)

Arguments

fitted
the original fitted model object.
which
the original model parameters which should be profiled. This can be a numeric
or character vector. By default, all parameters are profiled.
alpha
highest significance level allowed for the profile t-statistics.
maxsteps
maximum number of points to be used for profiling each parameter.
del
suggested change on the scale of the profile t-statistics. Default value chosen to
allow profiling at about 10 parameter values.
trace
logical: should the progress of profiling be reported?
... further arguments passed to or from other methods.
Details

The profile t-statistic is defined as the square root of change in sum-of-squares divided by residual standard error with an appropriate sign.

Value

A list of classes "profile.glm" and "profile" with an element for each parameter being profiled. The elements are data-frames with two variables

- par.vals: a matrix of parameter values for each fitted model.
- tau: the profile t-statistics.

Author(s)

Originally, D. M. Bates and W. N. Venables. (For S in 1996.)

See Also

glm, profile, plot.profile

Examples

```r
options(contrasts = c("contr.treatment", "contr.poly"))
ldose <- rep(0:5, 2)
umdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
budworm.lg <- glm(SF ~ sex*ldose, family = binomial)
pr1 <- profile(budworm.lg)
plot(pr1)
pairs(pr1)
```

---

qda

### Quadratic Discriminant Analysis

Description

Quadratic discriminant analysis.

Usage

```r
qda(x, ...)
```

## S3 method for class 'formula'
qda(formula, data, ..., subset, na.action)

## Default S3 method:
qda(x, grouping, prior = proportions,
    method, CV = FALSE, nu, ...)

## S3 method for class 'data.frame'
qda(x, ...)
## S3 method for class 'matrix'
qda(x, grouping, ..., subset, na.action)

### Arguments

- **formula**: A formula of the form `groups ~ x1 + x2 + ...`. That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
- **data**: An optional data frame, list or environment from which variables specified in `formula` are preferentially to be taken.
- **x**: (required if no formula is given as the principal argument.) a matrix or data frame or Matrix containing the explanatory variables.
- **grouping**: (required if no formula principal argument is given.) a factor specifying the class for each observation.
- **prior**: the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If specified, the probabilities should be specified in the order of the factor levels.
- **subset**: An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
- **na.action**: A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is `na.omit`, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
- **method**: "moment" for standard estimators of the mean and variance, "mle" for MLEs, "mve" to use `cov.mve`, or "t" for robust estimates based on a t distribution.
- **CV**: If true, returns results (classes and posterior probabilities) for leave-out-out cross-validation. Note that if the prior is estimated, the proportions in the whole dataset are used.
- **nu**: degrees of freedom for `method = "t"`.
- **...**: arguments passed to or from other methods.

### Details

Uses a QR decomposition which will give an error message if the within-group variance is singular for any group.

### Value

An object of class "qda" containing the following components:

- **prior**: the prior probabilities used.
- **means**: the group means.
- **scaling**: for each group i, `scaling[,i]` is an array which transforms observations so that within-groups covariance matrix is spherical.
- **ldet**: a vector of half log determinants of the dispersion matrix.
- **lev**: the levels of the grouping factor.
- **terms**: (if formula is a formula) an object of mode expression and class term summarizing the formula.
call the (matched) function call.

unless CV=TRUE, when the return value is a list with components:

- **class**: The MAP classification (a factor)
- **posterior**: posterior probabilities for the classes

**References**


**See Also**

`predict.qda`, `lda`

**Examples**

```r
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
z <- qda(train, cl)
predict(z,test)$class
```

---

**Description**

The *quine* data frame has 146 rows and 5 columns. Children from Walgett, New South Wales, Australia, were classified by Culture, Age, Sex and Learner status and the number of days absent from school in a particular school year was recorded.

**Usage**

`quine`

**Format**

This data frame contains the following columns:

- **Eth**: ethnic background: Aboriginal or Not ("A" or "N").
- **Sex**: sex: factor with levels ("F" or "M").
- **Age**: age group: Primary ("F0"), or forms "F1", "F2" or "F3".
- **Lrn**: learner status: factor with levels Average or Slow learner, ("AL" or "SL").
- **Days**: days absent from school in the year.

**Source**

Rabbit

References


---

**Blood Pressure in Rabbits**

**Description**

Five rabbits were studied on two occasions, after treatment with saline (control) and after treatment with the $5-HT_3$ antagonist MDL 72222. After each treatment ascending doses of phenylbiguanide were injected intravenously at 10 minute intervals and the responses of mean blood pressure measured. The goal was to test whether the cardiogenic chemoreflex elicited by phenylbiguanide depends on the activation of $5-HT_3$ receptors.

**Usage**

Rabbit

**Format**

This data frame contains 60 rows and the following variables:

- `BPchange` change in blood pressure relative to the start of the experiment.
- `Dose` dose of Phenylbiguanide in micrograms.
- `Run` label of run ("C1" to "C5", then "M1" to "M5").
- `Treatment` placebo or the $5-HT_3$ antagonist MDL 72222.
- `Animal` label of animal used ("R1" to "R5").

**Source**


[The numerical data are not in the paper but were supplied by Professor Ludbrook]

**References**

rational

Rational Approximation

Description

Find rational approximations to the components of a real numeric object using a standard continued fraction method.

Usage

rational(x, cycles = 10, max.denominator = 2000, ...)

Arguments

x
Any object of mode numeric. Missing values are now allowed.
cycles
The maximum number of steps to be used in the continued fraction approximation process.
max.denominator
An early termination criterion. If any partial denominator exceeds max.denominator the continued fraction stops at that point.
...
arguments passed to or from other methods.

Details

Each component is first expanded in a continued fraction of the form

\[ x = \text{floor}(x) + \frac{1}{p_1 + \frac{1}{p_2 + \ldots}} \]

where \( p_1, p_2, \ldots \) are positive integers, terminating either at cycles terms or when a \( p_j > \) max.denominator. The continued fraction is then re-arranged to retrieve the numerator and denominator as integers and the ratio returned as the value.

Value

A numeric object with the same attributes as \( x \) but with entries rational approximations to the values. This effectively rounds relative to the size of the object and replaces very small entries by zero.

See Also

fractions

Examples

X <- matrix(runif(25), 5, 5)
zapsmall(solve(X, X/5)) # print near-zeroes as zero
rational(solve(X, X/5))
Description

*denumerate* converts a formula written using the conventions of *loglm* into one that *terms* is able to process. *renumerate* converts it back again to a form like the original.

Usage

renumerate(x)

Arguments

x

A formula, normally as modified by *denumerate*.

Details

This is an inverse function to *denumerate*. It is only needed since *terms* returns an expanded form of the original formula where the non-marginal terms are exposed. This expanded form is mapped back into a form corresponding to the one that the user originally supplied.

Value

A formula where all variables with names of the form .*vn*, where *n* is an integer, converted to numbers, *n*, as allowed by the formula conventions of *loglm*.

See Also

denumerate

Examples

denumerate(~(1+2+3)^3 + a/b)
## ~ (.v1 + .v2 + .v3)^3 + a/b
renumerate(.Last.value)
## ~ (1 + 2 + 3)^3 + a/b

---

*r1m*  
Robust Fitting of Linear Models

Description

Fit a linear model by robust regression using an M estimator.
Usage

rlm(x, ...)

## S3 method for class 'formula'
rlm(formula, data, weights, ..., subset, na.action,
    method = c("M", "MM", "model.frame"),
    wt.method = c("inv.var", "case"),
    model = TRUE, x.ret = TRUE, y.ret = FALSE, contrasts = NULL)

## Default S3 method:
rlm(x, y, weights, ..., w = rep(1, nrow(x)),
    init = "ls", psi = psi.huber,
    scale.est = c("MAD", "Huber", "proposal 2"), k2 = 1.345,
    method = c("M", "MM"), wt.method = c("inv.var", "case"),
    maxit = 20, acc = 1e-4, test.vec = "resid", lqs.control = NULL)

psi.huber(u, k = 1.345, deriv = 0)
psi.hampel(u, a = 2, b = 4, c = 8, deriv = 0)
psi.bisquare(u, c = 4.685, deriv = 0)

Arguments

formula a formula of the form y ~ x1 + x2 + ....
data an optional data frame, list or environment from which variables specified in
formula are preferentially to be taken.
weights a vector of prior weights for each case.
subset An index vector specifying the cases to be used in fitting.
na.action A function to specify the action to be taken if NAs are found. The ‘factory-fresh’
default action in R is na.omit, and can be changed by options(na.action=).
x a matrix or data frame containing the explanatory variables.
y the response: a vector of length the number of rows of x.
method currently either M-estimation or MM-estimation or (for the formula method
only) find the model frame. MM-estimation is M-estimation with Tukey’s bi-
weight initialized by a specific S-estimator. See the ‘Details’ section.
wt.method are the weights case weights (giving the relative importance of case, so a weight
of 2 means there are two of these) or the inverse of the variances, so a weight of
two means this error is half as variable?
model should the model frame be returned in the object?
x.ret should the model matrix be returned in the object?
y.ret should the response be returned in the object?
contrasts optional contrast specifications: see lm.
w (optional) initial down-weighting for each case.
init (optional) initial values for the coefficients OR a method to find initial values
OR the result of a fit with a coef component. Known methods are "ls" (the
default) for an initial least-squares fit using weights w*weights, and "lts"
for an unweighted least-trimmed squares fit with 200 samples.
psi the psi function is specified by this argument. It must give (possibly by name)
a function g(x, ..., deriv) that for deriv=0 returns psi(x)/x and for deriv=1
returns psi’(x). Tuning constants will be passed in via ....
scale.est method of scale estimation: re-scaled MAD of the residuals (default) or Huber’s proposal 2 (which can be selected by either "Huber" or "proposal 2").
k2 tuning constant used for Huber proposal 2 scale estimation.
maxit the limit on the number of IWLS iterations.
acc the accuracy for the stopping criterion.
test.vec the stopping criterion is based on changes in this vector.
... additional arguments to be passed to rlm.default or to the psi function.
lqs.control An optional list of control values for lqs.
u numeric vector of evaluation points.
k, a, b, c tuning constants.
deriv 0 or 1: compute values of the psi function or of its first derivative.

Details

Fitting is done by iterated re-weighted least squares (IWLS).
Psi functions are supplied for the Huber, Hampel and Tukey bisquare proposals as psi.huber, psi.hampel and psi.bisquare. Huber’s corresponds to a convex optimization problem and gives a unique solution (up to collinearity). The other two will have multiple local minima, and a good starting point is desirable.
Selecting method = "MM" selects a specific set of options which ensures that the estimator has a high breakdown point. The initial set of coefficients and the final scale are selected by an S-estimator with k0 = 1.548; this gives (for n >> p) breakdown point 0.5. The final estimator is an M-estimator with Tukey’s biweight and fixed scale that will inherit this breakdown point provided c > k0; this is true for the default value of c that corresponds to 95% relative efficiency at the normal. Case weights are not supported for method = "MM".

Value

An object of class "rlm" inheriting from "lm". Note that the df.residual component is deliberately set to NA to avoid inappropriate estimation of the residual scale from the residual mean square by "lm" methods.

The additional components not in an lm object are

s the robust scale estimate used
w the weights used in the IWLS process
psi the psi function with parameters substituted
conv the convergence criteria at each iteration
converged did the IWLS converge?
wresid a working residual, weighted for "inv.var" weights only.

Note

Prior to version 7.3-52, offset terms in formula were omitted from fitted and predicted values.
rms.curv

Relative Curvature Measures for Non-Linear Regression

Description

Calculates the root mean square parameter effects and intrinsic relative curvatures, $c^\theta$ and $c^\iota$, for a fitted nonlinear regression, as defined in Bates & Watts, section 7.3, p. 253ff

Usage

rms.curv(obj)

Arguments

obj Fitted model object of class "nls". The model must be fitted using the default algorithm.

Details

The method of section 7.3.1 of Bates & Watts is implemented. The function deriv3 should be used to generate a model function with first derivative (gradient) matrix and second derivative (Hessian) array attributes. This function should then be used to fit the nonlinear regression model.

A print method, print.rms.curv, prints the pc and ic components only, suitably annotated.

If either pc or ic exceeds some threshold (0.3 has been suggested) the curvature is unacceptably high for the planar assumption.

Value

A list of class rms.curv with components pc and ic for parameter effects and intrinsic relative curvatures multiplied by sqrt(F), ct and ci for $c^\theta$ and $c^\iota$ (unmultiplied), and C the C-array as used in section 7.3.1 of Bates & Watts.

References


See Also

lm, lqs.

Examples

summary(rlm(stack.loss ~ ., stackloss))
rlm(stack.loss ~ ., stackloss, psi = psi.hampel, init = "lts")
rlm(stack.loss ~ ., stackloss, psi = psi.bisquare)
References


See Also

deriv3

Examples

# The treated sample from the Puromycin data
mmcurve <- deriv3(~ Vm * conc/(K + conc), c("Vm", "K"),
                  function(Vm, K, conc) NULL)
Treated <- Puromycin[Puromycin$state == "treated", ]
(Purfit1 <- nls(rate ~ mmcurve(Vm, K, conc), data = Treated,
                 start = list(Vm=200, K=0.1)))
rms.curv(Purfit1)
##Parameter effects: c^theta x sqrt(F) = 0.2121
## Intrinsic: c^iota x sqrt(F) = 0.092

---

**rnegbin**

*Simulate Negative Binomial Variates*

**Description**

Function to generate random outcomes from a Negative Binomial distribution, with mean $\mu$ and variance $\mu + \mu^2/\theta$.

**Usage**

`rnegbin(n, mu = n, theta = stop("\theta must be specified"))`

**Arguments**

- `n` If a scalar, the number of sample values required. If a vector, `length(n)` is the number required and $n$ is used as the mean vector if $\mu$ is not specified.
- `mu` The vector of means. Short vectors are recycled.
- `theta` Vector of values of the $\theta$ parameter. Short vectors are recycled.

**Details**

The function uses the representation of the Negative Binomial distribution as a continuous mixture of Poisson distributions with Gamma distributed means. Unlike `rnbinom` the index can be arbitrary.

**Value**

Vector of random Negative Binomial variate values.

**Side Effects**

Changes `.Random.seed` in the usual way.
Examples

```r
# Negative Binomials with means fitted(fm) and theta = 4.5
fm <- glm.nb(Days ~ ., data = quine)
dummy <- rnegbin(fitted(fm), theta = 4.5)
```

---

**road**  
*Road Accident Deaths in US States*

**Description**

A data frame with the annual deaths in road accidents for half the US states.

**Usage**

`road`

**Format**

Columns are:

- `state` name.
- `deaths` number of deaths.
- `drivers` number of drivers (in 10,000s).
- `popden` population density in people per square mile.
- `rural` length of rural roads, in 1000s of miles.
- `temp` average daily maximum temperature in January.
- `fuel` fuel consumption in 10,000,000 US gallons per year.

**Source**

Imperial College, London M.Sc. exercise

---

**rotifer**  
*Numbers of Rotifers by Fluid Density*

**Description**

The data give the numbers of rotifers falling out of suspension for different fluid densities. There are two species, *Polyarthra major* and *Keratella cochlearis* and for each species the number falling out and the total number are given.

**Usage**

`rotifer`
**Rubber**

**Format**

- density specific density of fluid.
- pm.y number falling out for *P. major*.
- pm.total total number of *P. major*.
- kc.y number falling out for *K. cochlearis*.
- kc.tot total number of *K. cochlearis*.

**Source**


---

**Accelerated Testing of Tyre Rubber**

<table>
<thead>
<tr>
<th>Rubber</th>
<th>Accelerated Testing of Tyre Rubber</th>
</tr>
</thead>
</table>

**Description**

Data frame from accelerated testing of tyre rubber.

**Usage**

Rubber

**Format**

- loss the abrasion loss in gm/hr.
- hard the hardness in Shore units.
- tens tensile strength in kg/sq m.

**Source**


**References**

**Sammon's Non-Linear Mapping**

**Description**

One form of non-metric multidimensional scaling.

**Usage**

```r
sammon(d, y = cmdscale(d, k), k = 2, niter = 100, trace = TRUE,
       magic = 0.2, tol = 1e-4)
```

**Arguments**

- `d`: distance structure of the form returned by `dist`, or a full, symmetric matrix. Data are assumed to be dissimilarities or relative distances, but must be positive except for self-distance. This can contain missing values.
- `y`: An initial configuration. If none is supplied, `cmdscale` is used to provide the classical solution. (If there are missing values in `d`, an initial configuration must be provided.) This must not have duplicates.
- `k`: The dimension of the configuration.
- `niter`: The maximum number of iterations.
- `trace`: Logical for tracing optimization. Default `TRUE`.
- `magic`: Initial value of the step size constant in diagonal Newton method.
- `tol`: Tolerance for stopping, in units of stress.

**Details**

This chooses a two-dimensional configuration to minimize the stress, the sum of squared differences between the input distances and those of the configuration, weighted by the distances, the whole sum being divided by the sum of input distances to make the stress scale-free.

An iterative algorithm is used, which will usually converge in around 50 iterations. As this is necessarily an $O(n^2)$ calculation, it is slow for large datasets. Further, since the configuration is only determined up to rotations and reflections (by convention the centroid is at the origin), the result can vary considerably from machine to machine. In this release the algorithm has been modified by adding a step-length search (`magic`) to ensure that it always goes downhill.

**Value**

Two components:

- `points`: A two-column vector of the fitted configuration.
- `stress`: The final stress achieved.

**Side Effects**

If `trace` is true, the initial stress and the current stress are printed out every 10 iterations.
ships

References


See Also

cmdscale, isoMDS

Examples

```r
swiss.x <- as.matrix(swiss[, -1])
swiss.sam <- sammon(dist(swiss.x))
plot(swiss.sam$points, type = "n")
text(swiss.sam$points, labels = as.character(1:nrow(swiss.x)))
```

---

ships  

*Ships Damage Data*

Description

Data frame giving the number of damage incidents and aggregate months of service by ship type, year of construction, and period of operation.

Usage

ships

Format

<table>
<thead>
<tr>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>type</code></td>
<td>type: &quot;A&quot; to &quot;E&quot;.</td>
</tr>
<tr>
<td><code>year</code></td>
<td>year of construction: 1960–64, 65–69, 70–74, 75–79 (coded as &quot;60&quot;, &quot;65&quot;, &quot;70&quot;, &quot;75&quot;).</td>
</tr>
<tr>
<td><code>period</code></td>
<td>period of operation: 1960–74, 75–79.</td>
</tr>
<tr>
<td><code>service</code></td>
<td>aggregate months of service.</td>
</tr>
<tr>
<td><code>incidents</code></td>
<td>number of damage incidents.</td>
</tr>
</tbody>
</table>

Source

shoes

Description

A list of two vectors, giving the wear of shoes of materials A and B for one foot each of ten boys.

Usage

shoes

Source


References


shrimp

Description

A numeric vector with 18 determinations by different laboratories of the amount (percentage of the declared total weight) of shrimp in shrimp cocktail.

Usage

shrimp

Source


shuttle

Space Shuttle Autolander Problem

Description

The shuttle data frame has 256 rows and 7 columns. The first six columns are categorical variables giving example conditions; the seventh is the decision. The first 253 rows are the training set, the last 3 the test conditions.

Usage

shuttle

Format

This data frame contains the following factor columns:

- stability: stable positioning or not (stab/xstab).
- error: size of error (MM/SS/LX/XL).
- sign: sign of error, positive or negative (pp/nn).
- wind: wind sign (head/tail).
- magn: wind strength (Light/Medium/Strong/Out of Range).
- vis: visibility (yes/no).
- use: use the autolander or not (auto/noauto).

Source


References


Sitka

Growth Curves for Sitka Spruce Trees in 1988

Description

The Sitka data frame has 395 rows and 4 columns. It gives repeated measurements on the log-size of 79 Sitka spruce trees, 54 of which were grown in ozone-enriched chambers and 25 were controls. The size was measured five times in 1988, at roughly monthly intervals.

Usage

Sitka
This data frame contains the following columns:

- **size**: measured size (height times diameter squared) of tree, on log scale.
- **Time**: time of measurement in days since 1 January 1988.
- **tree**: number of tree.
- **treat**: either "ozone" for an ozone-enriched chamber or "control".

**Source**


**References**


**See Also**

Sitka89.
Description

The Skye data frame has 23 rows and 3 columns.

Usage

Skye

Format

This data frame contains the following columns:

A Percentage of sodium and potassium oxides.
F Percentage of iron oxide.
M Percentage of magnesium oxide.

Source


References


Examples

# ternary() is from the on-line answers.
ternary <- function(X, pch = par("pch"), lcex = 1,
    add = FALSE, ord = 1:3, ...)
{
  X <- as.matrix(X)
  if(any(X < 0)) stop("X must be non-negative")
  s <- drop(X %*% rep(1, ncol(X)))
  if(any(s<=0)) stop("each row of X must have a positive sum")
  if(max(abs(s-1)) > 1e-6) {
    warning("row(s) of X will be rescaled")
    X <- X / s
  }
  X <- X[, ord]
  s3 <- sqrt(1/3)
  if(!add)
    {
      oldpty <- par("pty")
      on.exit(par(pty=oldpty))
      par(pty="s")
      plot(c(-s3, s3), c(0.5-s3, 0.5+s3), type="n", axes=FALSE,
           xlab="", ylab="")
      polygon(c(0, -s3, s3), c(1, 0, 0), density=0)
Groups of 20 snails were held for periods of 1, 2, 3 or 4 weeks in carefully controlled conditions of temperature and relative humidity. There were two species of snail, A and B, and the experiment was designed as a 4 by 3 by 4 by 2 completely randomized design. At the end of the exposure time the snails were tested to see if they had survived; the process itself is fatal for the animals. The object of the exercise was to model the probability of survival in terms of the stimulus variables, and in particular to test for differences between species.

The data are unusual in that in most cases fatalities during the experiment were fairly small.

The data frame contains the following components:

- **Species**: snail species A (1) or B (2).
- **Exposure**: exposure in weeks.
- **Rel.Hum**: relative humidity (4 levels).
- **Temp**: temperature, in degrees Celsius (3 levels).
- **Deaths**: number of deaths.
- **N**: number of snails exposed.

**Description**

**Usage**

```
> snails
```

**Format**

```
snails  Snail Mortality Data

Description

Groups of 20 snails were held for periods of 1, 2, 3 or 4 weeks in carefully controlled conditions of temperature and relative humidity. There were two species of snail, A and B, and the experiment was designed as a 4 by 3 by 4 by 2 completely randomized design. At the end of the exposure time the snails were tested to see if they had survived; the process itself is fatal for the animals. The object of the exercise was to model the probability of survival in terms of the stimulus variables, and in particular to test for differences between species.

The data are unusual in that in most cases fatalities during the experiment were fairly small.

**Usage**

```
> snails
```

**Format**

The data frame contains the following components:

- **Species**: snail species A (1) or B (2).
- **Exposure**: exposure in weeks.
- **Rel.Hum**: relative humidity (4 levels).
- **Temp**: temperature, in degrees Celsius (3 levels).
- **Deaths**: number of deaths.
- **N**: number of snails exposed.

**Source**

Zoology Department, The University of Adelaide.

**References**

Description

Returns of the Standard and Poors 500 Index in the 1990’s

Usage

SP500

Format


References


stdres

Extract Standardized Residuals from a Linear Model

Description

The standardized residuals. These are normalized to unit variance, fitted including the current data point.

Usage

stdres(object)

Arguments

object any object representing a linear model.

Value

The vector of appropriately transformed residuals.

References


See Also

residuals, studres
steampressure

The Saturated Steam Pressure Data

Description

Temperature and pressure in a saturated steam driven experimental device.

Usage

steampressure

Format

The data frame contains the following components:

- **Temp** : temperature, in degrees Celsius.
- **Press** : pressure, in Pascals.

Source


References


stepAIC

Choose a model by AIC in a Stepwise Algorithm

Description

Performs stepwise model selection by AIC.

Usage

```
stepAIC(object, scope, scale = 0,
        direction = c("both", "backward", "forward"),
        trace = 1, keep = NULL, steps = 1000, use.start = FALSE,
        k = 2, ...)  
```

Arguments

- **object** : an object representing a model of an appropriate class. This is used as the initial model in the stepwise search.
- **scope** : defines the range of models examined in the stepwise search. This should be either a single formula, or a list containing components `upper` and `lower`, both formulae. See the details for how to specify the formulae and how they are used.
- **scale** : used in the definition of the AIC statistic for selecting the models, currently only for `lm` and `aov` models (see `extractAIC` for details).
direction: the mode of stepwise search, can be one of "both", "backward", or "forward", with a default of "both". If the scope argument is missing the default for direction is "backward".

trace: if positive, information is printed during the running of stepAIC. Larger values may give more information on the fitting process.

keep: a filter function whose input is a fitted model object and the associated AIC statistic, and whose output is arbitrary. Typically keep will select a subset of the components of the object and return them. The default is not to keep anything.

steps: the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early.

use.start: if true the updated fits are done starting at the linear predictor for the currently selected model. This may speed up the iterative calculations for glm (and other fits), but it can also slow them down. Not used in R.

k: the multiple of the number of degrees of freedom used for the penalty. Only $k = 2$ gives the genuine AIC: $k = \log(n)$ is sometimes referred to as BIC or SBC.

... any additional arguments to extractAIC. (None are currently used.)

Details

The set of models searched is determined by the scope argument. The right-hand-side of its lower component is always included in the model, and right-hand-side of the model is included in the upper component. If scope is a single formula, it specifies the upper component, and the lower model is empty. If scope is missing, the initial model is used as the upper model.

Models specified by scope can be templates to update object as used by update.formula.

There is a potential problem in using glm fits with a variable scale, as in that case the deviance is not simply related to the maximized log-likelihood. The glm method for extractAIC makes the appropriate adjustment for a gaussian family, but may need to be amended for other cases. (The binomial and poisson families have fixed scale by default and do not correspond to a particular maximum-likelihood problem for variable scale.)

Where a conventional deviance exists (e.g. for lm, aov and glm fits) this is quoted in the analysis of variance table: it is the unscaled deviance.

Value

the stepwise-selected model is returned, with up to two additional components. There is an "anova" component corresponding to the steps taken in the search, as well as a "keep" component if the keep= argument was supplied in the call. The "Resid. Dev" column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood: it will be a deviance only in cases where a saturated model is well-defined (thus excluding lm, aov and survreg fits, for example).

Note

The model fitting must apply the models to the same dataset. This may be a problem if there are missing values and an na.action other than na.fail is used (as is the default in R). We suggest you remove the missing values first.

References

The Stormer Viscometer Data

Description

The stormer viscometer measures the viscosity of a fluid by measuring the time taken for an inner cylinder in the mechanism to perform a fixed number of revolutions in response to an actuating weight. The viscometer is calibrated by measuring the time taken with varying weights while the mechanism is suspended in fluids of accurately known viscosity. The data comes from such a calibration, and theoretical considerations suggest a nonlinear relationship between time, weight and viscosity, of the form \( \text{Time} = \frac{B_1 \times \text{Viscosity}}{\text{Weight} - B_2} + E \) where \( B_1 \) and \( B_2 \) are unknown parameters to be estimated, and \( E \) is error.

Usage

stormer
Format

The data frame contains the following components:

- **Viscosity**: viscosity of fluid.
- **Wt**: actuating weight.
- **Time**: time taken.

Source


References


studres

*Extract Studentized Residuals from a Linear Model*

Description

The Studentized residuals. Like standardized residuals, these are normalized to unit variance, but the Studentized version is fitted ignoring the current data point. (They are sometimes called jackknifed residuals).

Usage

```r
studres(object)
```

Arguments

- **object**: any object representing a linear model.

Value

The vector of appropriately transformed residuals.

References


See Also

- `residuals`, `stdres`
Summary Method Function for Objects of Class 'loglm'

Description

Returns a summary list for log-linear models fitted by iterative proportional scaling using loglm.

Usage

## S3 method for class 'loglm'
summary(object, fitted = FALSE, ...)

Arguments

object a fitted loglm model object.
fitted if TRUE return observed and expected frequencies in the result. Using fitted = TRUE may necessitate re-fitting the object.
...
arguments to be passed to or from other methods.

Details

This function is a method for the generic function summary() for class "loglm". It can be invoked by calling summary(x) for an object x of the appropriate class, or directly by calling summary.loglm(x) regardless of the class of the object.

Value

a list is returned for use by print.summary.loglm. This has components

formula the formula used to produce object
tests the table of test statistics (likelihood ratio, Pearson) for the fit.
oe if fitted = TRUE, an array of the observed and expected frequencies, otherwise NULL.

References


See Also

loglm, summary
Summary Method Function for Objects of Class 'negbin'

Description

Identical to summary.glm, but with three lines of additional output: the ML estimate of theta, its standard error, and twice the log-likelihood function.

Usage

## S3 method for class 'negbin'
summary(object, dispersion = 1, correlation = FALSE, ...)

Arguments

object fitted model object of class negbin inheriting from glm and lm. Typically the output of glm.nb.
dispersion as for summary.glm, with a default of 1.
correlation as for summary.glm.
... arguments passed to or from other methods.

Details

summary.glm is used to produce the majority of the output and supply the result. This function is a method for the generic function summary() for class "negbin". It can be invoked by calling summary(x) for an object x of the appropriate class, or directly by calling summary.negbin(x) regardless of the class of the object.

Value

As for summary.glm; the additional lines of output are not included in the resultant object.

Side Effects

A summary table is produced as for summary.glm, with the additional information described above.

References


See Also

summary.glm.nb, negative.binomial, anova.negbin

Examples

## IGNORE_RDIFF_BEGIN
summary(glm.nb(Days ~ Eth*Age*Lrn*Sex, quine, link = log))
## IGNORE_RDIFF_END
Summary Method for Robust Linear Models

Description

summary method for objects of class "rlm"

Usage

## S3 method for class 'rlm'
summary(object, method = c("XtX", "XtWX"), correlation = FALSE, ...)

Arguments

object the fitted model. This is assumed to be the result of some fit that produces an
object inheriting from the class rlm, in the sense that the components returned
by the rlm function will be available.

method Should the weighted (by the IWLS weights) or unweighted cross-products ma-
trix be used?

correlation logical. Should correlations be computed (and printed)?

... arguments passed to or from other methods.

Details

This function is a method for the generic function summary() for class "rlm". It can be invoked by
calling summary(x) for an object x of the appropriate class, or directly by calling summary.rlm(x)
regardless of the class of the object.

Value

If printing takes place, only a null value is returned. Otherwise, a list is returned with the following
components. Printing always takes place if this function is invoked automatically as a method for
the summary function.

correlation The computed correlation coefficient matrix for the coefficients in the model.

cov.unscaled The unscaled covariance matrix; i.e, a matrix such that multiplying it by an
estimate of the error variance produces an estimated covariance matrix for the
coefficients.

sigma The scale estimate.

stddev A scale estimate used for the standard errors.

df The number of degrees of freedom for the model and for residuals.

coefficients A matrix with three columns, containing the coefficients, their standard errors
and the corresponding t statistic.

terms The terms object used in fitting this model.

References

survey

See Also
summary

Examples

summary(rlm(calls ~ year, data = phones, maxit = 50))

---

survey  Student Survey Data

Description

This data frame contains the responses of 237 Statistics I students at the University of Adelaide to a number of questions.

Usage

survey

Format

The components of the data frame are:

- **Sex**  The sex of the student. (Factor with levels "Male" and "Female".)
- **Wr.Hnd**  span (distance from tip of thumb to tip of little finger of spread hand) of writing hand, in centimetres.
- **NW.Hnd**  span of non-writing hand.
- **W.Hnd**  writing hand of student. (Factor, with levels "Left" and "Right".)
- **Fold**  "Fold your arms! Which is on top" (Factor, with levels "R on L", "L on R", "Neither").
- **Pulse**  pulse rate of student (beats per minute).
- **Clap**  'Clap your hands! Which hand is on top?' (Factor, with levels "Right", "Left", "Neither").
- **Exer**  how often the student exercises. (Factor, with levels "Freq" (frequently), "Some", "None").
- **Smoke**  how much the student smokes. (Factor, levels "Heavy", "Regul" (regularly), "Occas" (occasionally), "Never").
- **Height**  height of the student in centimetres.
- **M.I**  whether the student expressed height in imperial (feet/inches) or metric (centimetres/metres) units. (Factor, levels "Metric", "Imperial").
- **Age**  age of the student in years.

References

**Description**

The synth.tr data frame has 250 rows and 3 columns. The synth.te data frame has 100 rows and 3 columns. It is intended that synth.tr be used from training and synth.te for testing.

**Usage**

```r
synth.tr
synth.te
```

**Format**

These data frames contain the following columns:

- **xs**: x-coordinate
- **ys**: y-coordinate
- **yc**: class, coded as 0 or 1.

**Source**


---

**theta.md**

**Estimate theta of the Negative Binomial**

**Description**

Given the estimated mean vector, estimate theta of the Negative Binomial Distribution.

**Usage**

```r
theta.md(y, mu, dfr, weights, limit = 20, eps = .Machine$double.eps^0.25)
theta.ml(y, mu, n, weights, limit = 10, eps = .Machine$double.eps^0.25, trace = FALSE)
theta.mm(y, mu, dfr, weights, limit = 10, eps = .Machine$double.eps^0.25)
```
Arguments

- \( y \): Vector of observed values from the Negative Binomial.
- \( \mu \): Estimated mean vector.
- \( n \): Number of data points (defaults to the sum of weights).
- \( \text{dfr} \): Residual degrees of freedom (assuming \( \theta \) known). For a weighted fit this is the sum of the weights minus the number of fitted parameters.
- \( \text{weights} \): Case weights. If missing, taken as 1.
- \( \text{limit} \): Limit on the number of iterations.
- \( \text{eps} \): Tolerance to determine convergence.
- \( \text{trace} \): Logical: should iteration progress be printed?

Details

\text{theta.md} estimates by equating the deviance to the residual degrees of freedom, an analogue of a moment estimator.

\text{theta.ml} uses maximum likelihood.

\text{theta.mm} calculates the moment estimator of \( \theta \) by equating the Pearson chi-square \( \sum (y - \mu)^2 / (\mu + \mu^2 / \theta) \) to the residual degrees of freedom.

Value

The required estimate of \( \theta \), as a scalar. For \text{theta.ml}, the standard error is given as attribute "SE".

See Also

\text{glm.nb}

Examples

```r
quine.nb <- glm.nb(Days ~ .^2, data = quine)
theta.md(quine$Days, fitted(quine.nb), dfr = df.residual(quine.nb))
theta.ml(quine$Days, fitted(quine.nb))
theta.mm(quine$Days, fitted(quine.nb), dfr = df.residual(quine.nb))

## weighted example
yeast <- data.frame(cbind(numbers = 0:5, fr = c(213, 128, 37, 18, 3, 1)))
fit <- glm.nb(numbers ~ 1, weights = fr, data = yeast)
## IGNORE_RDIFF_BEGIN
summary(fit)
## IGNORE_RDIFF_END
mu <- fitted(fit)
theta.md(yeast$numbers, mu, dfr = 399, weights = yeast$fr)
theta.ml(yeast$numbers, mu, limit = 15, weights = yeast$fr)
theta.mm(yeast$numbers, mu, dfr = 399, weights = yeast$fr)
```
**topo**  
*Spatial Topographic Data*

**Description**

The topo data frame has 52 rows and 3 columns, of topographic heights within a 310 feet square.

**Usage**

topo

**Format**

This data frame contains the following columns:

- **x** x coordinates (units of 50 feet)
- **y** y coordinates (units of 50 feet)
- **z** heights (feet)

**Source**

Davis, J.C. (1973) *Statistics and Data Analysis in Geology*. Wiley.

**References**


**Traffic**  
*Effect of Swedish Speed Limits on Accidents*

**Description**

An experiment was performed in Sweden in 1961–2 to assess the effect of a speed limit on the motorway accident rate. The experiment was conducted on 92 days in each year, matched so that day $j$ in 1962 was comparable to day $j$ in 1961. On some days the speed limit was in effect and enforced, while on other days there was no speed limit and cars tended to be driven faster. The speed limit days tended to be in contiguous blocks.

**Usage**

Traffic

**Format**

This data frame contains the following columns:

- **year** 1961 or 1962.
- **day** of year.
- **limit** was there a speed limit?
- **y** traffic accident count for that day.
truehist

Source


References


truehist

Plot a Histogram

Description

Creates a histogram on the current graphics device.

Usage

truehist(data, nbins = "Scott", h, x0 = -h/1000, breaks, prob = TRUE, xlim = range(breaks), ymax = max(est), col = "cyan", xlab = deparse(substitute(data)), bty = "n", ...)

Arguments

data numeric vector of data for histogram. Missing values (NAs) are allowed and omitted.
nbins The suggested number of bins. Either a positive integer, or a character string naming a rule: "Scott" or "Freedman–Diaconis" or "FD". (Case is ignored.)
h The bin width, a strictly positive number (takes precedence over nbins).
x0 Shift for the bins - the breaks are at x0 + h x (..., -1, 0, 1, ...)
breaks The set of breakpoints to be used. (Usually omitted, takes precedence over h and nbins).
prob If true (the default) plot a true histogram. The vertical axis has a relative frequency density scale, so the product of the dimensions of any panel gives the relative frequency. Hence the total area under the histogram is 1 and it is directly comparable with most other estimates of the probability density function. If false plot the counts in the bins.
xlim The limits for the x-axis.
ymax The upper limit for the y-axis.
col The colour for the bar fill: the default is colour 5 in the default R palette.
xlab label for the plot x-axis. By default, this will be the name of data.
bty The box type for the plot - defaults to none.
... additional arguments to rect or plot.
Details

This plots a true histogram, a density estimate of total area 1. If breaks is specified, those break-points are used. Otherwise if h is specified, a regular grid of bins is used with width h. If neither breaks nor h is specified, nbins is used to select a suitable h.

Side Effects

A histogram is plotted on the current device.

References


See Also

hist

---

ucv

*Unbiased Cross-Validation for Bandwidth Selection*

Description

Uses unbiased cross-validation to select the bandwidth of a Gaussian kernel density estimator.

Usage

```r
ucv(x, nb = 1000, lower, upper)
```

Arguments

- `x` a numeric vector
- `nb` number of bins to use.
- `lower, upper` Range over which to minimize. The default is almost always satisfactory.

Value

a bandwidth.

References


See Also

bcv, width.SJ, density

Examples

```r
ucv(geyser$duration)
```
UScereal

Nutritional and Marketing Information on US Cereals

Description

The UScereal data frame has 65 rows and 11 columns. The data come from the 1993 ASA Statistical Graphics Exposition, and are taken from the mandatory F&DA food label. The data have been normalized here to a portion of one American cup.

Usage

UScereal

Format

This data frame contains the following columns:

mfr  Manufacturer, represented by its first initial:  G=General Mills, K=Kelloggs, N=Nabisco, P=Post, Q=Quaker Oats, R=Ralston Purina.
calories  number of calories in one portion.
protein  grams of protein in one portion.
fat  grams of fat in one portion.
sodium  milligrams of sodium in one portion.
fibre  grams of dietary fibre in one portion.
carbo  grams of complex carbohydrates in one portion.
sugars  grams of sugars in one portion.
shelf  display shelf (1, 2, or 3, counting from the floor).
potassium  grams of potassium.
vitamins  vitamins and minerals (none, enriched, or 100%).

Source

The original data are available at http://lib.stat.cmu.edu/datasets/1993.expo/.

References

UScrime

The Effect of Punishment Regimes on Crime Rates

Description

Criminologists are interested in the effect of punishment regimes on crime rates. This has been studied using aggregate data on 47 states of the USA for 1960 given in this data frame. The variables seem to have been re-scaled to convenient numbers.

Usage

UScrime

Format

This data frame contains the following columns:

- So: indicator variable for a Southern state.
- Ed: mean years of schooling.
- Po1: police expenditure in 1960.
- Po2: police expenditure in 1959.
- LF: labour force participation rate.
- M.F: number of males per 1000 females.
- Pop: state population.
- NW: number of non-whites per 1000 people.
- U1: unemployment rate of urban males 14–24.
- U2: unemployment rate of urban males 35–39.
- GDP: gross domestic product per head.
- Ineq: income inequality.
- Prob: probability of imprisonment.
- Time: average time served in state prisons.
- y: rate of crimes in a particular category per head of population.

Source


References

**Veteran's Administration Lung Cancer Trial**

**Description**

Veteran’s Administration lung cancer trial from Kalbfleisch & Prentice.

**Usage**

VA

**Format**

A data frame with columns:

- **stime**: survival or follow-up time in days.
- **status**: dead or censored.
- **treat**: treatment: standard or test.
- **age**: patient’s age in years.
- **Karn**: Karnofsky score of patient’s performance on a scale of 0 to 100.
- **diag.time**: times since diagnosis in months at entry to trial.
- **cell**: one of four cell types.
- **prior**: prior therapy?

**Source**


**References**


---

**Waders**

**Counts of Waders at 15 Sites in South Africa**

**Description**

The waders data frame has 15 rows and 19 columns. The entries are counts of waders in summer.

**Usage**

waders
## Format

This data frame contains the following columns (species):

- S1 Oystercatcher
- S2 White-fronted Plover
- S3 Kitt Lutz’s Plover
- S4 Three-banded Plover
- S5 Grey Plover
- S6 Ringed Plover
- S7 Bar-tailed Godwit
- S8 Whimbrel
- S9 Marsh Sandpiper
- S10 Greenshank
- S11 Common Sandpiper
- S12 Turnstone
- S13 Knot
- S14 Sanderling
- S15 Little Stint
- S16 Curlew Sandpiper
- S17 Ruff
- S18 Avocet
- S19 Black-winged Stilt

The rows are the sites:
- A = Namibia North coast
- B = Namibia North wetland
- C = Namibia South coast
- D = Namibia South wetland
- E = Cape North coast
- F = Cape North wetland
- G = Cape West coast
- H = Cape West wetland
- I = Cape South coast
- J = Cape South wetland
- K = Cape East coast
- L = Cape East wetland
- M = Transkei coast
- N = Natal coast
- O = Natal wetland

## Source

J.C. Gower and D.J. Hand (1996) *Biplots* Chapman & Hall Table 9.1. Quoted as from:


## Examples

```r
plot(corresp(waders, nf=2))
```
Example usage of the Whiteside dataset:

```r
require(lattice)
xyplot(Gas ~ Temp | Insul, whiteside, panel =
  function(x, y, ...) {
    panel.xyplot(x, y, ...)
    panel.lmline(x, y, ...)
  }, xlab = "Average external temperature (deg. C)",
ylab = "Gas consumption (1000 cubic feet)", aspect = "xy",
strip = function(...) strip.default(..., style = 1))

gasB <- lm(Gas ~ Temp, whiteside, subset = Insul=="Before")
gasA <- update(gasB, subset = Insul=="After")
summary(gasB)
summary(gasA)
gasBA <- lm(Gas ~ Insul/Temp - 1, whiteside)
summary(gasBA)
```
gasQ <- lm(Gas ~ Insul/(Temp + I(Temp^2)) - 1, whiteside)
coef(summary(gasQ))

gaspR <- lm(Gas ~ Insul + Temp, whiteside)
anova(gaspR, gasBA)
options(contrasts = c("contr.treatment", "contr.poly"))
gasBA1 <- lm(Gas ~ Insul*Temp, whiteside)
coef(summary(gasBA1))

width.SJ

Bandwidth Selection by Pilot Estimation of Derivatives

Description

Uses the method of Sheather & Jones (1991) to select the bandwidth of a Gaussian kernel density estimator.

Usage

width.SJ(x, nb = 1000, lower, upper, method = c("ste", "dpi"))

Arguments

x
a numeric vector

nb
number of bins to use.

upper, lower
range over which to search for solution if method = "ste".

method
Either "ste" ("solve-the-equation") or "dpi" ("direct plug-in").

Value

a bandwidth.

Note

A faster version for large n (thousands) is available in R ≥ 3.4.0 as part of bw.SJ: quadruple its value for comparability with this version.

References


See Also

ucv, bcv, density
write.matrix

Examples

width.SJ(geyser$duration, method = "dpi")
width.SJ(geyser$duration)

width.SJ(galaxies, method = "dpi")
width.SJ(galaxies)

write.matrix write a Matrix or Data Frame

Description

Writes a matrix or data frame to a file or the console, using column labels and a layout respecting columns.

Usage

write.matrix(x, file = "", sep = " ", blocksize)

Arguments

x matrix or data frame.
file name of output file. The default ("") is the console.
sep The separator between columns.
blocksize If supplied and positive, the output is written in blocks of blocksize rows. Choose as large as possible consistent with the amount of memory available.

Details

If x is a matrix, supplying blocksize is more memory-efficient and enables larger matrices to be written, but each block of rows might be formatted slightly differently.

If x is a data frame, the conversion to a matrix may negate the memory saving.

Side Effects

A formatted file is produced, with column headings (if x has them) and columns of data.

References


See Also

write.table
wtloss

Weight Loss Data from an Obese Patient

Description
The data frame gives the weight, in kilograms, of an obese patient at 52 time points over an 8 month period of a weight rehabilitation programme.

Usage
wtloss

Format
This data frame contains the following columns:

Days  time in days since the start of the programme.
Weight  weight in kilograms of the patient.

Source
Dr T. Davies, Adelaide.

References

Examples
```r
## IGNORE_RDIFF_BEGIN
wtloss.fm <- nls(Weight ~ b0 + b1*2^(-Days/th),
                 data = wtloss, start = list(b0=90, b1=95, th=120))
wtloss.fm
## IGNORE_RDIFF_END
plot(wtloss)
with(wtloss, lines(Days, fitted(wtloss.fm)))
```
Chapter 17

The Matrix package

abIndex-class  Class "abIndex" of Abstract Index Vectors

Description

The "abIndex" class, short for "Abstract Index Vector", is used for dealing with large index vectors more efficiently, than using integer (or numeric) vectors of the kind `2:1000000` or `c(0:1e5, 1000:1e6).

Note that the current implementation details are subject to change, and if you consider working with these classes, please contact the package maintainers (packageDescription("Matrix")$Maintainer).

Objects from the Class

Objects can be created by calls of the form `new("abIndex", ...)`, but more easily and typically either by `as(x, "abIndex")` where `x` is an integer (valued) vector, or directly by `abIseq()` and combination `c(...)` of such.

Slots

kind: a character string, one of ("int32", "double", "rleDiff"), denoting the internal structure of the abIndex object.
x: Object of class "numLike"; is used (i.e., not of length 0) only iff the object is not compressed, i.e., currently exactly when kind != "rleDiff".
rleD: object of class "rleDiff", used for compression via rle.

Methods

as.numeric, as.integer, as.vector  signature(x = "abIndex"): ...
[  signature(x = "abIndex", i = "index", j = "ANY", drop = "ANY"): ...
coerce  signature(from = "numeric", to = "abIndex"): ...
coerce  signature(from = "abIndex", to = "numeric"): ...
coerce  signature(from = "abIndex", to = "integer"): ...
length  signature(x = "abIndex"): ...
abIseq

Sequence Generation of "abIndex", Abstract Index Vectors

Description

Generation of abstract index vectors, i.e., objects of class "abIndex".

abIseq() is designed to work entirely like seq, but producing "abIndex" vectors.
abIseq1() is its basic building block, where abIseq1(n,m) corresponds to n:m.
c(x, ...) will return an "abIndex" vector, when x is one.

Usage

abIseq1(from = 1, to = 1)
abIseq(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
length.out = NULL, along.with = NULL)

## S3 method for class 'abIndex'
c(...)
all.equal-methods

Arguments

- **from, to**: the starting and (maximal) end value of the sequence.
- **by**: number: increment of the sequence.
- **length.out**: desired length of the sequence. A non-negative number, which for seq and seq.int will be rounded up if fractional.
- **along.with**: take the length from the length of this argument.
- **...**: in general an arbitrary number of R objects; here, when the first is an "abIndex" vector, these arguments will be concatenated to a new "abIndex" object.

Value

An abstract index vector, i.e., object of class "abIndex".

See Also

the class abIndex documentation; rep2abI() for another constructor; rle (base).

Examples

```r
target = "Matrix", current = "Matrix" \
target = "ANY", current = "Matrix" \
target = "Matrix", current = "ANY" these three methods are simply using all.equal.numeric directly and work via as.vector().
```

Description

Methods for function all.equal() (from R package base) are defined for all Matrix classes.

```r
Methods

target = "Matrix", current = "Matrix" \
target = "ANY", current = "Matrix" \
target = "Matrix", current = "ANY" these three methods are simply using all.equal.numeric directly and work via as.vector().
```

There are more methods, notably also for "sparseVector"'s, see showMethods("all.equal").
Examples

```r
deft <- as.matrix(c(1:3, 2:1), x = 1:5)
```

```r
stopifnot(all.equal(ex, all.equal(with(ex, all.equal(as(P %*% A %*% t(Q), "CsparseMatrix"),
                 L %*% U)),
           with(ex, all.equal(as(A, "CsparseMatrix"),
                 t(P) %*% L %*% U %*% Q))))
```

---

**asUniqueT**  

*Standardize a Sparse Matrix in Triplet Format*

**Description**

Detect or standardize a `TsparseMatrix` with unsorted or duplicated `(i, j)` pairs.

**Usage**

```r
anyDuplicatedT(x, ...)
```

```r
isUniqueT(x, byrow = FALSE, isT = is(x, "TsparseMatrix"))
asUniqueT(x, byrow = FALSE, isT = is(x, "TsparseMatrix"))
```

**Arguments**

- **x**: an R object. `anyDuplicatedT` and `aggregateT` require `x` inheriting from `TsparseMatrix`. `asUniqueT` requires `x` inheriting from `Matrix` and coerces `x` to `TsparseMatrix` if necessary.
- **...**: optional arguments passed to the default method for generic function `anyDuplicated`.
- **byrow**: a logical indicating if `x` should be sorted by row then by column.
- **isT**: a logical indicating if `x` inherits from virtual class `TsparseMatrix`.

**Value**

- `anyDuplicatedT(x)` returns the index of the first duplicated `(i, j)` pair in `x` (0 if there are no duplicated pairs).
- `isUniqueT(x)` returns `TRUE` if `x` is a `TsparseMatrix` with sorted, nonduplicated `(i, j)` pairs and `FALSE` otherwise.
- `asUniqueT(x)` returns the unique `TsparseMatrix` representation of `x` with sorted, nonduplicated `(i, j)` pairs. Values corresponding to identical `(i, j)` pairs are aggregated by addition, where in the logical case “addition” refers to logical OR.
- `aggregateT(x)` aggregates without sorting.

**See Also**

Virtual class `TsparseMatrix`. 
Examples

```r
example("dgTMatrix-class", echo=FALSE)
## -> 'T2' with (i,j,x) slots of length 5 each
T2u <- asUniqueT(T2)
stopifnot(# They "are" the same (and print the same):
  all.equal(T2, T2u, tol=0),
  # but not internally:
  anyDuplicatedT(T2) == 2,
  anyDuplicatedT(T2u) == 0,
  length(T2 @x) == 5,
  length(T2u@x) == 3)
isUniqueT(T2) # FALSE
isUniqueT(T2u) # TRUE

T3 <- T2u
T3[1, c(1,3)] <- 10; T3[2, c(1,5)] <- 20
T3u <- asUniqueT(T3)
str(T3u) # sorted in 'j', and within j, sorted in i
stopifnot(isUniqueT(T3u))

## Logical l.TMatrix and n.TMatrix :
(L2 <- T2 > 0)
validObject(L2u <- asUniqueT(L2))
(N2 <- as(L2, "nMatrix"))
validObject(N2u <- asUniqueT(N2))
stopifnot(N2u@i == L2u@i, L2u@i == T2u@i, N2@i == L2@i, L2@i == T2@i,
  N2u@j == L2u@j, L2u@j == T2u@j, N2@j == L2@j, L2@j == T2@j)
# now with a nasty NA [partly failed in Matrix 1.1-5]:
L.0N <- L.1N <- L2
L.0N@x[1:2] <- c(FALSE, NA)
L.1N@x[1:2] <- c(TRUE, NA)
validObject(L.0N)
validObject(L.1N)
(m.0N <- as.matrix(L.0N))
(m.1N <- as.matrix(L.1N))
stopifnot(identical(10L, which(is.na(m.0N))), !anyNA(m.1N))
symnum(m.0N)
symnum(m.1N)
```

atomicVector-class

Virtual Class "atomicVector" of Atomic Vectors

Description

The class "atomicVector" is a virtual class containing all atomic vector classes of base R, as also implicitly defined via is.atomic.

Objects from the Class

A virtual Class: No objects may be created from it.
Methods

In the Matrix package, the "atomicVector" is used in signatures where typically "old-style" "matrix" objects can be used and can be substituted by simple vectors.

Extends

The atomic classes "logical", "integer", "double", "numeric", "complex", "raw" and "character" are extended directly. Note that "numeric" already contains "integer" and "double", but we want all of them to be direct subclasses of "atomicVector".

Author(s)

Martin Maechler

See Also

is.atomic, integer, numeric, complex, etc.

Examples

showClass("atomicVector")

band-methods

Extract bands of a matrix

Description

Return the matrix obtained by setting to zero elements below a diagonal (triu), above a diagonal (tril), or outside of a general band (band).

Usage

band(x, k1, k2, ...)
triu(x, k = 0L, ...)
tril(x, k = 0L, ...)

Arguments

x a matrix-like object
k,k1,k2 integers specifying the diagonals that are not set to zero. These are interpreted relative to the main diagonal, which is k=0. Positive and negative values of k indicate diagonals above and below the main diagonal, respectively.

... optional arguments passed methods (currently unused by package Matrix)

Details

triu(x, k) is equivalent to band(x, k, dim(x)[2]). Similarly, tril(x, k) is equivalent to band(x, -dim(x)[1], k).
Value

An object of a suitable matrix class, inheriting from `triangularMatrix` where appropriate. It inherits from `sparseMatrix` if and only if `x` does.

Methods

- `x = "CsparseMatrix"` method for compressed, sparse, column-oriented matrices.
- `x = "RsparseMatrix"` method for compressed, sparse, row-oriented matrices.
- `x = "TsparseMatrix"` method for sparse matrices in triplet format.
- `x = "diagonalMatrix"` method for diagonal matrices.
- `x = "denseMatrix"` method for dense matrices in packed or unpacked format.
- `x = "matrix"` method for traditional matrices of implicit class `matrix`.

See Also

`bandSparse` for the construction of a banded sparse matrix directly from its non-zero diagonals.

Examples

```r
## A random sparse matrix:
set.seed(7)
m <- matrix(0, 5, 5)
m[sample(length(m), size = 14)] <- rep(1:9, length=14)
(mm <- as(m, "CsparseMatrix"))

tril(mm)       # lower triangle
tril(mm, -1)   # strict lower triangle
triu(mm, 1)    # strict upper triangle
band(mm, -1, 2) # general band

(m5 <- Matrix(rnorm(25), ncol = 5))

tril(m5)       # lower triangle
tril(m5, -1)   # strict lower triangle
triu(m5, 1)    # strict upper triangle
band(m5, -1, 2) # general band

(m65 <- Matrix(rnorm(30), ncol = 5)) # not square
triu(m65)      # result not "dtrMatrix" unless square
(sm5 <- crossprod(m65)) # symmetric

band(sm5, -1, 1) # "dsyMatrix": symmetric band preserves symmetry property
as(band(sm5, -1, 1), "sparseMatrix") # often preferable
(sm <- round(crossprod(triu(mm/2)))) # sparse symmetric ("dsC高新技术")
band(sm, -1, 1) # remains "dsC", however
band(sm, -2, 1) # -> "dgC"
```
Construct Sparse Banded Matrix from (Sup-/Super-) Diagonals

Description
Construct a sparse banded matrix by specifying its non-zero sup- and super-diagonals.

Usage
bandSparse(n, m = n, k, diagonals, symmetric = FALSE,
  repr = "C", giveCsparse = (repr == "C"))

Arguments
n,m the matrix dimension \((n, m) = (\text{row}, \text{col})\).
k integer vector of "diagonal numbers", with identical meaning as in \text{band}(*, k),
i.e., relative to the main diagonal, which is \(k=0\).
diagonals optional list of sub-/super- diagonals; if missing, the result will be a pattern
  matrix, i.e., inheriting from class \text{nMatrix}.
  diagonals can also be \(n^\prime \times d\) matrix, where \(d \leftarrow \text{length}(k)\) and \(n^\prime \geq
  \min(n, m)\). In that case, the sub-/super- diagonals are taken from the columns
  of diagonals, where only the first several rows will be used (typically) for off-
  diagonals.
symmetric logical; if true the result will be symmetric (inheriting from class
  \text{symmetricMatrix}) and only the upper or lower triangle must be specified (via
  \(k\) and diagonals).
repr character string, one of "C", "T", or "R", specifying the sparse representation
  to be used for the result, i.e., one from the super classes \text{CsparseMatrix},
  \text{TsparseMatrix}, or \text{RsparseMatrix}.
giveCsparse \text{(deprecated, replaced with repr): logical indicating if the result should be a}
  \text{CsparseMatrix} or a \text{TsparseMatrix}, where the default was \text{TRUE}, and now is
  determined from \text{repr}; very often \text{Csparse} matrices are more efficient subsequ-
  ently, but not always.

Value
a sparse matrix (of class \text{CsparseMatrix}) of dimension \(n \times m\) with diagonal “bands” as specified.

See Also
\text{band}, for extraction of matrix bands; \text{bdiag, diag, sparseMatrix, Matrix}.

Examples
```r
diags <- list(1:30, 10*(1:20), 100*(1:20))
s1 <- bandSparse(13, k = -c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
s1
s2 <- bandSparse(13, k = c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
stopifnot(identical(s1, t(s2)), is(s1,"dsCMatrix"))
```
### a pattern Matrix of *full* (sub-)diagonals:

```r
bk <- c(0:4, 7, 9)
(s3 <- bandSparse(30, k = bk, symm = TRUE))
```

### If you want a pattern matrix, but with "sparse"-diagonals, 
### you currently need to go via logical sparse:

```r
llis <- lapply(list(rpois(20, 2), rpois(20, 1), rpois(20, 3))[, c(1:3, 2:3, 3:2)],
              as.logical)
(s4 <- bandSparse(20, k = bk, symm = TRUE, diag = llis))
(s4. <- as(drop0(s4), "nsparseMatrix"))
```

```r
n <- 1e4
bk <- c(0:5, 7, 11)
bMat <- matrix(1:8, n, 8, byrow=TRUE)
blis <- as.data.frame(bMat)
B <- bandSparse(n, k = bk, diag = blis)
Bs <- bandSparse(n, k = bk, diag = blis, symmetric=TRUE)
B[1:15, 1:30]
Bs[1:15, 1:30]
```

```r
## can use a list *or* a matrix for specifying the diagonals:
stopifnot(identical(B, bandSparse(n, k = bk, diag = bMat)),
          identical(Bs, bandSparse(n, k = bk, diag = bMat, symmetric=TRUE))
          , inherits(B, "dtCMatrix") # triangular!
)
```

---

**bdiag**

**Construct a Block Diagonal Matrix**

**Description**

Build a block diagonal matrix given several building block matrices.

**Usage**

```r
bdiag(...)
.bdiag(lst)
```

**Arguments**

- `...`: individual matrices or a *list* of matrices.
- `lst`: non-empty *list* of matrices.

**Details**

For non-trivial argument list, bdiag() calls .bdiag(). The latter maybe useful to programmers.

**Value**

A *sparse* matrix obtained by combining the arguments into a block diagonal matrix.

The value of bdiag() inherits from class *CsparseMatrix*, whereas .bdiag() returns a *TsparseMatrix*. 
Note

This function has been written and is efficient for the case of relatively few block matrices which are typically sparse themselves.

It is currently inefficient for the case of many small dense block matrices. For the case of many dense $k \times k$ matrices, the `bdiag_m()` function in the ‘Examples’ is an order of magnitude faster.

Author(s)

Martin Maechler, built on a version posted by Berton Gunter to R-help; earlier versions have been posted by other authors, notably Scott Chasalow to S-news. Doug Bates’s faster implementation builds on `TsparseMatrix` objects.

See Also

`Diagonal` for constructing matrices of class `diagonalMatrix`, or `kronecker` which also works for "Matrix" inheriting matrices.

`bandSparse` constructs a banded sparse matrix from its non-zero sub-/super - diagonals.

Note that other CRAN `R` packages have own versions of `bdiag()` which return traditional matrices.

Examples

```r
bdiag(matrix(1:4, 2), diag(3))
## combine "Matrix" class and traditional matrices:
bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))

mlist <- list(1, 2:3, diag(x=5:3), 27, cbind(1:3:6), 100:101)
bdiag(mlist)
stopifnot(identical(bdiag(mlist),
                  bdiag(lapply(mlist, as.matrix))))

ml <- c(as(matrix((1:24)%% 11 == 0, 6,4),"nMatrix"),
         rep(list(Diagonal(2, x=TRUE)), 3))
mln <- c(ml, Diagonal(x = 1:3))
stopifnot(is(bdiag(ml), "lsparseMatrix"),
          is(bdiag(mln),"dsparseMatrix")
)

## random (diagonal-)block-triangular matrices:
rblockTri <- function(nb, max.ni, lambda = 3) {
  .bdiag(replicate(nb, {
    n <- sample.int(max.ni, 1)
    tril(Matrix(rpois(n * n, lambda = lambda), n, n))
  }))
}(T4 <- rblockTri(4, 10, lambda = 1))
image(T4 <- rblockTri(12, 20))
```

```r
##' Fast version of Matrix :: .bdiag() -- for the case of *many* (k x k) matrices:
##' @param lmat list(<mat1>, <mat2>, ......, <mat_N>) where each mat_j is a k x k 'matrix'
##' @return a sparse (N*k x N*k) matrix of class 'code("dgCMatrix")'.
bdiag_m <- function(lmat) {
  # Copyright (C) 2016 Martin Maechler, ETH Zurich
  if(!length(lmat)) return(new("dgCMatrix"))
  stopifnot(is.list(lmat), is.matrix(lmat[[1]]),
            lengths(lmat) == length(lmat))
  m <- matrix(0, nrow = length(lmat), ncol = length(lmat)
```

```r
```
\[(k \leftarrow (d \leftarrow \text{dim(lmat[[1]])}[1])) == d[2], \# \ k \times k \n\]
\[\text{all(vapply(lmat, \text{dim}, \text{integer}(2)) == k))} \# \text{all of them} \n\]
\[N \leftarrow \text{length(lmat)} \n\]
\[\text{if}(N * k > \text{.Machine}\$\text{integer.max}) \n\]
\[\text{stop("resulting matrix too large; would be } \ M \times M, \text{with } M=", N*k) \n\]
\[M \leftarrow \text{as.integer}(N \times k) \n\]
\[\#\text{ result: an } M \times M \text{ matrix} \n\]
\[\text{new("dgCMatrix", } \text{Dim} = c(M,M), \n\]
\[\#\text{ 'i :'} \text{ maybe there's a faster way (w/o matrix indexing), but elegant?} \n\]
\[i = \text{as.vector(matrix(0L:(M-1L), nrow=k[, rep(seq_len(N), each=k))}),} \n\]
\[p = k \times 0L:M, \n\]
\[x = \text{as.double(unlist(lmat, recursive=False, use.names=False))})} \n\]
\]
\[112 \leftarrow \text{replicate(12, matrix(rpois(16, lambda = 6.4), 4, 4),} \n\]
\[\text{simplify=FALSE)} \n\]
\[\text{dim(T12 \leftarrow \text{bdiag_m(112)})} # 48 \times 48 \n\]
\[T12[1:20, 1:20] \n\]

---

**boolmatmult-methods**  
*Boolean Arithmetic Matrix Products: %&% and Methods*

**Description**

For boolean or “pattern” matrices, i.e., R objects of class `nMatrix`, it is natural to allow matrix products using boolean instead of numerical arithmetic.

In package Matrix, we use the binary operator %&% (aka “infix”) function) for this and provide methods for all our matrices and the traditional R matrices (see `matrix`).

**Value**

a pattern matrix, i.e., inheriting from "nMatrix", or an "ldiMatrix" in case of a diagonal matrix.

**Methods**

We provide methods for both the “traditional” (R base) matrices and numeric vectors and conceptually all matrices and `sparseVectors` in package Matrix.

signature(x = "ANY", y = "ANY")
signature(x = "ANY", y = "Matrix")
signature(x = "Matrix", y = "ANY")
signature(x = "nMatrix", y = "nMatrix")
signature(x = "nMatrix", y = "nsparseMatrix")
signature(x = "nsparseMatrix", y = "nMatrix")
signature(x = "nsparseMatrix", y = "nsparseMatrix")
signature(x = "sparseVector", y = "sparseVector")
Note

These boolean arithmetic matrix products had been newly introduced for `Matrix` 1.2.0 (March 2015). Its implementation has still not been tested extensively.

Originally, it was left unspecified how non-structural zeros, i.e., \(0\)'s as part of the \(M@x\) slot should be treated for numeric ("dMatrix") and logical ("lMatrix") sparse matrices. We now specify that boolean matrix products should behave as if applied to `drop0(M)`, i.e., as if dropping such zeros from the matrix before using it.

Equivalently, for all matrices \(M\), boolean arithmetic should work as if applied to \(M \neq 0\) (or \(M \neq FALSE\)).

The current implementation ends up coercing both \(x\) and \(y\) to (virtual) class `nsparseMatrix` which may be quite inefficient for dense matrices. A future implementation may well return a matrix with different class, but the “same” content, i.e., the same matrix entries \(m_{ij}\).

See Also

`%*%`, crossprod(), or `tcrossprod()`, for (regular) matrix product methods.

Examples

```r
set.seed(7)
L <- Matrix(rnorm(20) > 1, 4,5)
(N <- as(L, "nMatrix"))
L. <- L; L.[1:2,1] <- TRUE; L.@x[1:2] <- FALSE; L. # has "zeros" to drop0()
D <- Matrix(round(rnorm(30)), 5,6) # -> values in -1:1 (for this seed)
L %&% D

stopifnot(identical(L %&% D, N %&% D),
  all(L %&% D == as((L %*% abs(D)) > 0, "sparseMatrix")))
```

```r
## cross products , possibly with boolArith = TRUE :
crossprod(N) # -> sparse patter'n' (TRUE/FALSE : boolean arithmetic)
crossprod(N +0) # -> numeric Matrix (with same "pattern")

stopifnot(all(crossprod(N) == t(N) %&% N),
  identical(crossprod(N), crossprod(N +0, boolArith=TRUE)),
  identical(crossprod(L), crossprod(N , boolArith=FALSE)))
crossprod(D, boolArith = TRUE) # pattern: "nsCMatrix"
crossprod(L, boolArith = TRUE) # ditto
crossprod(L, boolArith = FALSE) # numeric: "dsCMatrix"
```

BunchKaufman-class

Dense Bunch-Kaufman Factorizations

Description

Classes `BunchKaufman` and `pBunchKaufman` represent Bunch-Kaufman factorizations of \(n \times n\) real, symmetric matrices \(A\), having the general form

\[
A = U D_U U' = LD_L L'
\]

where \(D_U\) and \(D_L\) are symmetric, block diagonal matrices composed of \(b_U\) and \(b_L\) 1 \(\times\) 1 or 2 \(\times\) 2 diagonal blocks; \(U = \prod_{k=1}^{b_U} P_k U_k\) is the product of \(b_U\) row-permuted unit upper triangular matrices, each having nonzero entries above the diagonal in 1 or 2 columns; and \(L = \prod_{k=1}^{b_L} P_k L_k\)
BunchKaufman-class

is the product of \( b_L \) row-permuted unit lower triangular matrices, each having nonzero entries below the diagonal in 1 or 2 columns.

These classes store the nonzero entries of the \( 2b_U + 1 \) or \( 2b_L + 1 \) factors, which are individually sparse, in a dense format as a vector of length \( nn \) (BunchKaufman) or \( n(n+1)/2 \) (pBunchKaufman), the latter giving the “packed” representation.

Slots

- \( \text{Dim}, \text{Dimnames} \) inherited from virtual class \( \text{MatrixFactorization} \).
- \( \text{uplo} \) a string, either "U" or "L", indicating which triangle (upper or lower) of the factorized symmetric matrix was used to compute the factorization and in turn how the \( x \) slot is partitioned.
- \( x \) a numeric vector of length \( n(n) \) (BunchKaufman) or \( n(n+1)/2 \) (pBunchKaufman), where \( n=\text{Dim}[1] \). The details of the representation are specified by the manual for LAPACK routines \( \text{dsytrf} \) and \( \text{dsptrf} \).
- \( \text{perm} \) an integer vector of length \( n=\text{Dim}[1] \) specifying row and column interchanges as described in the manual for LAPACK routines \( \text{dsytrf} \) and \( \text{dsptrf} \).

Extends

Class \( \text{BunchKaufmanFactorization} \), directly. Class \( \text{MatrixFactorization} \), by class \( \text{BunchKaufmanFactorization} \), distance 2.

Instantiation

Objects can be generated directly by calls of the form \( \text{new("BunchKaufman", ...)} \) or \( \text{new("pBunchKaufman", ...)} \), but they are more typically obtained as the value of \( \text{BunchKaufman}(x) \) for \( x \) inheriting from \( \text{dsyMatrix} \) or \( \text{dspMatrix} \).

Methods

- \( \text{coerce signature(from = "BunchKaufman", to = "dtrMatrix")}: \) returns a \( \text{dtrMatrix} \), useful for inspecting the internal representation of the factorization; see ‘Notes’.
- \( \text{coerce signature(from = "pBunchKaufman", to = "dtpMatrix")}: \) returns a \( \text{dtpMatrix} \), useful for inspecting the internal representation of the factorization; see ‘Notes’.
- \( \text{determinant signature(from = "p?BunchKaufman", logarithm = "logical")}: \) computes the determinant of the factorized matrix \( A \) or its logarithm.
- \( \text{expand1 signature(x = "p?BunchKaufman")}: \) see \( \text{expand1-methods} \).
- \( \text{expand2 signature(x = "p?BunchKaufman")}: \) see \( \text{expand2-methods} \).
- \( \text{solve signature(a = "p?BunchKaufman", b = .)}: \) see \( \text{solve-methods} \).

Note

In \( \text{Matrix} < 1.6-0 \), class \( \text{BunchKaufman} \) extended \( \text{dtrMatrix} \) and class \( \text{pBunchKaufman} \) extended \( \text{dtpMatrix} \), reflecting the fact that the internal representation of the factorization is fundamentally triangular: there are \( n(n+1)/2 \) “parameters”, and these can be arranged systematically to form an \( n \times n \) triangular matrix. \( \text{Matrix} 1.6-0 \) removed these extensions so that methods would no longer be inherited from \( \text{dtrMatrix} \) and \( \text{dtpMatrix} \). The availability of such methods gave the wrong impression that \( \text{BunchKaufman} \) and \( \text{pBunchKaufman} \) represent a (singular) matrix, when in fact they represent an ordered set of matrix factors.

The coercions \( \text{as}(., "dtrMatrix") \) and \( \text{as}(., "dtpMatrix") \) are provided for users who understand the caveats.
References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dsytrf.f and https://netlib.org/lapack/double/dsptrf.f.


See Also

Class dsyMatrix and its packed counterpart.

Generic functions BunchKaufman, expand1, and expand2.

Examples

```r
showClass("BunchKaufman")
set.seed(1)

n <- 6L
(A <- forceSymmetric(Matrix(rnorm(n * n), n, n)))
## With dimnames, to see that they are propagated:
dimnames(A) <- rep.int(list(paste0("x", seq_len(n))), 2L)

(bk.A <- BunchKaufman(A))
str(bk.A <- expand2(bk.A, complete = FALSE), max.level = 2L)
str(bk.A <- expand2(bk.A, complete = TRUE), max.level = 2L)

## Underlying LAPACK representation
(m.bk.A <- as(bk.A, "dtrMatrix"))
stopifnot(identical(as(m.bk.A, "matrix"), `dim<-`(bk.A@x, bk.A@Dim)))

## Number of factors is 2*b+1, b <= n, which can be nontrivial ...
(b <- (length(E.bk.A) - 1L) %/% 2L)
ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ U DU U', U := prod(Pk Uk) in floating point
stopifnot(exprs = {
  identical(names(e.bk.A), c("U", "DU", "U."))
  identical(e.bk.A[["U"]], Reduce("%*%", E.bk.A[seq_len(b)]))
  identical(e.bk.A[["U."]], t(e.bk.A[["U"]]))
  ae1(A, with(e.bk.A, U %*% DU %*% U.))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(bk.A)),
  identical(solve(A, b), solve(bk.A, b)))
```

BunchKaufman-methods Methods for Bunch-Kaufman Factorization
Description

Computes the Bunch-Kaufman factorization of an $n \times n$ real, symmetric matrix $A$, which has the general form

$$A = U D_U U' = L D_L L'$$

where $D_U$ and $D_L$ are symmetric, block diagonal matrices composed of $b_U$ and $b_L$ $1 \times 1$ or $2 \times 2$ diagonal blocks; $U = \prod_{k=1}^{b_U} P_k U_k$ is the product of $b_U$ row-permuted unit upper triangular matrices, each having nonzero entries above the diagonal in 1 or 2 columns; and $L = \prod_{k=1}^{b_L} P_k L_k$ is the product of $b_L$ row-permuted unit lower triangular matrices, each having nonzero entries below the diagonal in 1 or 2 columns.

Methods are built on LAPACK routines $\text{dsytrf}$ and $\text{dsptrf}$.

Usage

```r
BunchKaufman(x, ...)  
## S4 method for signature 'dsyMatrix'
BunchKaufman(x, warnSing = TRUE, ...)  
## S4 method for signature 'dspMatrix'
BunchKaufman(x, warnSing = TRUE, ...)  
## S4 method for signature 'matrix'
BunchKaufman(x, uplo = "U", ...)  
```

Arguments

- `x`: a finite symmetric matrix or `Matrix` to be factorized. If `x` is square but not symmetric, then it will be treated as symmetric; see `uplo`.
- `warnSing`: a logical indicating if a warning should be signaled for singular `x`.
- `uplo`: a string, either "U" or "L", indicating which triangle of `x` should be used to compute the factorization.
- `...`: further arguments passed to or from methods.

Value

An object representing the factorization, inheriting from virtual class `BunchKaufmanFactorization`. The specific class is `BunchKaufman` unless `x` inherits from virtual class `packedMatrix`, in which case it is `pBunchKaufman`.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dsytrf.f and https://netlib.org/lapack/double/dsptrf.f.


See Also

Classes `BunchKaufman` and `pBunchKaufman` and their methods.
Classes `dsyMatrix` and `dspMatrix`.
Generic functions `expand1` and `expand2`, for constructing matrix factors from the result.
Generic functions `Cholesky`, `Schur`, `lu`, and `qr`, for computing other factorizations.
Examples

```r
showMethods("BunchKaufman", inherited = FALSE)
set.seed(0)

data(CAex, package = "Matrix")
class(CAex) # dgCMat
isSymmetric(CAex) # symmetric, but not formally

A <- as(CAex, "symmetricMatrix")
class(A) # dsCMat

## Have methods for denseMatrix (unpacked and packed),
## but not yet sparseMatrix ...
## Not run:
(bk.A <- BunchKaufman(A))

## End(Not run)
(bk.A <- BunchKaufman(as(A, "unpackedMatrix")))

## A ~ U DU U' in floating point
str(e.bk.A <- expand2(bk.A), max.level = 2L)
stopifnot(all.equal(as(A, "matrix"), as(Reduce("%*%", e.bk.A), "matrix")))
```

CAex  Albers' example Matrix with "Difficult" Eigen Factorization

Description

An example of a sparse matrix for which `eigen()` seemed to be difficult, an unscaled version of this has been posted to the web, accompanying an E-mail to R-help ([https://stat.ethz.ch/mailman/listinfo/r-help](https://stat.ethz.ch/mailman/listinfo/r-help)), by Casper J Albers, Open University, UK.

Usage

```r
data(CAex)
```

Format

This is a 72 x 72 symmetric matrix with 216 non-zero entries in five bands, stored as sparse matrix of class `dgCMat`.

Details

Historical note (2006-03-30): In earlier versions of R, `eigen(CAex)` fell into an infinite loop whereas `eigen(CAex, EISPACK=TRUE)` had been okay.

Examples

```r
data(CAex, package = "Matrix")
str(CAex) # of class "dgCMat"

image(CAex)# -> it's a simple band matrix with 5 bands
## and the eigen values are basically 1 (42 times) and 0 (30 x):
zapsmall(ev <- eigen(CAex, only.values=TRUE)$values)
## i.e., the matrix is symmetric, hence
sCA <- as(CAex, "symmetricMatrix")
## and
stopifnot(class(sCA) == "dsCMatrix",
    as(sCA, "matrix") == as(CAex, "matrix"))

### Description

The base functions `cbind` and `rbind` are defined for an arbitrary number of arguments and hence have the first formal argument `...`. Now, when S4 objects are found among the arguments, base `cbind()` and `rbind()` internally “dispatch” recursively, calling `cbind2()` or `rbind2()` respectively, where these have methods defined and so should dispatch appropriately.

`cbind2()` and `rbind2()` are from the `methods` package, i.e., standard R, and have been provided for binding together two matrices, where in `Matrix`, we have defined methods for these and the 'Matrix' matrices.

### Usage

```r
## cbind(..., deparse.level = 1)
## rbind(..., deparse.level = 1)

## S4 method for signature 'Matrix,Matrix'
cbind2(x, y, ...)
## S4 method for signature 'Matrix,Matrix'
rbind2(x, y, ...)
```

### Arguments

- `...` for `[cr]bind`, vector- or matrix-like R objects to be bound together; for `[cr]bind2`, further arguments passed to or from methods; see `cbind` and `cbind2`.
- `deparse.level` integer controlling the construction of labels in the case of non-matrix-like arguments; see `cbind`.
- `x, y` vector- or matrix-like R objects to be bound together.

### Value

typically a ‘matrix-like’ object of a similar `class` as the first argument in `...`. Note that sometimes by default, the result is a `sparseMatrix` if one of the arguments is (even in the case where this is not efficient). In other cases, the result is chosen to be sparse when there are more zero entries is than non-zero ones (as the default sparse in `Matrix()`).

### Author(s)

Martin Maechler
CHMfactor-class

Sparse Cholesky Factorizations

Description

CHMfactor is the virtual class of sparse Cholesky factorizations of \( n \times n \) real, symmetric matrices \( A \), having the general form

\[
P_1 A P_1' = L_1 D L_1' \quad D_{jj} \geq 0 \quad LL'
\]

or (equivalently)

\[
A = P_1' L_1 D L_1' P_1 \quad D_{jj} \geq 0 \quad P_1' LL' P_1
\]

where \( P_1 \) is a permutation matrix, \( L_1 \) is a unit lower triangular matrix, \( D \) is a diagonal matrix, and \( L = L_1 \sqrt{D} \). The second equalities hold only for positive semidefinite \( A \), for which the diagonal entries of \( D \) are non-negative and \( \sqrt{D} \) is well-defined.

The implementation of class CHMfactor is based on CHOLMOD’s C-level cholmod_factor_struct. Virtual subclasses CHMsimpl and CHMsuper separate the simpli- cial and supernodal variants. These have nonvirtual subclasses [dn]CHMsimpl and [dn]CHMsuper, where prefix ‘d’ and prefix ‘n’ are reserved for numeric and symbolic factorizations, respectively.

Usage

isLDL(x)

Arguments

x an object inheriting from virtual class CHMfactor, almost always the result of a call to generic function Cholesky.

Value

isLDL(x) returns TRUE or FALSE: TRUE if \( x \) stores the lower triangular entries of \( L_1 - I + D \), FALSE if \( x \) stores the lower triangular entries of \( L \).

See Also
cbind, cbind2.

Our class definition help pages mentioning cbind2() and rbind2() methods: "denseMatrix", "diagonalMatrix", "indMatrix".

Examples

(a <- matrix(c(2:1,1:2), 2,2))

(M1 <- cbind(0, rbind(a, 7))) # a traditional matrix

D <- Diagonal(2)

(M2 <- cbind(4, a, D, -1, D, 0)) # a sparse Matrix

stopifnot(validObject(M2), inherits(M2, "sparseMatrix"),
          dim(M2) == c(2,9))
**Slots**

Of `CHMfactor`:

- `Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.
  
- `colcount` an integer vector of length `Dim[1]` giving an estimate of the number of nonzero entries in each column of the lower triangular Cholesky factor. If symbolic analysis was performed prior to factorization, then the estimate is exact.

- `perm` a 0-based integer vector of length `Dim[1]` specifying the permutation applied to the rows and columns of the factorized matrix. `perm` of length 0 is valid and equivalent to the identity permutation, implying no pivoting.

- `type` an integer vector of length 6 specifying details of the factorization. The elements correspond to members `ordering`, `is_ll`, `is_super`, `is_monotonic`, `maxcsize`, and `maxesize` of the original `cholmod_factor_struct`. Simplicial and supernodal factorizations are distinguished by `is_super`. Simplicial factorizations do not use `maxcsize` or `maxesize`. Supernodal factorizations do not use `is_ll` or `is_monotonic`.

Of `CHMsimpl` (all unused by `nCHMsimpl`):

- `nz` an integer vector of length `Dim[1]` giving the number of nonzero entries in each column of the lower triangular Cholesky factor. There is at least one nonzero entry in each column, because the diagonal elements of the factor are stored explicitly.

- `p` an integer vector of length `Dim[1]+1`. Row indices of nonzero entries in column `j` of the lower triangular Cholesky factor are obtained as `i[p[j]+seq_len(nz[j])]+1`.

- `i` an integer vector of length greater than or equal to `sum(nz)` containing the row indices of nonzero entries in the lower triangular Cholesky factor. These are grouped by column and sorted within columns, but the columns themselves need not be ordered monotonically. Columns may be overallocated, i.e., the number of elements of `i` reserved for column `j` may exceed `nz[j]`.

- `prv`, `nxt` integer vectors of length `Dim[1]+2` indicating the order in which the columns of the lower triangular Cholesky factor are stored in `i` and `x`. Starting from `j <- Dim[1]+2`, the recursion `j <- nxt[j+1]+1` traverses the columns in forward order and terminates when `nxt[j+1] = -1`. Starting from `j <- Dim[1]+1`, the recursion `j <- prv[j+1]+1` traverses the columns in backward order and terminates when `prv[j+1] = -1`.

Of `dCHMsimpl`:

- `x` a numeric vector parallel to `i` containing the corresponding nonzero entries of the lower triangular Cholesky factor `L` or (if and only if `type[2]` is 0) of the lower triangular matrix `L_1 - I + D`.

Of `CHMsuper`:

- `super`, `pi`, `px` integer vectors of length `nsuper+1`, where `nsuper` is the number of supernodes. `super[j]+1` is the index of the leftmost column of supernode `j`. The row indices of supernode `j` are obtained as `s[pi[j]+seq_len(pi[j+1]-pi[j])]+1`. The numeric entries of supernode `j` are obtained as `x[px[j]+seq_len(px[j+1]-px[j])]+1` (if slot `x` is available).

- `s` an integer vector of length greater than or equal to `Dim[1]` containing the row indices of the supernodes. `s` may contain duplicates, but not within a supernode, where the row indices must be increasing.

Of `dCHMsuper`:

- `x` a numeric vector of length less than or equal to `prod(Dim)` containing the numeric entries of the supernodes.
Extends

Class `MatrixFactorization`, directly.

Instantiation

Objects can be generated directly by calls of the form `new("dCHMsimpl", ...)`, etc., but `dCHMsimpl` and `dCHMsuper` are more typically obtained as the value of `Cholesky(x, ...)` for `x` inheriting from `sparseMatrix` (often `dsCMatrix`).

There is currently no API outside of calls to `new` for generating `nCHMsimpl` and `nCHMsuper`. These classes are vestigial and may be formally deprecated in a future version of `Matrix`.

Methods

coerce signature(from = "CHMsimpl", to = "dtCMatrix"): returns a `dtCMatrix` representing the lower triangular Cholesky factor `L` or the lower triangular matrix `L_1 - I + D`, the latter if and only if `from@type[2]` is 0.

coerce signature(from = "CHMsuper", to = "dgCMatrix"): returns a `dgCMatrix` representing the lower triangular Cholesky factor `L`. Note that, for supernodes spanning two or more columns, the supernodal algorithm by design stores non-structural zeros above the main diagonal, hence `dgCMatrix` is indeed more appropriate than `dtCMatrix` as a coercion target.

determinant signature(from = "CHMfactor", logarithm = "logical"): behaves according to an optional argument `sqrt`. If `sqrt = FALSE`, then this method computes the determinant of the factorized matrix `A` or its logarithm. If `sqrt = TRUE`, then this method computes the determinant of the factor `L = L_1 sqrt(D)` or its logarithm, giving NaN for the modulus when `D` has negative diagonal elements. For backwards compatibility, the default value of `sqrt` is `TRUE`, but that can be expected change in a future version of `Matrix`, hence defensive code will always set `sqrt` (to `TRUE`, if the code must remain backwards compatible with `Matrix < 1.6-0`). Calls to this method not setting `sqrt` may warn about the pending change. The warnings can be disabled with `options(Matrix.warnSqrtDefault = 0)`.

diag signature(x = "CHMfactor"): returns a numeric vector of length `n` containing the diagonal elements of `D`, which (if they are all non-negative) are the squared diagonal elements of `L`.

expand signature(x = "CHMfactor"): see `expand-methods`.

expand1 signature(x = "CHMsimpl"): see `expand1-methods`.

expand2 signature(x = "CHMsimpl"): see `expand2-methods`.

expand signature(x = "CHMsuper"): see `expand-methods`.

image signature(x = "CHMfactor"): see `image-methods`.

nnzero signature(x = "CHMfactor"): see `nnzero-methods`.

determinate signature(update = ".", C = ".", object = "CHMfactor"): see `update-methods`.

determinate signature(update = ".", C = ".", object = "CHMfactor"): see `solve-methods`.

updown signature(update = ".", C = ".", object = "CHMfactor"): see `updown-methods`. 
The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file ‘CHOLMOD/Include/cholmod.h’ defining cholmod_factor_struct.


See Also

Class `dsCMatrix`.

Generic functions `Cholesky`, `updown`, `expand1` and `expand2`.

Examples

```r
showClass("dCHMsimpl")
showClass("dCHMsuper")

set.seed(2)

m <- 1000L
n <- 200L
M <- rsparsematrix(m, n, 0.01)
A <- crossprod(M)
## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- rep.int(list(paste0("x", seq_len(n))), 2L)

(ch.A <- Cholesky(A)) # pivoted, by default
str(e.ch.A <- expand2(ch.A, LDL = TRUE), max.level = 2L)
str(E.ch.A <- expand2(ch.A, LDL = FALSE), max.level = 2L)

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L1 D L1' P1 ~ P1' L L' P1 in floating point
stopifnot(exprs = {
  identical(names(e.ch.A), c("P1.", "L1", "D", "L1.", "P1"))
  identical(names(E.ch.A), c("P1.", "L", "L.", "P1"))
  identical(e.ch.A[["P1"]],
    new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
      margin = 2L, perm = invertPerm(ch.A$perm, 0L, 1L)))
  identical(e.ch.A[["P1"]], t(e.ch.A[["P1"]]))
  identical(e.ch.A[["L1"]], t(e.ch.A[["L1"]]))
  identical(E.ch.A[["L"]], t(E.ch.A[["L"]]))
  identical(e.ch.A[["D"]], Diagonal(x = diag(ch.A)))
  all.equal(E.ch.A[["L"]], with(e.ch.A, L1 %*% sqrt(D)))
  ae1(A, with(e.ch.A, P1. %*% L1 %*% D %*% L1. %*% P1))
  ae1(A, with(e.ch.A, P1. %*% L %*% D %*% L %*% P1))
  ae2(A[ch.A$perm + 1L, ch.A$perm + 1L], with(e.ch.A, L1 %*% D %*% L1.))
})
```
chol-methods

Factorization handled as factorized matrix

(in some cases only optionally, depending on arguments)

```
b <- rnorm(n)
stopifnot(identical(det(A), det(ch.A, sqrt = FALSE)),
          identical(solve(A, b), solve(ch.A, b, system = "A")))
u1 <- update(ch.A, A, mult = sqrt(2))
u2 <- update(ch.A, t(M), mult = sqrt(2)) # updating with crossprod(M), not M
stopifnot(all.equal(u1, u2, tolerance = 1e-14))
```

chol-methods

Compute the Cholesky Factor of a Matrix

Description

Computes the upper triangular Cholesky factor of an \(n \times n\) real, symmetric, positive semidefinite matrix \(A\), optionally after pivoting. That is the factor \(L'\) in

\[P_1A P_1' = LL'\]

or (equivalently)

\[A = P_1' LL' P_1\]

where \(P_1\) is a permutation matrix.

Methods for \texttt{denseMatrix} are built on LAPACK routines \texttt{dpstrf}, \texttt{dpotrf}, and \texttt{dpptrf}. The latter two do not permute rows or columns, so that \(P_1\) is an identity matrix.

Methods for \texttt{sparseMatrix} are built on CHOLMOD routines \texttt{cholmod_analyze} and \texttt{cholmod_factorize_p}.

Usage

```
chol(x, ...)
## S4 method for signature 'dsyMatrix'
chol(x, pivot = FALSE, tol = -1, ...)
## S4 method for signature 'dsyMatrix'
chol(x, ...)
## S4 method for signature 'dsyMatrix'
chol(x, pivot = FALSE, ...)
## S4 method for signature 'dsyMatrix'
chol(x, ...)
## S4 method for signature 'dsyMatrix'
chol(x, pivot = FALSE, ...)
## S4 method for signature 'dsyMatrix'
chol(x, ...)
## S4 method for signature 'generalMatrix'
chol(x, uplo = "U", ...)  # for sparse (but not diagonal) x require positive definiteness unconditionally.
```

Arguments

- \(x\) a finite, symmetric, positive semidefinite matrix or \texttt{Matrix} to be factorized. If \(x\) is square but not symmetric, then it will be treated as symmetric; see \texttt{uplo}.

Methods for dense \(x\) require positive definiteness when \texttt{pivot = FALSE}. Methods for sparse (but not diagonal) \(x\) require positive definiteness unconditionally.
pivot a logical indicating if the rows and columns of \( x \) should be pivoted. Methods for sparse \( x \) employ the approximate minimum degree (AMD) algorithm in order to reduce fill-in, i.e., without regard for numerical stability.

tol a finite numeric tolerance, used only if \( pivot = \text{TRUE} \). The factorization algorithm stops if the pivot is less than or equal to \( tol \). Negative \( tol \) is equivalent to \( nrow(x) \times .Machine\$double.eps \times \max(\text{diag}(x)) \).

uplo a string, either "U" or "L", indicating which triangle of \( x \) should be used to compute the factorization. The default is "U", even for lower triangular \( x \), to be consistent with \texttt{chol} from \texttt{base}.

... further arguments passed to or from methods.

Details

For \( x \) inheriting from \texttt{diagonalMatrix}, the diagonal result is computed directly and without pivoting, i.e., bypassing CHOLMOD.

For all other \( x \), \texttt{chol}(\( x \), \( pivot = \text{value} \)) calls \texttt{Cholesky}(\( x \), \( perm = \text{value} \), ...) under the hood. If you must know the permutation \( P_1 \) in addition to the Cholesky factor \( L' \), then call \texttt{Cholesky} directly, as the result of \texttt{chol}(\( x \), \( pivot = \text{TRUE} \)) specifies \( L' \) but not \( P_1 \).

Value

A matrix, \texttt{triangularMatrix}, or \texttt{diagonalMatrix} representing the upper triangular Cholesky factor \( L' \). The result is a traditional matrix if \( x \) is a traditional matrix, dense if \( x \) is dense, and sparse if \( x \) is sparse.

References

The LAPACK source code, including documentation; see \url{https://netlib.org/lapack/\double/dpstrf.f}, \url{https://netlib.org/lapack/\double/dpotrf.f}, and \url{https://netlib.org/lapack/\double/dpptrf.f}.

The CHOLMOD source code; see \url{https://github.com/DrTimothyAldenDavis/SuiteSparse}, notably the header file ‘\texttt{CHOLMOD}\/Include/\texttt{cholmod.h}’ defining \texttt{cholmod\_factor\_struct}.


See Also

The default method from \texttt{base}, \texttt{chol}, called for traditional matrices \( x \).

Generic function \texttt{Cholesky}, for more flexibility notably when computing the Cholesky factorization and not only the factor \( L' \).
Examples

```
showMethods("chol", inherited = FALSE)
set.seed(0)

## ---- Dense ----------------------------------------------------------
## chol(x, pivot = value) wrapping Cholesky(x, perm = value)
selectMethod("chol", "dsyMatrix")
## Except in packed cases where pivoting is not yet available
selectMethod("chol", "dspMatrix")
## .... Positive definite ..............................................
(A1 <- new("dsyMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 5)))
(R1.nopivot <- chol(A1))
(R1 <- chol(A1, pivot = TRUE))
## In 2-by-2 cases, we know that the permutation is 1:2 or 2:1,
## even if in general 'chol' does not say ...
stopifnot(exprs = {
  all.equal( A1, as(crossprod(R1.nopivot), "dsyMatrix"))
  all.equal(t(A1[2:1, 2:1]), as(crossprod(R1), "dsyMatrix"))
  identical(Cholesky(A1)@perm, 2:1) # because 5 > 1
})
## .... Positive semidefinite but not positive definite ..............
(A2 <- new("dpoMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 4)))
try(R2.nopivot <- chol(A2)) # fails as not positive definite
(R2 <- chol(A2, pivot = TRUE)) # returns, with a warning and ...
stopifnot(exprs = {
  all.equal(t(A2[2:1, 2:1]), as(crossprod(R2), "dsyMatrix"))
  identical(Cholesky(A2)@perm, 2:1) # because 4 > 1
})
## .... Not positive semidefinite ......................................
(A3 <- new("dsyMatrix", Dim = c(2L, 2L), x = c(1, 2, 2, 3)))
try(R3.nopivot <- chol(A3)) # fails as not positive definite
(R3 <- chol(A3, pivot = TRUE)) # returns, with a warning and ...
## _Not_ equal: see details and examples in help("Cholesky")
all.equal(t(A3[2:1, 2:1]), as(crossprod(R3), "dsyMatrix"))
## ---- Sparse ---------------------------------------------------------
## chol(x, pivot = value) wrapping
## Cholesky(x, perm = value, LDL = FALSE, super = FALSE)
selectMethod("chol", "dsCMatrix")
## Except in diagonal cases which are handled "directly"
selectMethod("chol", "ddiMatrix")
```
chol2inv-methods

(A4 <- toeplitz(as(c(10, 0, 1, 0, 3), "sparseVector")))
(ch.A4.nopivot <- Cholesky(A4, perm = FALSE, LDL = FALSE, super = FALSE))
(ch.A4 <- Cholesky(A4, perm = TRUE, LDL = FALSE, super = FALSE))
(R4.nopivot <- chol(A4))
(R4 <- chol(A4, pivot = TRUE))
det4 <- det(A4)
b4 <- rnorm(5L)
x4 <- solve(A4, b4)

stopifnot(exprs = {
  identical(R4.nopivot, expand1(ch.A4.nopivot, "L."))
  identical(R4, expand1(ch.A4, "L.") )
  all.equal(A4, crossprod(R4.nopivot))
  all.equal(A4[ch.A4@perm + 1L, ch.A4@perm + 1L], crossprod(R4))
  all.equal(diag(R4.nopivot), sqrt(diag(ch.A4.nopivot)))
  all.equal(diag(R4), sqrt(diag(ch.A4)))
  all.equal(sqrt(det4), det(R4.nopivot))
  all.equal(sqrt(det4), det(R4))
  all.equal(det4, det(ch.A4.nopivot, sqrt = FALSE))
  all.equal(det4, det(ch.A4, sqrt = FALSE))
  all.equal(x4, solve(R4.nopivot, solve(t(R4.nopivot), b4)))
  all.equal(x4, solve(ch.A4.nopivot, b4))
  all.equal(x4, solve(ch.A4, b4))
})

---

chol2inv-methods Inverse from Cholesky Factor

Description

Given formally upper and lower triangular matrices \(U\) and \(L\), compute \((U'U)^{-1}\) and \((LL')^{-1}\), respectively. This function can be seen as way to compute the inverse of a symmetric positive definite matrix given its Cholesky factor. Equivalently, it can be seen as a way to compute \((X'X)^{-1}\) given the \(R\) part of the QR factorization of \(X\), if \(R\) is constrained to have positive diagonal entries.

Usage

chol2inv(x, ...)
## S4 method for signature 'dtrMatrix'
chol2inv(x, ...)
## S4 method for signature 'dtCMatrix'
chol2inv(x, ...)
## S4 method for signature 'generalMatrix'
chol2inv(x, uplo = "U", ...)

Arguments

- \(x\) a square matrix or \texttt{Matrix}, typically the result of a call to \texttt{chol}. If \(x\) is square but not (formally) triangular, then only the upper or lower triangle is considered, depending on optional argument \texttt{uplo} if \(x\) is a \texttt{Matrix}.  

---

chol2inv-methods Inverse from Cholesky Factor

Description

Given formally upper and lower triangular matrices \(U\) and \(L\), compute \((U'U)^{-1}\) and \((LL')^{-1}\), respectively. This function can be seen as way to compute the inverse of a symmetric positive definite matrix given its Cholesky factor. Equivalently, it can be seen as a way to compute \((X'X)^{-1}\) given the \(R\) part of the QR factorization of \(X\), if \(R\) is constrained to have positive diagonal entries.

Usage

chol2inv(x, ...)
## S4 method for signature 'dtrMatrix'
chol2inv(x, ...)
## S4 method for signature 'dtCMatrix'
chol2inv(x, ...)
## S4 method for signature 'generalMatrix'
chol2inv(x, uplo = "U", ...)

Arguments

- \(x\) a square matrix or \texttt{Matrix}, typically the result of a call to \texttt{chol}. If \(x\) is square but not (formally) triangular, then only the upper or lower triangle is considered, depending on optional argument \texttt{uplo} if \(x\) is a \texttt{Matrix}.  

---
uplo  a string, either "U" or "L", indicating which triangle of \( x \) contains the Cholesky factor. The default is "U", to be consistent with \texttt{chol2inv} from \texttt{base}.

... further arguments passed to or from methods.

Value

A matrix, \texttt{symmetricMatrix}, or \texttt{diagonalMatrix} representing the inverse of the positive definite matrix whose Cholesky factor is \( x \). The result is a traditional matrix if \( x \) is a traditional matrix, dense if \( x \) is dense, and sparse if \( x \) is sparse.

See Also

The default method from \texttt{base}, \texttt{chol2inv}, called for traditional matrices \( x \).

Generic function \texttt{chol}, for computing the upper triangular Cholesky factor \( L' \) of a symmetric positive semidefinite matrix.

Generic function \texttt{solve}, for solving linear systems and (as a corollary) for computing inverses more generally.

Examples

\begin{verbatim}
(A <- Matrix(cbind(c(1, 1, 1), c(1, 2, 4), c(1, 4, 16))))
(R <- chol(A))
(L <- t(R))
(R2i <- chol2inv(R))
(L2i <- chol2inv(R))
stopifnot(exprs = {
  all.equal(R2i, tcrossprod(solve(R)))
  all.equal(L2i, crossprod(solve(L)))
  all.equal(as(R2i %%% A, "matrix"), diag(3L)) # the identity
  all.equal(as(L2i %%% A, "matrix"), diag(3L)) # ditto
})
\end{verbatim}

Cholesky-class

Dense Cholesky Factorizations

Description

Classes \texttt{Cholesky} and \texttt{pCholesky} represent dense, pivoted Cholesky factorizations of \( n \times n \) real, symmetric, positive semidefinite matrices \( A \), having the general form

\[ P_1 A P_1' = L_1 D L_1' = LL' \]

or (equivalently)

\[ A = P_1' L_1 D L_1' P_1 = P_1' L L' P_1 \]

where \( P_1 \) is a permutation matrix, \( L_1 \) is a unit lower triangular matrix, \( D \) is a non-negative diagonal matrix, and \( L = L_1 \sqrt{D} \).

These classes store the entries of the Cholesky factor \( L \) or its transpose \( L' \) in a dense format as a vector of length \( nn \) (\texttt{Cholesky}) or \( n(n + 1)/2 \) (\texttt{pCholesky}), the latter giving the “packed” representation.
Slots

Dim, Dimnames inherited from virtual class MatrixFactorization.

uplo a string, either "U" or "L", indicating which triangle (upper or lower) of the factorized symmetric matrix was used to compute the factorization and in turn whether x stores $L'$ or $L$.

x a numeric vector of length $n^2$ (Cholesky) or $n(n+1)/2$ (pCholesky), where $n=\text{Dim}[1]$, listing the entries of the Cholesky factor $L$ or its transpose $L'$ in column-major order.

perm a 1-based integer vector of length Dim[1] specifying the permutation applied to the rows and columns of the factorized matrix. perm of length 0 is valid and equivalent to the identity permutation, implying no pivoting.

Extends

Class CholeskyFactorization, directly. Class MatrixFactorization, by class CholeskyFactorization, distance 2.

Instantiation

Objects can be generated directly by calls of the form new("Cholesky", ...) or new("pCholesky", ...), but they are more typically obtained as the value of Cholesky(x) for x inheriting from dsyMatrix or dspMatrix (often the subclasses of those reserved for positive semidefinite matrices, namely dpoMatrix and dppMatrix).

Methods

coerce signature(from = "Cholesky", to = "dtrMatrix"): returns a dtrMatrix representing the Cholesky factor $L$ or its transpose $L'$; see 'Note'.

coeerce signature(from = "pCholesky", to = "dtpMatrix"): returns a dtpMatrix representing the Cholesky factor $L$ or its transpose $L'$; see 'Note'.

determinant signature(from = "p?Cholesky", logarithm = "logical"): computes the determinant of the factorized matrix $A$ or its logarithm.

diag signature(x = "p?Cholesky"): returns a numeric vector of length $n$ containing the diagonal elements of $D$, which are the squared diagonal elements of $L$.

expand1 signature(x = "p?Cholesky"): see expand1-methods.

expand2 signature(x = "p?Cholesky"): see expand2-methods.

solve signature(a = "p?Cholesky", b = .): see solve-methods.

Note

In Matrix <1.6-0, class Cholesky extended dtrMatrix and class pCholesky extended dtpMatrix, reflecting the fact that the factor $L$ is indeed a triangular matrix. Matrix 1.6-0 removed these extensions so that methods would no longer be inherited from dtrMatrix and dtpMatrix. The availability of such methods gave the wrong impression that Cholesky and pCholesky represent a (singular) matrix, when in fact they represent an ordered set of matrix factors.

The coercions as(., "dtrMatrix") and as(., "dtpMatrix") are provided for users who understand the caveats.
References

The LAPACK source code, including documentation; see https://netlib.org/lapack/
pack/double/dpptrf.f.

Lucas, C. (2004). LAPACK-style codes for level 2 and 3 pivoted Cholesky factorizations. LAPACK

Press. doi:10.56021/9781421407944

See Also

Class ChMMfactor for sparse Cholesky factorizations.

Classes dpoMatrix and dppMatrix.

Generic functions Cholesky, expand1 and expand2.

Examples

showClass("Cholesky")
set.seed(1)

m <- 30L
n <- 6L
(A <- crossprod(Matrix(rnorm(m*n), m, n)))

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- rep.int(list(paste0("x", seq_len(n))), 2L)

(ch.A <- Cholesky(A)) # pivoted, by default
str(e.ch.A <- expand2(ch.A, LDL = TRUE), max.level = 2L)
str(E.ch.A <- expand2(ch.A, LDL = FALSE), max.level = 2L)

## Underlying LAPACK representation
(m.ch.A <- as(ch.A, "dtrMatrix")) # which is L', not L, because
A@uplo == "U"
stopifnot(identical(as(m.ch.A, "matrix"), dim<-(ch.A@x, ch.A@Dim)))

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L1 D L1' P1 ~ P1' L L' P1 in floating point
stopifnot(exprs = {
  identical(names(e.ch.A), c("P1.", "L1", "D", "L1.", "P1"))
  identical(names(E.ch.A), c("P1.", "L", "L.", "P1"))
  identical(e.ch.A[["P1"]],
    new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
      margin = 2L, perm = invertPerm(ch.A@perm))
  identical(e.ch.A[["P1"]], t(e.ch.A[["P1"]]))
  identical(e.ch.A[["L1"]], t(e.ch.A[["L1"]]))
  identical(E.ch.A[["L"]], t(E.ch.A[["L"]]))
  identical(E.ch.A[["D"]], Diagonal(x = diag(ch.A)))
  all.equal(E.ch.A[["L"]], with(e.ch.A, L1 %*% sort(D)))
  ae1(A, with(e.ch.A, P1 %*% L1 %*% D %*% L1 %*% P1))
  ae1(A, with(E.ch.A, P1 %*% L %*% L %*% P1))
  ae2(A[ch.A@perm, ch.A@perm], with(e.ch.A, L1 %*% D %*% L1))}
## Cholesky-methods

### Methods for Cholesky Factorization

#### Description

Computes the pivoted Cholesky factorization of an $n \times n$ real, symmetric matrix $A$, which has the general form

$$P_1 A P_1' = L_1 D L_1' \quad D_{jj} \geq 0 \quad LL'$$

or (equivalently)

$$A = P_1' L_1 D L_1' P_1 \quad D_{jj} \geq 0 \quad P_1' LL' P_1$$

where $P_1$ is a permutation matrix, $L_1$ is a unit lower triangular matrix, $D$ is a diagonal matrix, and $L = L_1 \sqrt{D}$. The second equalities hold only for positive semidefinite $A$, for which the diagonal entries of $D$ are non-negative and $\sqrt{D}$ is well-defined.

Methods for `denseMatrix` are built on LAPACK routines `dpstrf`, `dpotrf`, and `dpptrf`. The latter two do not permute rows or columns, so that $P_1$ is an identity matrix.

Methods for `sparseMatrix` are built on CHOLMOD routines `cholmod_analyze` and `cholmod_factorize_p`.

#### Usage

- `Cholesky(A, ...)`
  - ## S4 method for signature 'dsyMatrix'
  - `Cholesky(A, perm = TRUE, tol = -1, ...)`
  - ## S4 method for signature 'dspMatrix'
  - `Cholesky(A, ...)`
  - ## S4 method for signature 'dsCMatrix'
  - `Cholesky(A, perm = TRUE, LDL = !super, super = FALSE, Imult = 0, ...)`
  - ## S4 method for signature 'ddiMatrix'
  - `Cholesky(A, ...)`
  - ## S4 method for signature 'generalMatrix'
  - `Cholesky(A, uplo = "U", ...)`
  - ## S4 method for signature 'triangularMatrix'
  - `Cholesky(A, uplo = "U", ...)`
  - ## S4 method for signature 'matrix'
  - `Cholesky(A, uplo = "U", ...)`
Arguments

A  a finite, symmetric matrix or Matrix to be factorized. If A is square but not symmetric, then it will be treated as symmetric; see uplo. Methods for dense A require positive definiteness when perm = FALSE and positive semidefiniteness when perm = TRUE. Methods for sparse A require positive definiteness when LDL = TRUE and nonzero leading principal minors (after pivoting) when LDL = FALSE. Methods for sparse, diagonal A are an exception, requiring positive semidefiniteness unconditionally.

perm a logical indicating if the rows and columns of A should be pivoted. Methods for sparse A employ the approximate minimum degree (AMD) algorithm in order to reduce fill-in, i.e., without regard for numerical stability. Pivoting for sparsity may introduce nonpositive leading principal minors, causing the factorization to fail, in which case it may be necessary to set perm = FALSE.

tol a finite numeric tolerance, used only if perm = TRUE. The factorization algorithm stops if the pivot is less than or equal to tol. Negative tol is equivalent to nrow(A) * .Machine$double.eps * max(diag(A)).

LDL a logical indicating if the simplicial factorization should be computed as $P_1'L_1D_1P_1$, such that the result stores the lower triangular entries of $L_1 - I + D$. The alternative is $P_1'L_1'L_1P_1$, such that the result stores the lower triangular entries of $L = L_1\sqrt{D}$. This argument is ignored if super = TRUE (or if super = NA and the supernodal algorithm is chosen), as the supernodal code does not yet support the LDL = TRUE variant.

super a logical indicating if the factorization should use the supernodal algorithm. The alternative is the simplicial algorithm. Setting super = NA leaves the choice to a CHOLMOD-internal heuristic.

Imult a finite number. The matrix that is factorized is $A + \text{Imult} \times \text{diag(nrow}(A))$, i.e., $A$ plus Imult times the identity matrix. This argument is useful for symmetric, indefinite $A$, as $\text{Imult} > \max(\text{rowSums(abs}(A)) - \text{diag(abs}(A))$ ensures that $A + \text{Imult} \times \text{diag(nrow}(A))$ is diagonally dominant. (Symmetric, diagonally dominant matrices are positive definite.)

uplo a string, either "U" or "L", indicating which triangle of $A$ should be used to compute the factorization. The default is "U", even for lower triangular $A$, to be consistent with chol from base.

... further arguments passed to or from methods.

Details

Note that the result of a call to Cholesky inherits from CholeskyFactorization but not Matrix. Users who just want a matrix should consider using chol, whose methods are simple wrappers around Cholesky returning just the upper triangular Cholesky factor $L'$, typically as a triangularMatrix. However, a more principled approach would be to construct factors as needed from the CholeskyFactorization object, e.g., with expand1(x, "L"), if $x$ is the object.

The behaviour of Cholesky(A, perm = TRUE) for dense $A$ is somewhat exceptional, in that it expects without checking that $A$ is positive semidefinite. By construction, if $A$ is positive semidefinite and the exact algorithm encounters a zero pivot, then the unfactorized trailing submatrix is the zero matrix, and there is nothing left to do. Hence when the finite precision algorithm encounters a pivot less than tol, it signals a warning instead of an error and zeros the trailing submatrix in order to guarantee that $P'LL'P$ is positive semidefinite even if $A$ is not. It follows that one way to test for
Cholesky-methods

positive semidefiniteness of $A$ in the event of a warning is to analyze the error

$$\frac{\|A - P'LL'P\|}{\|A\|}.$$ 

See the examples and LAPACK Working Note ("LAWN") 161 for details.

**Value**

An object representing the factorization, inheriting from virtual class `CholeskyFactorization`. For a traditional matrix $A$, the specific class is `Cholesky`. For $A$ inheriting from `unpackedMatrix`, `packedMatrix`, and `sparseMatrix`, the specific class is `Cholesky`, `pCholesky`, and `dCHMsimpl` or `dCHMsuper`, respectively.

**References**

The LAPACK source code, including documentation; see https://netlib.org/lapack/

The CHOLMOD source code; see https://github.com/DrTimothyAldenDavis/SuiteSparse, notably the header file ‘CHOLMOD/Include/cholmod.h’ defining cholmod_factor_struct.


**See Also**

Classes `Cholesky`, `pCholesky`, `dCHMsimpl` and `dCHMsuper` and their methods.

Classes `dpoMatrix`, `dppMatrix`, and `dsCMatrix`.

Generic function `chol`, for obtaining the upper triangular Cholesky factor $L'$ as a matrix or `Matrix`.

Generic functions `expand1` and `expand2`, for constructing matrix factors from the result.

Generic functions `BunchKaufman`, `Schur`, `lu`, and `qr`, for computing other factorizations.

**Examples**

```r
showMethods("Cholesky", inherited = FALSE)
set.seed(0)

# ---- Dense -----------------------------------------------

# ... Positive definite -------------------------------------

n <- 6L
(A1 <- crossprod(Matrix(rnorm(n * n), n, n)))
(ch.A1.nopivot <- Cholesky(A1, perm = FALSE))
```
(ch.A1 <- Cholesky(A1))
stopifnot(exprs = {
  length(ch.A1@perm) == ncol(A1)
  isPerm(ch.A1@perm)
  is.unsorted(ch.A1@perm) # typically not the identity permutation
  length(ch.A1.nopivot@perm) == 0L
})

## A ~ P1 L D L L' P1 = P1' L L' P1 in floating point
str(e.ch.A1 <- expand2(ch.A1, LDL = TRUE), max.level = 2L)
str(E.ch.A1 <- expand2(ch.A1, LDL = FALSE), max.level = 2L)
stopifnot(exprs = {
  all.equal(as(A1, "matrix"), as(Reduce("%*%", e.ch.A1), "matrix"))
  all.equal(as(A1, "matrix"), as(Reduce("%*%", E.ch.A1), "matrix"))
})

## .... Positive semidefinite but not positive definite .................
A2 <- A1
A2[1L, ] <- A2[, 1L] <- 0
A2
try(Cholesky(A2, perm = FALSE)) # fails as not positive definite
ch.A2 <- Cholesky(A2) # returns, with a warning and ...
A2.hat <- Reduce("%*%", expand2(ch.A2, LDL = FALSE))
norm(A2 - A2.hat, "2") / norm(A2, "2") # 7.678858e-17

## .... Not positive semidefinite ......................................
A3 <- A1
A3[1L, ] <- A3[, 1L] <- -1
A3
try(Cholesky(A3, perm = FALSE)) # fails as not positive definite
ch.A3 <- Cholesky(A3) # returns, with a warning and ...
A3.hat <- Reduce("%*%", expand2(ch.A3, LDL = FALSE))
norm(A3 - A3.hat, "2") / norm(A3, "2") # 1.781568

## Indeed, 'A3' is not positive semidefinite, but 'A3.hat' _is_
ch.A3.hat <- Cholesky(A3.hat)
A3.hat.hat <- Reduce("%*%", expand2(ch.A3.hat, LDL = FALSE))

## ---- Sparse ---------------------------------------------------------
## Really just three cases modulo permutation :
##
## | type | factorization | minors of P1 A P1' |
##|------|--------------|-------------------|
##| 1 simplicial | P1 A P1' = L1 D L1' | nonzero |
##| 2 simplicial | P1 A P1' = L L' | positive |
##| 3 supernodal | P1 A P2' = L L' | positive |

data(KNex, package = "Matrix")
A4 <- crossprod(KNex[["mm"]])
ch.A4 <-
list(pivoted = list(simpl11 = Cholesky(A4, perm = TRUE, super = FALSE, LDL = TRUE),
simpl01 = Cholesky(A4, perm = TRUE, super = FALSE, LDL = FALSE),
...
Cholesky-methods

\[
\text{super0 = Cholesky(A4, perm = TRUE, super = TRUE })
\]

\[
\text{unpivoted = list(simpl1 = Cholesky(A4, perm = FALSE, super = FALSE, LDL = TRUE),}
\text{simpl0 = Cholesky(A4, perm = FALSE, super = FALSE, LDL = FALSE),}
\text{super0 = Cholesky(A4, perm = FALSE, super = TRUE })]
\]

ch.A4

\[
s <- simplify2array
rapply2 <- function(object, f, ...) rapply(object, f, , , how = "list", ...)
\]

\[
s(rapply2(ch.A4, isLDL))
\]

\[
s(m.ch.A4 <- rapply2(ch.A4, expand1, "L")) # giving L = L1 sqrt(D)
\]

## By design, the pivoted and simplicial factorizations
## are more sparse than the unpivoted and supernodal ones ...

\[
s(rapply2(m.ch.A4, object.size))
\]

## Which is nicely visualized by lattice-based methods for 'image'
inm <- c("pivoted", "unpivoted")
jnm <- c("simpl1", "simpl0", "super0")
for(i in 1:2)
  for(j in 1:3)
    print(image(m.ch.A4[[c(i, j)]]), main = paste(inm[i], jnm[j]),
            split = c(j, i, 3L, 2L), more = i * j < 6L)

simpl1 <- ch.A4[[c("pivoted", "simpl1")]]
stopifnot(exprs = {
  length(simpl1@perm) == ncol(A4)
  isPerm(simpl1@perm, 0L)
  is.unsorted(simpl1@perm) # typically not the identity permutation
})

## One can expand with and without D regardless of isLDL(.),
## but "without" requires L = L1 sqrt(D), which is conditional
## on min(diag(D)) >= 0, hence "with" is the default

isLDL(simpl1)
stopifnot(min(diag(simpl1)) >= 0)

\[
\text{str(e.ch.A4 <- expand2(simpl1, LDL = TRUE), max.level = 2L) # default}
\]

\[
\text{str(E.ch.A4 <- expand2(simpl1, LDL = FALSE), max.level = 2L)}
\]

stopifnot(exprs = {
  all.equal(E.ch.A4["L" ], e.ch.A4[["L1" ]] %*% sqrt(e.ch.A4[["D"]]))
  all.equal(E.ch.A4["L."] , sqrt(e.ch.A4[["D"]])) %*% e.ch.A4[["L1."]])
  all.equal(A4, as(Reduce(\%\%", e.ch.A4), "symmetricMatrix"))
  all.equal(A4, as(Reduce(\%\%", E.ch.A4), "symmetricMatrix"))
})

## The "same" permutation matrix with "alternate" representation
## [i, perm[i]] {margin=1} <-> [invertPerm(perm)[j], j} {margin=2}

alt <- function(P) {
  P@margin <- 1L + !(P@margin - 1L) # 1 <-> 2
  P@perm <- invertPerm(P@perm)
P
}

## Expansions are elegant but inefficient (transposes are redundant)
## hence programmers should consider methods for 'expand1' and 'diag'

stopifnot(exprs = {
...
identical(expand1(simpl1, "P1"), alt(e.ch.A4["P1"], E.ch.A4["P1"]))
identical(expand1(simpl1, "L"), E.ch.A4["L"], Diagonal(x = diag(simpl1), e.ch.A4["D"]))

## chol(A, pivot = value) is a simple wrapper around
## Cholesky(A, perm = value, LDL = FALSE, super = FALSE),
## returning L = sqrt(D) L1 _but_ giving no information
## about the permutation P1
selectMethod("chol", "dsCMatrix")
stopifnot(all.equal(chol(A4, pivot = TRUE), E.ch.A4["L."]))

## Now a symmetric matrix with positive _and_ negative eigenvalues,
## hence _not_ positive semidefinite
A5 <- new("dsCMatrix",
  Dim = c(7L, 7L),
  p = c(0:1, 3L, 6:7, 10:11, 15L),
  i = c(0L, 0:1, 0:3, 2:5, 3:6),
  x = c(1, 6, 38, 10, 60, 103, -4, 6, -32, -247, -2, -16, -128, -2, -67))
(ev <- eigen(A5, only.values = TRUE)$values)
(t.ev <- table(factor(sign(ev), -1:1))) # the matrix "inertia"
ch.A5 <- Cholesky(A5)
isLDL(ch.A5)
(d.A5 <- diag(ch.A5)) # diag(D) is partly negative

## Sylvester’s law of inertia holds here, but not in general
## in finite precision arithmetic
stopifnot(identical(table(factor(sign(d.A5), -1:1)), t.ev))
try(expand1(ch.A5, "L")) # unable to compute L = L1 sqrt(D)
try(expand2(ch.A5, LDL = FALSE)) # ditto
try(chol(A5, pivot = TRUE)) # ditto

## The default expansion is "square root free" and still works here
str(e.ch.A5 <- expand2(ch.A5, LDL = TRUE, max.level = 2L))
stopifnot(all.equal(A5, as(Reduce(`%*%`, e.ch.A5), "symmetricMatrix")))

## Version of the SuiteSparse library, which includes CHOLMOD
Mv <- Matrix.Version()
Mv["SuiteSparse"]

---

**Description**

Since 2005, package **Matrix** has supported coercions to and from class **graph** from package **graph**. Since 2013, this functionality has been exposed via functions **T2graph** and **graph2T**, which, unlike methods for **as**(from, "<Class>"), support optional arguments.

**Usage**

```r
graph2T(from, use.weights = )
T2graph(from, need.uniq = !isUniqueT(from), edgemode = NULL)
```
Arguments

from for graph2T(), an R object of class "graph";
for T2graph(), a sparse matrix inheriting from "TsparseMatrix".

use.weights logical indicating if weights should be used, i.e., equivalently the result will be
numeric, i.e. of class dgTMatrix; otherwise the result will be ngTMatrix or
nsTMatrix, the latter if the graph is undirected. The default looks if there are
weights in the graph, and if any differ from 1, weights are used.

need.uniq a logical indicating if from may need to be internally “uniqified”; do not set this
and hence rather use the default, unless you know what you are doing!

edgemode one of NULL, "directed", or "undirected". The default NULL looks if the
matrix is symmetric and assumes "undirected" in that case.

Value

For graph2T(), a sparse matrix inheriting from "TsparseMatrix".
For T2graph() an R object of class "graph".

See Also

Package igraph, which provides similar coercions to and from its class igraph via functions
graph_from_adjacency_matrix and as_adjacency_matrix.

Examples

if(requireNamespace("igraph")) {
  n4 <- LETTERS[1:4]; dns <- list(n4,n4)
  show(a1 <- sparseMatrix(i= c(1:4), j=c(2:4,1), x = 2, dimnames=dns))
  show(g1 <- as(a1, "graph")) # directed
  unlist(graph::edgeWeights(g1)) # all '2'

  show(a2 <- sparseMatrix(i= c(1:4,4), j=c(2:4,1:2), x = TRUE, dimnames=dns))
  show(g2 <- as(a2, "graph")) # directed
  # now if you want it undirected:
  show(g3 <- T2graph(as(a2,"TsparseMatrix"), edgemode="undirected"))
  show(m3 <- as(g3,"Matrix"))
  show( graph2T(g3) ) # a "pattern Matrix" (nsTMatrix)

  a. <- sparseMatrix(i=4:1, j=1:4, dimnames=list(n4, n4), repr="T") # no 'x'
  show(a.) # "ngTMatrix"
  show(g. <- as(a., "graph"))
  }

---

coerce-methods-SparseM

Sparse Matrix Coercion from and to those from package SparseM
Methods for coercion from and to sparse matrices from package SparseM are provided here, for ease of porting functionality to the Matrix package, and comparing functionality of the two packages. All these work via the usual as(. , "<class>") coercion,

\[
as(\text{from}, \text{Class})
\]

Methods

\[
\text{from} = \"\text{matrix.csr}\", \text{to} = \"\text{dgRMatrix}\" \\
\text{from} = \"\text{matrix.csc}\", \text{to} = \"\text{dgCMatrix}\" \\
\text{from} = \"\text{matrix.coo}\", \text{to} = \"\text{dgTMatrix}\" \\
\text{from} = \"\text{dgRMatrix}\", \text{to} = \"\text{matrix.csr}\" \\
\text{from} = \"\text{dgCMatrix}\", \text{to} = \"\text{matrix.csc}\" \\
\text{from} = \"\text{dgTMatrix}\", \text{to} = \"\text{matrix.coo}\" \\
\text{from} = \"\text{Matrix}\", \text{to} = \"\text{matrix.csr}\" \\
\text{from} = \"\text{matrix.csr}\", \text{to} = \"\text{dgCMatrix}\" \\
\text{from} = \"\text{matrix.coo}\", \text{to} = \"\text{dgCMatrix}\" \\
\text{from} = \"\text{matrix.csr}\", \text{to} = \"\text{Matrix}\" \\
\text{from} = \"\text{matrix.csc}\", \text{to} = \"\text{Matrix}\" \\
\text{from} = \"\text{matrix.coo}\", \text{to} = \"\text{Matrix}\"
\]

See Also

The documentation in CRAN package SparseM, such as SparseM.ontology, and one important class, matrix.csr.

---

Form Row and Column Sums and Means

Description

Form row and column sums and means for objects, for sparseMatrix the result may optionally be sparse (sparseVector), too. Row or column names are kept respectively as for base matrices and colSums methods, when the result is numeric vector.

Usage

\[
\text{colSums}(x, \text{na.rm} = \text{FALSE}, \text{dims} = 1L, \ldots) \\
\text{rowSums}(x, \text{na.rm} = \text{FALSE}, \text{dims} = 1L, \ldots) \\
\text{colMeans}(x, \text{na.rm} = \text{FALSE}, \text{dims} = 1L, \ldots) \\
\text{rowMeans}(x, \text{na.rm} = \text{FALSE}, \text{dims} = 1L, \ldots)
\]

\[
\text{colSums}(x, \text{na.rm} = \text{FALSE}, \text{dims} = 1L, \text{sparseResult} = \text{FALSE}, \ldots) \\
\text{rowSums}(x, \text{na.rm} = \text{FALSE}, \text{dims} = 1L, \ldots)
\]
Arguments

x  a Matrix, i.e., inheriting from Matrix.
na.rm logical. Should missing values (including NaN) be omitted from the calculations?
dims  completely ignored by the Matrix methods.
...  potentially further arguments, for method <-> generic compatibility.
sparseResult logical indicating if the result should be sparse, i.e., inheriting from class sparseVector. Only applicable when x is inheriting from a sparseMatrix class.

Value

returns a numeric vector if sparseResult is FALSE as per default. Otherwise, returns a sparseVector.

dimnames(x) are only kept (as names(v)) when the resulting v is numeric, since sparseVectors do not have names.

See Also
colSums and the sparseVector classes.

Examples

(M <- bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))) # 7 x 8
colSums(M)
d <- Diagonal(10, c(0,0,10,0,2,rep(0,5)))
MM <- kronecker(d, M)
dim(MM) # 70 80
length(MM@x) # 160, but many are '0'; drop those:
MM <- drop0(MM)
length(MM@x) # 32

cm <- colSums(MM)
(scm <- colSums(MM, sparseResult = TRUE))
stopifnot(is(scm, "sparseVector"),
  identical(cm, as.numeric(scm)))

rowSums (MM, sparseResult = TRUE) # 14 of 70 are not zero
colMeans(MM, sparseResult = TRUE) # 16 of 80 are not zero

## Since we have no 'NA's, these two are equivalent:
stopifnot(identical(rowMeans(MM, sparseResult = TRUE),
  rowMeans(MM, sparseResult = TRUE, na.rm = TRUE)),
  rowMeans(Diagonal(16)) == 1/16,
  colSums(Diagonal(7)) == 1)

## dimnames(x) --> names(<value> )

dimnames(M) <- list(paste0("r", 1:7), paste0("V",1:8))
M
## Assertions:

```r
## Assertions:
stopifnot(exprs = {
  all.equal(colSums(M),
    structure(c(1,1,6,6,6,6,3,2), names = colnames(M)))
  all.equal(rowMeans(M),
    structure(c(1,1,4,8,12,3,2)/8, names = paste0("r", 1:7)))
})
```

---

### Description

Virtual class of *composite* matrices; i.e., matrices that can be *factorized*, typically as a product of simpler matrices.

### Objects from the Class

A virtual Class: No objects may be created from it.

### Slots

- **factors**: Object of class "list" - a list of factorizations of the matrix. Note that this is typically empty, i.e., `list()`, initially and is *updated automagically* whenever a matrix factorization is computed.

- **Dim, Dimnames**: inherited from the `Matrix` class, see there.

### Extends

Class "Matrix", directly.

### Methods

- **dimnames<-**: signature(x = "compMatrix", value = "list"): set the dimnames to a *list* of length 2, see `dimnames<-`. The factors slot is currently reset to empty, as the factorization dimnames would have to be adapted, too.

### See Also

The matrix factorization classes "MatrixFactorization" and their generators, `lu()`, `qr()`, `chol()` and `Cholesky()`, `BunchKaufman()`, `Schur()`.
**condest**

*Compute Approximate CONDition number and 1-Norm of (Large) Matrices*

**Description**

“Estimate”, i.e. compute approximately the CONDition number of a (potentially large, often sparse) matrix $A$. It works by apply a fast randomized approximation of the 1-norm, \( \|A\|_1 \), through `onenormest(.)`.

**Usage**

```r
condest(A, t = min(n, 5), normA = norm(A, "1"), silent = FALSE, quiet = TRUE)

onenormest(A, t = min(n, 5), A.x, At.x, n, silent = FALSE, quiet = silent, iter.max = 10, eps = 4 * .Machine$double.eps)
```

**Arguments**

- **A**
  - a square matrix, optional for `onenormest()`, where instead of $A$, $A.x$ and $At.x$ can be specified, see there.
- **t**
  - number of columns to use in the iterations.
- **normA**
  - number; (an estimate of) the 1-norm of $A$, by default `norm(A, "1")`; may be replaced by an estimate.
- **silent**
  - logical indicating if warning and (by default) convergence messages should be displayed.
- **quiet**
  - logical indicating if convergence messages should be displayed.
- **A.x, At.x**
  - when $A$ is missing, these two must be given as functions which compute $A \times x$, or $t(A) \times x$, respectively.
- **n**
  - $n = \text{ncol}(A)$, only needed when $A$ is not specified.
- **iter.max**
  - maximal number of iterations for the 1-norm estimator.
- **eps**
  - the relative change that is deemed irrelevant.

**Details**

`condest()` calls `lu(A)`, and subsequently `onenormest(A.x = , At.x = )` to compute an approximate norm of the inverse of $A$, $A^{-1}$, in a way which keeps using sparse matrices efficiently when $A$ is sparse.

Note that `onenormest()` uses random vectors and hence both functions’ results are random, i.e., depend on the random seed, see, e.g., `set.seed()`.

**Value**

Both functions return a list; `condest()` with components,

- **est**
  - a number $> 0$, the estimated (1-norm) condition number $\hat{\kappa}$; when $r := rcond(A), 1/\hat{\kappa} \approx r$.
The maximal $Ax$ column, scaled to $\text{norm}(v) = 1$. Consequently, $\text{norm}(Av) = \text{norm}(A) / \text{est}$; when $\text{est}$ is large, $v$ is an approximate null vector.

The function `onenormest()` returns a list with components,

- `est` a number $> 0$, the estimated $\text{norm}(A, "1")$.
- `v` 0-1 integer vector length $n$, with an 1 at the index $j$ with maximal column $A[,j]$ in $A$.
- `w` numeric vector, the largest $Ax$ found.
- `iter` the number of iterations used.

Author(s)

This is based on octave’s `condest()` and `onenormest()` implementations with original author Jason Riedy, U Berkeley; translation to R and adaption by Martin Maechler.

References


See Also

`norm`, `rcond`.

Examples

data(KNex, package = "Matrix")
mtn <- with(KNex, crossprod(mm))
system.time(ce <- condest(mtm))
sum(abs(ce$v)) # | | v | |_1 == 1
## Prove that | | A v | | = | | A | | / est (as | |v| | = 1):
stopifnot(all.equal(norm(mtm %*% ce$v),
                 norm(mtm) / ce$est))

## reciprocal
1 / ce$est
system.time(rc <- rcond(mtm)) # takes ca 3 x longer
rc
all.equal(rc, 1/ce$est) # TRUE -- the approximation was good

one <- onenormest(mtm)
str(one) # est = 12.3
## the maximal column:
which(one$v == 1) # mostly 4, rarely 1, depending on random seed
CsparseMatrix-class

Class "CsparseMatrix" of Sparse Matrices in Column-compressed Form

Description

The "CsparseMatrix" class is the virtual class of all sparse matrices coded in sorted compressed column-oriented form. Since it is a virtual class, no objects may be created from it. See showClass("CsparseMatrix") for its subclasses.

Slots

i: Object of class "integer" of length nnzero (number of non-zero elements). These are the 0-based row numbers for each non-zero element in the matrix, i.e., i must be in 0:(nrow(.)-1).

p: integer vector for providing pointers, one for each column, to the initial (zero-based) index of elements in the column. .@p is of length ncol(.)+1, with p[1] == 0 and p[length(p)] == nnzero, such that in fact, diff(.@p) are the number of non-zero elements for each column.

In other words, m@p[1:ncol(m)] contains the indices of those elements in m@x that are the first elements in the respective column of m.

Dim, Dimnames: inherited from the superclass, see the sparseMatrix class.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

matrix products %*%, crossprod() and tcrossprod(), several solve methods, and other matrix methods available:

signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

Arith signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

Math signature(x = "CsparseMatrix"): ...

band signature(x = "CsparseMatrix"): ...

- signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

- signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

+ signature(e1 = "CsparseMatrix", e2 = "numeric"): ...

+ signature(e1 = "numeric", e2 = "CsparseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "TsparseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "denseMatrix"): ...

coerce signature(from = "CsparseMatrix", to = "matrix"): ...

coeff signature(from = "TsparseMatrix", to = "CsparseMatrix"): ...

coeff signature(from = "denseMatrix", to = "CsparseMatrix"): ...

diag signature(x = "CsparseMatrix"): ...

gamma signature(x = "CsparseMatrix"): ...

lgamma signature(x = "CsparseMatrix"): ...
```r
log signature(x = "CsparseMatrix"): ...

t signature(x = "CsparseMatrix"): ...

tril signature(x = "CsparseMatrix"): ...

triu signature(x = "CsparseMatrix"): ...
```

**Note**

All classes extending `CsparseMatrix` have a common validity (see `validObject`) check function. That function additionally checks the i slot for each column to contain increasing row numbers. In earlier versions of `Matrix` (<= 0.999375-16), `validObject` automatically re-sorted the entries when necessary, and hence `new()` calls with somewhat permuted `i` and `x` slots worked, as `new(...)` (with slot arguments) automatically checks the validity.

Now, you have to use `sparseMatrix` to achieve the same functionality or know how to use `.validateCsparse()` to do so.

**See Also**

`colSums`, `kronecker`, and other such methods with own help pages.

Further, the super class of `CsparseMatrix`, `sparseMatrix`, and, e.g., class `dgCMatrix` for the links to other classes.

**Examples**

```r
class("CsparseMatrix")
```

```r
## The common validity check function (based on C code):
getValidity(class("CsparseMatrix"))
```

---

**ddenseMatrix-class**

**Virtual Class** "ddenseMatrix" **of Numeric Dense Matrices**

**Description**

This is the virtual class of all dense numeric (i.e., `double`, hence "`ddense`") S4 matrices. Its most important subclass is the `dgeMatrix` class.

**Extends**

Class "`dMatrix`" directly; class "`Matrix`", by the above.

**Slots**

the same slots at its subclass `dgeMatrix`, see there.

**Methods**

Most methods are implemented via `as(*, "generalMatrix")` and are mainly used as "fallbacks" when the subclass doesn’t need its own specialized method.

Use `showMethods(class = "ddenseMatrix", where = "package:Matrix")` for an overview.
See Also

The virtual classes Matrix, dMatrix, and dsparseMatrix.

Examples

showClass("ddenseMatrix")

showMethods(class = "ddenseMatrix", where = "package:Matrix")
denseLU-class

Dense LU Factorizations

Description

denseLU is the class of dense, row-pivoted LU factorizations of \( m \times n \) real matrices \( A \), having the general form

\[
P_1 A = LU
\]

or (equivalently)

\[
A = P_1'LU
\]

where \( P_1 \) is an \( m \times m \) permutation matrix, \( L \) is an \( m \times \min(m, n) \) unit lower trapezoidal matrix, and \( U \) is a \( \min(m, n) \times n \) upper trapezoidal matrix. If \( m = n \), then the factors \( L \) and \( U \) are triangular.

Slots

- \( \text{Dim, Dimnames} \) inherited from virtual class \text{MatrixFactorization}.
- \( \text{x} \) a numeric vector of length \( \prod(\text{Dim}) \) storing the triangular \( L \) and \( U \) factors together in a packed format. The details of the representation are specified by the manual for LAPACK routine \text{dgetrf}.
- \( \text{perm} \) an integer vector of length \( \min(\text{Dim}) \) specifying the permutation \( P_1 \) as a product of transpositions. The corresponding permutation vector can be obtained as \text{asPerm}(\text{perm})

Extends

Class \text{LU}, directly. Class \text{MatrixFactorization}, by class \text{LU}, distance 2.

Instantiation

Objects can be generated directly by calls of the form \text{new("denseLU", ...)}, but they are more typically obtained as the value of \text{lu(x)} for \( x \) inheriting from \text{denseMatrix} (often \text{dgeMatrix}).
denseLU-class

Methods

coerce signature(from = "denseLU", to = "dgeMatrix"): returns a dgeMatrix with the dimensions of the factorized matrix \( A \), equal to \( L \) below the diagonal and equal to \( U \) on and above the diagonal.

determinant signature(from = "denseLU", logarithm = "logical"): computes the determinant of the factorized matrix \( A \) or its logarithm.

expand signature(x = "denseLU"): see expand-methods.

expand1 signature(x = "denseLU"): see expand1-methods.

expand2 signature(x = "denseLU"): see expand2-methods.

solve signature(a = "denseLU", b = "missing"): see solve-methods.

References

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgetrf.f.


See Also

Class sparseLU for sparse LU factorizations.

Class dgeMatrix.

Generic functions lu, expand1 and expand2.

Examples

showClass("denseLU")

set.seed(1)

n <- 3L

(A <- Matrix(round(rnorm(n * n), 2L), n, n))

## With dimnames, to see that they are propagated :

dimnames(A) <- dn <- list(paste0("r", seq_len(n)),
                        paste0("c", seq_len(n)))

(lu.A <- lu(A))

str(e.lu.A <- expand2(lu.A), max.level = 2L)

## Underlying LAPACK representation

(m.lu.A <- as(lu.A, "dgeMatrix")) # which is L and U interlaced

stopifnot(identical(as(m.lu.A, "matrix"), `dim<-`(l.u.A@x, l.u.A@Dim)))

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)

ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' L U in floating point

stopifnot(exprs = {
    identical(names(e.lu.A), c("P1.", "L", "U"))
    identical(e.lu.A[['P1.']],
        new("pMatrix", Dim = c(n, n), Dimnames = c(dn[1L], list(NULL)),
            margin = 1L, perm = invertPerm(asPerm(lu.A@perm))))
})
identical(e.lu.A[["L"]],
    new("dtrMatrix", Dim = c(n, n), Dimnames = list(NULL, NULL),
        uplo = "L", diag = "U", x = lu.A@x))
identical(e.lu.A[["U"]],
    new("dtrMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
        uplo = "U", diag = "N", x = lu.A@x))
ae1(A, with(e.lu.A, P1. %*% L %*% U))
ae2(A[asPerm(lu.A@perm), ], with(e.lu.A, L %*% U))
})
## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(identical(det(A), det(lu.A)),
    identical(solve(A, b), solve(lu.A, b)))

denseMatrix-class

Virtual Class "denseMatrix" of All Dense Matrices

Description

This is the virtual class of all dense (S4) matrices. It partitions into two subclasses \texttt{packedMatrix} and \texttt{unpackedMatrix}. Alternatively into the (currently) three subclasses \texttt{ddenseMatrix}, \texttt{ldenseMatrix}, and \texttt{ndenseMatrix}.
denseMatrix is (hence) the direct superclass of these (\(2 + 3 = 5\)) classes.

Extends

class "Matrix" directly.

Slots

exactly those of its superclass "Matrix", i.e., "Dim" and "Dimnames".

Methods

Use \texttt{showMethods(class = "denseMatrix", where = "package:Matrix")} for an overview of
methods.

Extraction ("\[\]" methods, see \texttt{\[-methods\].

See Also

\texttt{colSums}, \texttt{kronecker}, and other such methods with own help pages.

Its superclass \texttt{Matrix}, and main subclasses, \texttt{ddenseMatrix} and \texttt{sparseMatrix}.

Examples

\texttt{showClass("denseMatrix")}
The **dgCMatrix** class is a class of sparse numeric matrices in the compressed, sparse, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order. **dgCMatrix** is the "standard" class for sparse numeric matrices in the **Matrix** package.

**Objects from the Class**

Objects can be created by calls of the form `new("dgCMatrix", ...),` more typically via `as(*, "CsparseMatrix")` or similar. Often however, more easily via `Matrix(*, sparse = TRUE),` or most efficiently via `sparseMatrix().`

**Slots**

- `x`: Object of class "numeric" - the non-zero elements of the matrix.
- `...`: all other slots are inherited from the superclass "CsparseMatrix".

**Methods**

- Matrix products (e.g., `crossprod-methods`), and (among other)
  - `coerce` signature(`from = "matrix", to = "dgCMatrix"`)
  - `diag` signature(`x = "dgCMatrix")`: returns the diagonal of `x`
  - `dim` signature(`x = "dgCMatrix")`: returns the dimensions of `x`
  - `image` signature(`x = "dgCMatrix")`: plots an image of `x` using the `levelplot` function
  - `solve` signature(`a = "dgCMatrix", b = "..."): see `solve-methods`, notably the extra argument `sparse`.
  - `lu` signature(`x = "dgCMatrix")`: computes the LU decomposition of a square `dgCMatrix` object

**See Also**

Classes `dsCMatrix, dtCMatrix, lu`

**Examples**

```r
(m <- Matrix(c(0,0,2:0), 3,5))
str(m)
m[,1]
```
dgeMatrix-class

Class "dgeMatrix" of Dense Numeric (S4 Class) Matrices

Description

A general numeric dense matrix in the S4 Matrix representation. dgeMatrix is the “standard” class for dense numeric matrices in the Matrix package.

Objects from the Class

Objects can be created by calls of the form new("dgeMatrix", ...) or, more commonly, by coercion from the Matrix class (see Matrix) or by Matrix(...).

Slots

x: Object of class "numeric" - the numeric values contained in the matrix, in column-major order.

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: a list of length two - inherited from class Matrix.

factors: Object of class "list" - a list of factorizations of the matrix.

Methods

The are group methods (see, e.g., Arith)

Arith signature(e1 = "dgeMatrix", e2 = "dgeMatrix"): ...

Arith signature(e1 = "dgeMatrix", e2 = "numeric"): ...

Arith signature(e1 = "numeric", e2 = "dgeMatrix"): ...

Math signature(x = "dgeMatrix"): ...

Math2 signature(x = "dgeMatrix", digits = "numeric"): ...

matrix products %*%, crossprod() and tcrossprod(), several solve methods, and other matrix methods available:

Schur signature(x = "dgeMatrix", vectors = "logical"): ...

Schur signature(x = "dgeMatrix", vectors = "missing"): ...

colMeans signature(x = "dgeMatrix"): columnwise means (averages)

colSums signature(x = "dgeMatrix"): columnwise sums

diag signature(x = "dgeMatrix"): ...

dim signature(x = "dgeMatrix"): ...

dimnames signature(x = "dgeMatrix"): ...

eigen signature(x = "dgeMatrix", only.values= "logical"): ...

eigen signature(x = "dgeMatrix", only.values= "missing"): ...

norm signature(x = "dgeMatrix", type = "character"): ...

norm signature(x = "dgeMatrix", type = "missing"): ...
The `dgRMatrix` class is a class of sparse numeric matrices in the compressed, sparse, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

**Note:** The column-oriented sparse classes, e.g., `dgCMatrix`, are preferred and better supported in the `Matrix` package.

**Objects from the Class**

Objects can be created by calls of the form `new("dgRMatrix", ...)`. 

**Slots**

- `j`: Object of class "integer" of length `nnzero` (number of non-zero elements). These are the column numbers for each non-zero element in the matrix.
- `p`: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.
- `x`: Object of class "numeric" - the non-zero elements of the matrix.
- `Dim`: Object of class "integer" - the dimensions of the matrix.

**Methods**

- `diag` signature(x = "dgRMatrix"): returns the diagonal of x
- `dim` signature(x = "dgRMatrix"): returns the dimensions of x
- `image` signature(x = "dgRMatrix"): plots an image of x using the levelplot function

**See Also**

the RsparseMatrix class, the virtual class of all sparse compressed row-oriented matrices, with its methods. The `dgCMatrix` class (column compressed sparse) is really preferred.
**Description**

The "dgTMatrix" class is the class of sparse matrices stored as (possibly redundant) triplets. The internal representation is not at all unique, contrary to the one for class \texttt{dgCMatrix}.

**Objects from the Class**

Objects can be created by calls of the form \texttt{new("dgTMatrix", ...),} but more typically via \texttt{spMatrix()} or \texttt{sparseMatrix(*, repr = "T").}

**Slots**

- \texttt{i}: integer row indices of non-zero entries in 0-base, i.e., must be in $0:(\text{nrow(\cdot)-1})$.
- \texttt{j}: integer column indices of non-zero entries. Must be the same length as slot \texttt{i} and 0-based as well, i.e., in $0:(\text{ncol(\cdot)-1})$.
- \texttt{x}: numeric vector - the (non-zero) entry at position $(i, j)$. Must be the same length as slot \texttt{i}. If an index pair occurs more than once, the corresponding values of slot \texttt{x} are added to form the element of the matrix.
- \texttt{Dim}: Object of class "integer" of length 2 - the dimensions of the matrix.

**Methods**

- \texttt{+} signature(e1 = "dgTMatrix", e2 = "dgTMatrix")
- \texttt{image} signature(x = "dgTMatrix"): plots an image of \texttt{x} using the \texttt{levelplot} function
- \texttt{t} signature(x = "dgTMatrix"): returns the transpose of \texttt{x}

**Note**

Triplet matrices are a convenient form in which to construct sparse matrices after which they can be coerced to \texttt{dgCMatrix} objects.

Note that both \texttt{new(.)} and \texttt{spMatrix} constructors for "dgTMatrix" (and other "TsparseMatrix" classes) implicitly add \texttt{x_k’s} that belong to identical $(i_k, j_k)$ pairs.

However this means that a matrix typically can be stored in more than one possible "TsparseMatrix" representations. Use \texttt{asUniqueT()} in order to ensure uniqueness of the internal representation of such a matrix.

**See Also**

Class \texttt{dgCMatrix} or the superclasses \texttt{dsparseMatrix} and \texttt{TsparseMatrix}; \texttt{asUniqueT}. 
Examples

```r
m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[3, 1:4] <- 0
(mT <- as(m, "TsparseMatrix"))
str(mT)
mT[1,]
mT[4, drop = FALSE]
stopifnot(identical(mT[lower.tri(mT)],
   m [lower.tri(m) ]))
mT[lower.tri(mT, diag=TRUE)] <- 0
mT
```

```r
## Triplet representation with repeated (i,j) entries
## *adds* the corresponding x's:
T2 <- new("dgTMatrix",
   i = as.integer(c(1,1,0,3,3)),
   j = as.integer(c(2,2,4,0,0)), x=10*1:5, Dim=4:5)
str(T2) # contains (i,j,x) slots exactly as above, but
T2 ## has only three non-zero entries, as for repeated (i,j)'s,
   ## the corresponding x's are "implicitly" added
stopifnot(nnzero(T2) == 3)
```

Diagonal

**Construct a Diagonal Matrix**

Description

Construct a formally diagonal Matrix, i.e., an object inheriting from virtual class diagonalMatrix (or, if desired, a mathematically diagonal CsparseMatrix).

Usage

```r
Diagonal(n, x = NULL, names = FALSE)
.sparseDiagonal(n, x = NULL, uplo = "U", shape = "t", unitri = TRUE, kind, cols)
.trDiagonal(n, x = NULL, uplo = "U", unitri = TRUE, kind)
.symDiagonal(n, x = NULL, uplo = "U", kind)
```

Arguments

- `n` integer indicating the dimension of the (square) matrix. If missing, then `length(x)` is used.
- `x` numeric or logical vector listing values for the diagonal entries, to be recycled as necessary. If NULL (the default), then the result is a unit diagonal matrix. .sparseDiagonal() and friends ignore non-NULL x when kind = "n".
- `names` either logical TRUE or FALSE or then a character vector of length n. If true and names(x) is not NULL, use that as both row and column names for the resulting matrix. When a character vector, use it for both dimnames.
- `uplo` one of c("U", "L"), specifying the uplo slot of the result if the result is formally triangular of symmetric.
shape
  one of c("t","s","g"), indicating if the result should be formally triangular, symmetric, or "general". The result will inherit from virtual class triangularMatrix, symmetricMatrix, or generalMatrix, respectively.

unitri
  logical indicating if a formally triangular result with ones on the diagonal should be formally unit triangular, i.e., with diag slot equal to "U" rather than "N".

kind
  one of c("d","l","n"), indicating the "mode" of the result: numeric, logical, or pattern. The result will inherit from virtual class dsparseMatrix, lsparseMatrix, or nsparseMatrix, respectively. Values other than "n" are ignored when x is non-NULL; in that case the mode is determined by typeof(x).

cols
  optional integer vector with values in 0:(n-1), indexing columns of the specified diagonal matrix. If specified, then the result is (mathematically) D[, cols+1] rather than D, where D = Diagonal(n, x), and it is always "general" (i.e., shape is ignored).

Value

Diagonal() returns an object inheriting from virtual class diagonalMatrix.

.sparseDiagonal() returns a CsparseMatrix representation of Diagonal(n, x) or, if cols is given, of Diagonal(n, x)[, cols+1]. The precise class of the result depends on shape and kind.

.trDiagonal() and .symDiagonal() are simple wrappers, for .sparseDiagonal(shape = "t") and .sparseDiagonal(shape = "s"), respectively.

.sparseDiagonal() exists primarily to leverage efficient C-level methods available for CsparseMatrix.

Author(s)

Martin Maechler

See Also

the generic function diag for extraction of the diagonal from a matrix works for all "Matrices".

bandSparse constructs a banded sparse matrix from its non-zero sub-/super - diagonals. band(A) returns a band matrix containing some sub-/super - diagonals of A.

Matrix for general matrix construction; further, class diagonalMatrix.

Examples

Diagonal(3)
Diagonal(x = 10^(3:1))
Diagonal(x = (1:4) >= 2)# -> "ldiMatrix"

## Use Diagonal() + kronecker() for "repeated-block" matrices:
M1 <- Matrix(0+0:5, 2,3)
(M <- kronecker(Diagonal(3), M1))

(S <- crossprod(Matrix(rbinom(60, size=1, prob=0.1), 10,6)))
(SI <- S + 10*.symDiagonal(6)) # sparse symmetric still
stopifnot(is(SI, "dsCMatrix"))
(I4 <- .sparseDiagonal(4, shape="t"))# now (2012-10) unitriangular
stopifnot(I4@diag == "U", all(I4 == diag(4)))
diagonalMatrix-class

Class "diagonalMatrix" of Diagonal Matrices

Description

Class "diagonalMatrix" is the virtual class of all diagonal matrices.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

diag: character string, either "U" or "N", where "U" means 'unit-diagonal'.
Dim: matrix dimension, and
Dimnames: the dimnames, a list, see the Matrix class description. Typically list(NULL,NULL) for diagonal matrices.

Extends

Class "sparseMatrix", directly.

Methods

These are just a subset of the signature for which defined methods. Currently, there are (too) many explicit methods defined in order to ensure efficient methods for diagonal matrices.

coerce signature(from = "matrix", to = "diagonalMatrix"): ...
coerce signature(from = "Matrix", to = "diagonalMatrix"): ...
coerce signature(from = "diagonalMatrix", to = "generalMatrix"): ...
coerce signature(from = "diagonalMatrix", to = "triangularMatrix"): ...
coerce signature(from = "diagonalMatrix", to = "nMatrix"): ...
coerce signature(from = "diagonalMatrix", to = "matrix"): ...
coerce signature(from = "diagonalMatrix", to = "sparseVector"): ...
t signature(x = "diagonalMatrix"): ... and many more methods
solve signature(a = "diagonalMatrix", b, ...): is trivially implemented, of course; see also solve-methods.
which signature(x = "nMatrix"), semantically equivalent to base function which(x, arr.ind).
"Math" signature(x = "diagonalMatrix"): all these group methods return a "diagonalMatrix", apart from cumsum() etc which return a vector also for base matrix.
* signature(e1 = "ddiMatrix", e2="denseMatrix"): arithmetic and other operators from the Ops group have a few dozen explicit method definitions, in order to keep the results diagonal in many cases, including the following:
Signature(e1 = "ddiMatrix", e2="denseMatrix"): the result is from class ddiMatrix which is typically very desirable. Note that when e2 contains off-diagonal zeros or NAs, we implicitly use 0/x = 0, hence differing from traditional R arithmetic (where 0/0 → NaN), in order to preserve sparsity.

**summary** (object = "diagonalMatrix"): Returns an object of S3 class "diagSummary" which is the summary of the vector object@x plus a simple heading, and an appropriate print method.

**See Also**

Diagonal() as constructor of these matrices, and isDiagonal. ddiMatrix and ldiMatrix are “actual” classes extending "diagonalMatrix".

**Examples**

```r
I5 <- Diagonal(5)
D5 <- Diagonal(x = 10*(1:5))
## trivial (but explicitly defined) methods:
stopifnot(identical(crossprod(I5), I5),
  identical(tcrossprod(I5), I5),
  identical(crossprod(I5, D5), D5),
  identical(tcrossprod(D5, I5), D5),
  identical(solve(D5), solve(D5, I5)),
  all.equal(D5, solve(solve(D5)), tolerance = 1e-12)
)
solve(D5)# efficient as is diagonal
# an unusual way to construct a band matrix:
rbind2(cbind2(I5, D5),
  cbind2(D5, I5))
```

---

### diagU2N

**Transform Triangular Matrices from Unit Triangular to General Triangular and Back**

**Description**

Transform a triangular matrix x, i.e., of class triangularMatrix, from (internally)! unit triangular (“unitriangular”) to “general” triangular (diagU2N(x)) or back (diagN2U(x)). Note that the latter, diagN2U(x), also sets the diagonal to one in cases where diag(x) was not all one.

.diagU2N(x) and .diagN2U(x) assume without checking that x is a triangularMatrix with suitable diag slot ("U" and "N", respectively), hence they should be used with care.

**Usage**

```r
diagU2N(x, cl = getClassDef(class(x)), checkDense = FALSE)
diagN2U(x, cl = getClassDef(class(x)), checkDense = FALSE)
.diagU2N(x, cl = getClassDef(class(x)), checkDense = FALSE)
.diagN2U(x, cl = getClassDef(class(x)), checkDense = FALSE)
```
Arguments

x  a triangularMatrix, often sparse.
cl (optional, for speedup only:) class (definition) of x.
checkDense  logical indicating if dense (see denseMatrix) matrices should be considered at all; i.e., when false, as per default, the result will be sparse even when x is dense.

Details

The concept of unit triangular matrices with a diag slot of "U" stems from LAPACK.

Value

a triangular matrix of the same class but with a different diag slot. For diagU2N (semantically) with identical entries as x, whereas in diagN2U(x), the off-diagonal entries are unchanged and the diagonal is set to all 1 even if it was not previously.

Note

Such internal storage details should rarely be of relevance to the user. Hence, these functions really are rather internal utilities.

See Also

"triangularMatrix", "dtCMatrix".

Examples

(T <- Diagonal(7) + triu(Matrix(rpois(49, 1/4), 7, 7), k = 1))
(uT <- diagN2U(T)) # "unitriangular"
t.u <- diagN2U(10*T))# changes the diagonal!
stopifnot(all(T == uT), diag(t.u) == 1,
identical(T, diagU2N(uT)))
T[upper.tri(T)] <- 5 # still "dtC"
T <- diagN2U(as(T, "triangularMatrix"))
dT <- as(T, "denseMatrix") # (unitriangular)
dT.n <- diagU2N(dT, checkDense = TRUE)
sT.n <- diagU2N(dT)
stopifnot(is(dT.n, "denseMatrix"), is(sT.n, "sparseMatrix"),
dT@diag == "U", dT.n@diag == "N", sT.n@diag == "N",
all(dT == dT.n), all(dT == sT.n))
Usage

\[ \text{dimScale}(x, d1 = \sqrt{1/\text{diag}(x, \text{names} = \text{FALSE})}), \ d2 = d1) \]
\[ \text{rowScale}(x, d) \]
\[ \text{colScale}(x, d) \]

Arguments

- **x**: a matrix, possibly inheriting from virtual class `Matrix`.
- **d1, d2, d**: numeric vectors giving factors by which to scale the rows or columns of `x`; they are recycled as necessary.

Details

\[ \text{dimScale}(x) \] (with \(d1\) and \(d2\) unset) is only roughly equivalent to `cov2cor(x)`. `cov2cor` sets the diagonal entries of the result to 1 (exactly); `dimScale` does not.

Value

The result of scaling `x`, currently always inheriting from virtual class `dMatrix`.

It inherits from `triangularMatrix` if and only if `x` does. In the special case of `dimScale(x, d1, d2)` with identical `d1` and `d2`, it inherits from `symmetricMatrix` if and only if `x` does.

Author(s)

Mikael Jagan

See Also

cov2cor

Examples

```
n <- 6L
(x <- forceSymmetric(matrix(1, n, n)))
dimnames(x) <- rep.int(list(letters[seq_len(n)]), 2L)
d <- seq_len(n)
(D <- Diagonal(x = d))

(scx <- dimScale(x, d)) # symmetry and 'dimnames' kept
(mmx <- D %*% x %*% D) # symmetry and 'dimnames' lost
stopifnot(identical(unname(as(scx, "generalMatrix")), mmx))

rowScale(x, d)
colScale(x, d)
```
dMatrix-class

(Virtual) Class "dMatrix" of "double" Matrices

Description

The dMatrix class is a virtual class contained by all actual classes of numeric matrices in the Matrix package. Similarly, all the actual classes of logical matrices inherit from the lMatrix class.

Slots

Common to all matrix object in the package:

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: list of length two; each component containing NULL or a character vector length equal the corresponding Dim element.

Methods

There are (relatively simple) group methods (see, e.g., Arith)

Arith signature(e1 = "dMatrix", e2 = "dMatrix"): ...
Arith signature(e1 = "dMatrix", e2 = "numeric"): ...
Arith signature(e1 = "numeric", e2 = "dMatrix"): ...

Math signature(x = "dMatrix"): ...
Math2 signature(x = "dMatrix", digits = "numeric"): this group contains round() and signif().

Compare signature(e1 = "numeric", e2 = "dMatrix"): ...
Compare signature(e1 = "dMatrix", e2 = "numeric"): ...
Compare signature(e1 = "dMatrix", e2 = "dMatrix"): ...

Summary signature(x = "dMatrix"): The "Summary" group contains the seven functions max(), min(), range(), prod(), sum(), any(), and all().

The following methods are also defined for all double matrices:

expm signature(x = "dMatrix"): computes the "Matrix Exponential", see expm.

class signature(x = "dMatrix"): ...

The following methods are defined for all logical matrices:

which signature(x = "lsparseMatrix") and many other subclasses of "lMatrix": as the base function which(x, arr.ind) returns the indices of the TRUE entries in x; if arr.ind is true, as a 2-column matrix of row and column indices. Since Matrix version 1.2-9, if useNames is true, as by default, with dimnames, the same as base::which.

See Also

The nonzero-pattern matrix class nMatrix, which can be used to store non-NA logical matrices even more compactly.

The numeric matrix classes dgeMatrix, dgCMatrix, and Matrix.

drop0(x, tol=1e-10) is sometimes preferable to (and more efficient than) zapsmall(x, digits=10).
Examples

```r
showClass("dMatrix")

set.seed(101)
round(Matrix(rnorm(28), 4,7), 2)
M <- Matrix(rlnorm(56, sd=10), 4,14)
(M. <- zapsmall(M))
table(as.logical(M. == 0))
```

**dmperm**  
*Dulmage-Mendelsohn Permutation / Decomposition*

Description

For any $n \times m$ (typically) sparse matrix $x$ compute the Dulmage-Mendelsohn row and columns permutations which at first splits the $n$ rows and $m$ columns into coarse partitions each; and then a finer one, reordering rows and columns such that the permuted matrix is “as upper triangular” as possible.

Usage

```r
dmperm(x, nAns = 6L, seed = 0L)
```

Arguments

- **x**: a typically sparse matrix; internally coerced to either "dgCMatrix" or "dtCMatrix".
- **nAns**: an integer specifying the length of the resulting list. Must be 2, 4, or 6.
- **seed**: an integer code in -1,0,1; determining the (initial) permutation; by default, seed = 0, no (or the identity) permutation; seed = -1 uses the "reverse" permutation $k:1$; for seed = 1, it is a random permutation (using R’s RNG, seed, etc).

Details

See the book section by Tim Davis; page 122–127, in the References.

Value

- a named list with (by default) 6 components,
  - **p**: integer vector with the permutation $p$, of length nrow(x).
  - **q**: integer vector with the permutation $q$, of length ncol(x).
  - **r**: integer vector of length nb+1, where block $k$ is rows $r[k]$ to $r[k+1]-1$ in $A[p,q]$.
  - **s**: integer vector of length nb+1, where block $k$ is cols $s[k]$ to $s[k+1]-1$ in $A[p,q]$.
  - **rr5**: integer vector of length 5, defining the coarse row decomposition.
  - **cc5**: integer vector of length 5, defining the coarse column decomposition.

Author(s)

Martin Maechler, with a lot of “encouragement” by Mauricio Vargas.
References

Section 7.4 Dulmage-Mendelsohn decomposition, pp. 122 ff of
of Algorithms”.

See Also

Schur, the class of permutation matrices; "pMatrix".

Examples

```
set.seed(17)
(S9 <- rsparsematrix(9, 9, nnz = 10, symmetric=TRUE)) # dsCMatrix
str( dm9 <- dmperm(S9) )
(S9p <- with(dm9, S9[p, q]))
## looks good, but *not* quite upper triangular; these, too:
str(dm9.0 <- dmperm(S9, seed=-1)) # non-random too.
str(dm9.1 <- dmperm(S9, seed= 1)) # a random one
## The last two permutations differ, but have the same effect!
(S9p0 <- with(dm9.0, S9[p, q])) # .. hmm ..
stopifnot(all.equal(S9p0, S9p))# same as as default, but different from the random one

set.seed(11)
(M <- triu(rsparsematrix(9,11, 1/4)))
dM <- dmperm(M); with(dM, M[p, q])
(Mp <- M[sample.int(nrow(M)), sample.int(ncol(M))])
dMp <- dmperm(Mp); with(dMp, Mp[p, q])

set.seed(7)
(n7 <- rsparsematrix(5, 12, nnz = 10, rand.x = NULL))
str(dm.7 <- dmperm(n7 ))
stopifnot(exprs = {
    lengths(dm.7[1:2]) == dim(n7)
    identical(dm.7, dmperm(as(n7, "dMatrix")))
    identical(dm.7[1:4], dmperm(n7, nAns=4))
    identical(dm.7[1:2], dmperm(n7, nAns=2))
})
```

dpoMatrix-class

Positive Semi-definite Dense (Packed | Non-packed) Numeric Matrices

Description

The "dpoMatrix" class is the class of positive-semidefinite symmetric matrices in nonpacked
storage.

The "dppMatrix" class is the same except in packed storage. Only the upper triangle or the
lower triangle is required to be available.

The "corMatrix" and "pcorMatrix" classes represent correlation matrices. They extend
"dpoMatrix" and "dppMatrix", respectively, with an additional slot sd allowing restoration of
the original covariance matrix.
**Objects from the Class**

Objects can be created by calls of the form `new("dpoMatrix", ...)` or from `crossprod` applied to an "dgeMatrix" object.

**Slots**

- `uplo`: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- `x`: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.
- `Dim`: Object of class "integer". The dimensions of the matrix which must be a two-element vector of non-negative integers.
- `Dimnames`: inherited from class "Matrix".
- `factors`: Object of class "list". A named list of factorizations that have been computed for the matrix.
- `sd`: (for "corMatrix" and "pcorMatrix") a numeric vector of length `n` containing the (original) square root of the entries which allow reconstruction of a covariance matrix from the correlation matrix.

**Extends**

Class "dsyMatrix", directly.

Classes "dgeMatrix", "symmetricMatrix", and many more by class "dsyMatrix".

**Methods**

- `chol` signature(x = "dpoMatrix") : Returns (and stores) the Cholesky decomposition of `x`, see `chol`.
- `determinant` signature(x = "dpoMatrix") : Returns the determinant of `x`, via `chol(x)`, see above.
- `rcond` signature(x = "dpoMatrix", norm = "character") : Returns (and stores) the reciprocal of the condition number of `x`. The norm can be "O" for the one-norm (the default) or "I" for the infinity-norm. For symmetric matrices the result does not depend on the norm.
- `solve` signature(a = "dpoMatrix", b = "....") and `solve` signature(a = "dppMatrix", b = "....") work via the Cholesky composition, see also the Matrix `solve-methods`.

**Arith** signature(e1 = "dpoMatrix", e2 = "numeric") (and quite a few other signatures): The result of ("elementwise" defined) arithmetic operations is typically not positive-definite anymore. The only exceptions, currently, are multiplications, divisions or additions with positive length(.) == 1 numbers (or `logicals`).

**Note**

Currently the validity methods for these classes such as `getValidity(getClass("dpoMatrix"))` for efficiency reasons only check the diagonal entries of the matrix – they may not be negative. This is only necessary but not sufficient for a symmetric matrix to be positive semi-definite.

A more reliable (but often more expensive) check for positive semi-definiteness would look at the signs of `diag(BunchKaufman(.))` (with some tolerance for very small negative values), and for (strict) positive definiteness at something like `!inherits(tryCatch(chol(.),...`,
error=identity), "error"). Indeed, when coercing to these classes, a version of Cholesky() or chol() is typically used, e.g., see selectMethod("coerce", c(from="dsyMatrix", to="dpoMatrix")).

See Also

Classes dsyMatrix and dgeMatrix; further, Matrix, rcond, chol, solve, crossprod.

Examples

h6 <- Hilbert(6)
rcond(h6)
str(h6)
h6 * 27720 # is `integer'
solve(h6)
str(hp6 <- pack(h6))

### Note that as(*, "corMatrix") *scales* the matrix
(ch6 <- as(h6, "corMatrix"))
stopifnot(all.equal(as(h6 * 27720, "dsyMatrix"), round(27720 * h6),
                     tolerance = 1e-14),
        all.equal(ch6@sd^(-2), 2*(1:6)-1,
                     tolerance = 1e-12))

chch <- Cholesky(ch6, perm = FALSE)
stopifnot(identical(chch, ch6@factors$Cholesky),
          all(abs(crossprod(as(chch, "dtrMatrix")) - ch6) < 1e-10))

---

drop0

Drop Non-Structural Zeros from a Sparse Matrix

Description

Deletes “non-structural” zeros (i.e., zeros stored explicitly, in memory) from a sparse matrix and returns the result.

Usage

drop0(x, tol = 0, is.Csparse = NA, give.Csparse = TRUE)

Arguments

x a Matrix, typically inheriting from virtual class sparseMatrix. denseMatrix and traditional vectors and matrices are coerced to CsparseMatrix, with zeros dropped automatically, hence users passing such x should consider as(x, "CsparseMatrix") instead, notably in the tol = 0 case.

tol a non-negative number. If x is numeric, then entries less than or equal to tol in absolute value are deleted.

is.Csparse a logical used only if give.Csparse is TRUE, indicating if x already inherits from virtual class CsparseMatrix, in which case coercion is not attempted, permitting some (typically small) speed-up.

give.Csparse a logical indicating if the result must inherit from virtual class CsparseMatrix. If FALSE and x inherits from RsparseMatrix, TsparseMatrix, or indMatrix, then the result preserves the class of x. The default value is TRUE only for backwards compatibility.
Value

A `sparseMatrix`, the result of deleting non-structural zeros from `x`, possibly after coercion.

Note

drop0 is sometimes called in conjunction with `zapsmall`, e.g., when dealing with sparse matrix products; see the example.

See Also

Function `sparseMatrix`, for constructing objects inheriting from virtual class `sparseMatrix`; `nnzero`.

Examples

```r
(m <- sparseMatrix(i = 1:8, j = 2:9, x = c(0:2, 3:-1),
              dims = c(10L, 20L)))
drop0(m)
```

```r
## A larger example:
T5 <- new("dtCMatrix", Dim = c(5L, 5L), uplo = "L",
              x = c(10, 1, 3, 10, 1, 10, 1, 10, 10),
              i = c(0L,2L,4L, 1L, 3L,2L,4L, 3L, 4L),
              p = c(0L, 3L, 5L, 7:9))
TT <- kronecker(t5, kronecker(kronecker(t5, t5), t5))
IT <- solve(TT)
I. <- TT %x% IT ; nnzero(I.) # 697 ( == 625 + 72 )
I.0 <- drop0(zapsmall(I.))
## which actually can be more efficiently achieved by
I.. <- drop0(I., tol = 1e-15)
stopifnot(all(I.0 == Diagonal(625)), nnzero(I..) == 625)
```

---

dsCMatrix-class

**Numeric Symmetric Sparse (column compressed) Matrices**

Description

The `dsCMatrix` class is a class of symmetric, sparse numeric matrices in the compressed, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order.

The `dsTMatrix` class is the class of symmetric, sparse numeric matrices in triplet format.

Objects from the Class

Objects can be created by calls of the form `new("dsCMatrix",...)` or `new("dsTMatrix",...)`, or automatically via e.g., `as(*,"symmetricMatrix")`, or (for `dsCMatrix`) also from `Matrix(.)`. Creation “from scratch” most efficiently happens via `sparseMatrix(*, symmetric=TRUE)`.
Slots

- **uplo**: A character object indicating if the upper triangle ("U") or the lower triangle ("L") is stored.
- **i**: Object of class "integer" of length nnZ (half number of non-zero elements). These are the row numbers for each non-zero element in the lower triangle of the matrix.
- **p**: (only in class "dsCMatrix") an integer vector for providing pointers, one for each column, see the detailed description in CsparseMatrix.
- **j**: (only in class "dsTMatrix") Object of class "integer" of length nnZ (as i). These are the column numbers for each non-zero element in the lower triangle of the matrix.
- **x**: Object of class "numeric" of length nnZ – the non-zero elements of the matrix (to be duplicated for full matrix).
- **factors**: Object of class "list" - a list of factorizations of the matrix.
- **Dim**: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Extends

Both classes extend classes and symmetricMatrix dsparseMatrix directly; dsCMatrix further directly extends CsparseMatrix, where dsTMatrix does TsparseMatrix.

Methods

- **solve** signature(a = "dsCMatrix", b = "..."): x <- solve(a,b) solves \( Ax = b \) for \( x \); see solve-methods.
- **chol** signature(x = "dsCMatrix", pivot = "logical"): Returns (and stores) the Cholesky decomposition of \( x \), see chol.
- **Cholesky** signature(A = "dsCMatrix",...): Computes more flexibly Cholesky decompositions, see Cholesky.
- **determinant** signature(x = "dsCMatrix", logarithm = "missing"): Evaluate the determinant of \( x \) on the logarithm scale. This creates and stores the Cholesky factorization.
- **determinant** signature(x = "dsCMatrix", logarithm = "logical"): Evaluate the determinant of \( x \) on the logarithm scale or not, according to the logarithm argument. This creates and stores the Cholesky factorization.
- **t** signature(x = "dsCMatrix"): Transpose. As for all symmetric matrices, a matrix for which the upper triangle is stored produces a matrix for which the lower triangle is stored and vice versa, i.e., the uplo slot is swapped, and the row and column indices are interchanged.
- **t** signature(x = "dsTMatrix"): Transpose. The uplo slot is swapped from "U" to "L" or vice versa, as for a "dsCMatrix", see above.

See Also

Classes dgCMatrix, dgTMatrix, dgeMatrix and those mentioned above.

Examples

```r
mm <- Matrix(toeplitz(c(10, 0, 1, 0, 3)), sparse = TRUE)
mm # automatically dsCMatrix
str(mm)
mT <- as(as(mm, "generalMatrix"), "TsparseMatrix")
## Either
```
(symM <- as(mT, "symmetricMatrix")) # dsT
(symC <- as(symM, "CsparseMatrix")) # dsC
## or
sT <- Matrix(mT, sparse=TRUE, forceCheck=TRUE) # dsT

sym2 <- as(symC, "TsparseMatrix")
## --> the same as 'symM', a "dsTMatrix"

## dsparseMatrix-class

Virtual Class "dsparseMatrix" of Numeric Sparse Matrices

Description

The Class "dsparseMatrix" is the virtual (super) class of all numeric sparse matrices.

Slots

Dim: the matrix dimension, see class "Matrix".

Dimnames: see the "Matrix" class.

x: a numeric vector containing the (non-zero) matrix entries.

Extends

Class "dMatrix" and "sparseMatrix", directly.

Class "Matrix", by the above classes.

See Also

the documentation of the (non virtual) sub classes, see showClass("dsparseMatrix"); in particular, dgTMatrix, dgCMatrix, and dgRMatrix.

Examples

showClass("dsparseMatrix")

## dsRMatrix-class

Symmetric Sparse Compressed Row Matrices

Description

The dsRMatrix class is a class of symmetric, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

Objects from the Class

These ".RMatrix" classes are currently still mostly unimplemented!

Objects can be created by calls of the form new("dsRMatrix", ...).
Slots

uplo: A character object indicating if the upper triangle ("U") or the lower triangle ("L") is stored. At present only the lower triangle form is allowed.

j: Object of class "integer" of length n nonzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

p: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

factors: Object of class "list" - a list of factorizations of the matrix.

x: Object of class "numeric" - the non-zero elements of the matrix.

Dim: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: List of length two, see Matrix.

Extends

Classes RsparseMatrix, dsparseMatrix and symmetricMatrix, directly.

Class "dMatrix", by class "dsparseMatrix", class "sparseMatrix", by class "dsparseMatrix" or "RsparseMatrix"; class "compMatrix" by class "symmetricMatrix" and of course, class "Matrix".

Methods

forceSymmetric signature(x = "dsRMatrix", uplo = "missing"): a trivial method just returning x

forceSymmetric signature(x = "dsRMatrix", uplo = "character"): if uplo == x@uplo, this trivially returns x; otherwise t(x).

See Also

the classes dgCMatrix, dgTMatrix, and dgeMatrix.

Examples

(m0 <- new("dsRMatrix"))
m2 <- new("dsRMatrix", Dim = c(2L,2L),
x = c(3,1), j = c(1L,1L), p = 0:2)
m2
stopifnot(colSums(as(m2, "TsparseMatrix")) == 3:4)
str(m2)
(ds2 <- forceSymmetric(diag(2))) # dsy*
dR <- as(ds2, "RsparseMatrix")
dR # dsRMatrix
**dsyMatrix-class**

**Symmetric Dense (Packed or Unpacked) Numeric Matrices**

**Description**

- The "dsyMatrix" class is the class of symmetric, dense matrices in non-packed storage and
- "dspMatrix" is the class of symmetric dense matrices in packed storage, see `pack()`. Only the upper triangle or the lower triangle is stored.

**Objects from the Class**

Objects can be created by calls of the form `new("dsyMatrix", ...)` or `new("dspMatrix", ...)`, respectively.

**Slots**

- `uplo`: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- `x`: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.
- `Dim,Dimnames`: The dimension (a length-2 "integer") and corresponding names (or NULL), see the `Matrix`.
- `factors`: Object of class "list". A named list of factorizations that have been computed for the matrix.

**Extends**

"dsyMatrix" extends class "dgeMatrix", directly, whereas
"dspMatrix" extends class "ddenseMatrix", directly.

Both extend class "symmetricMatrix", directly, and class "Matrix" and others, indirectly, use `showClass("dsyMatrix")`, e.g., for details.

**Methods**

- `norm` signature(x = "dspMatrix", type = "character"), or x = "dsyMatrix" or type = "missing": Computes the matrix norm of the desired type, see `norm`.
- `rcond` signature(x = "dspMatrix", type = "character"), or x = "dsyMatrix" or type = "missing": Computes the reciprocal condition number, `rcond()`.
- `solve` signature(a = "dspMatrix", b = ". . ."), and
- `solve` signature(a = "dsyMatrix", b = ". . ."): x <- solve(a, b) solves $Ax = b$ for $x$; see `solve-methods`.
- `t` signature(x = "dsyMatrix"): Transpose; swaps from upper triangular to lower triangular storage, i.e., the uplo slot from "U" to "L" or vice versa, the same as for all symmetric matrices.

**See Also**

The **positive (Semi-)definite** dense (packed or non-packed numeric matrix classes `dpoMatrix`, `dppMatrix` and `corMatrix`.

Classes `dgeMatrix` and `Matrix`; `solve`, `norm`, `rcond`, `t`
Examples

```r
## Only upper triangular part matters (when uplo == "U" as per default)
(sy2 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, NA, 32, 77)))
str(t(sy2)) # uplo = "L", and the lower tri. (i.e. NA is replaced).

chol(sy2) #-> "Cholesky" matrix
(sp2 <- pack(sy2)) # a "dspMatrix"

## Coercing to dpoMatrix gives invalid object:
sy3 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, -1, 2, -7))
try(as(sy3, "dpoMatrix")) # -> error: not positive definite

## 4x4 example
m <- matrix(0,4,4); m[upper.tri(m)] <- 1:6
(sym <- m+t(m)+diag(11:14, 4))
(S1 <- pack(sym))
(S2 <- t(S1))
stopifnot(all(S1 == S2)) # equal "seen as matrix", but differ internally:
str(S1)
S2@x
```

Description

The "dtCMatrix" class is a class of triangular, sparse matrices in the compressed, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order.

The "dtTMatrix" class is a class of triangular, sparse matrices in triplet format.

Objects from the Class

Objects can be created by calls of the form new("dtCMatrix", ...) or calls of the form new("dtTMatrix", ...), but more typically automatically via Matrix() or coercions such as as(x, "triangularMatrix").

Slots

- `uplo`: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- `diag`: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see triangularMatrix.
- `p`: (only present in "dtCMatrix"): an integer vector for providing pointers, one for each column, see the detailed description in CsparseMatrix.
- `i`: Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.
- `j`: Object of class "integer" of length nnzero (number of non-zero elements). These are the column numbers for each non-zero element in the matrix. (Only present in the dtTMatrix class.)
**dtCMatrix-class**

- **x**: Object of class "numeric" - the non-zero elements of the matrix.
- **Dim,Dimnames**: The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the `Matrix`, see there.

**Extends**

Class "dgCMatrix", directly. Class "triangularMatrix", directly. Class "dMatrix", "sparseMatrix", and more by class "dgCMatrix" etc, see the examples.

**Methods**

- **solve** signature(a = "dtCMMatrix", b = "."): sparse triangular solve (aka "backsolve" or "forwardsolve"), see `solve-methods`.
- **t** signature(x = "dtCMMatrix"): returns the transpose of x
- **t** signature(x = "dtTMatrix"): returns the transpose of x

**See Also**

Classes `dgCMatrix`, `dgTMatrix`, `dgeMatrix`, and `dtrMatrix`.

**Examples**

```r
showClass("dtCMMatrix")
showClass("dtTMatrix")
t1 <- new("dtTMatrix", x = c(3,7), i= 0:1, j=3:2, Dim= as.integer(c(4,4)))
t1
## from 0-diagonal to unit-diagonal (low-level step):
tu <- t1 ; tu@diag <- "U"
tu
tu (cu <- as(tu, "CsparseMatrix"))
str(cu)# only two entries in @i and @x
stopifnot(cu@i == 1:0,
          all(2 * symmpart(cu) == Diagonal(4) + forceSymmetric(cu)))
t1[1,2:3] <- -1:-2
diag(t1) <- 10*c(1:2,3:2)
t1 # still triangular
(it1 <- solve(t1))
t1. <- solve(it1)
all(abs(t1 - t1.) < 10 * .Machine$double.eps)

## 2nd example
U5 <- new("dtCMMatrix", i= c(0L, 0:3), p=c(0L,0L,0:2, 5L), Dim = c(5L, 5L),
        x = rep(1, 5L), diag = "U")
U5
(iu <- solve(U5)) # contains one '0'
validObject(iu2 <- solve(U5, Diagonal(5)))# failed in earlier versions
I5 <- iu %*% U5 # should equal the identity matrix
I5 <- iu2 %*% U5
m53 <- matrix(1:15, 5,3, dimnames=list(NULL,letters[1:3]))
asDiag <- function(M) as(drop0(M), "diagonalMatrix")
stopifnot(
          all.equal(Diagonal(5), asDiag(I5), tolerance=1e-14) ,
          all.equal(Diagonal(5), asDiag(i5), tolerance=1e-14),
```
dtpMatrix-class

identical(list(NULL, dimnames(m53)[[2]]), dimnames(solve(U5, m53)))

DtpMatrix-class  Packed Triangular Dense Matrices - "dtpMatrix"

Description

The "dtpMatrix" class is the class of triangular, dense, numeric matrices in packed storage. The "dtrMatrix" class is the same except in nonpacked storage.

Objects from the Class

Objects can be created by calls of the form new("dtpMatrix", ...) or by coercion from other classes of matrices.

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see triangularMatrix.

x: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order. For a packed square matrix of dimension \(d \times d\), length(x) is of length \(d(d+1)/2\) (also when diag == "U"!).

Dim, Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the Matrix, see there.

Extends

Class "ddenseMatrix", directly. Class "triangularMatrix", directly. Class "dMatrix" and more by class "ddenseMatrix" etc, see the examples.

Methods

\%\%% signature(x = "dtpMatrix", y = "dgeMatrix"): Matrix multiplication; ditto for several other signature combinations, see showMethods("\%\%\%", class = "dtpMatrix").

determinant signature(x = "dtpMatrix", logarithm = "logical"): the determinant(x) trivially is prod(diag(x)), but computed on log scale to prevent over- and underflow.

diag signature(x = "dtpMatrix"): ...

norm signature(x = "dtpMatrix", type = "character"): ...

rcond signature(x = "dtpMatrix", norm = "character"): ...

solve signature(a = "dtpMatrix", b = "..."): efficiently using internal backsolve or forward-solve, see solve-methods.

t signature(x = "dtpMatrix"): t(x) remains a "dtpMatrix", lower triangular if x is upper triangular, and vice versa.
See Also

Class dtrMatrix

Examples

showClass("dtrMatrix")

eample("dtrMatrix-class", echo=FALSE)
(p1 <- pack(T2))
str(p1)
(pp <- pack(T))
ip1 <- solve(p1)
stopifnot(length(p1@x) == 3, length(pp@x) == 3,
  p1 @ uplo == T2 @ uplo, pp @ uplo == T @ uplo,
  identical(t(pp), p1), identical(t(p1), pp),
  all((l.d <- p1 - T2) == 0), is(l.d, "dtpMatrix"),
  all((u.d <- pp - T ) == 0), is(u.d, "dtpMatrix"),
  l.d@uplo == T2@uplo, u.d@uplo == T@uplo,
  identical(t(ip1), solve(pp)), is(ip1, "dtpMatrix"),
  all.equal(as(solve(p1,p1), "diagonalMatrix"), Diagonal(2)))

---

dtRMatrix-class  Triangular Sparse Compressed Row Matrices

Description

The dtRMatrix class is a class of triangular, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

Objects from the Class

This class is currently still mostly unimplemented!

Objects can be created by calls of the form new("dtRMatrix", ...).

Slots

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular. At present only the lower triangle form is allowed.

diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see triangularMatrix.

j: Object of class "integer" of length nnzero(.) (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

p: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row. (Only present in the dsRMatrix class.)

x: Object of class "numeric" - the non-zero elements of the matrix.

Dim: The dimension (a length-2 "integer")

Dimnames: corresponding names (or NULL), inherited from the Matrix, see there.
dtrMatrix-class

Extends

Class "dgRMatrix", directly. Class "dsparseMatrix", by class "dgRMatrix". Class "dMatrix", by class "dgRMatrix". Class "sparseMatrix", by class "dgRMatrix". Class "Matrix", by class "dgRMatrix".

Methods

No methods currently with class "dtrMatrix" in the signature.

See Also

Classes dgCMatrix, dgTMatrix, dgeMatrix

Examples

(m0 <- new("dtrMatrix"))
(m2 <- new("dtrMatrix", Dim = c(2L,2L),
          x = c(5, 1:2), p = c(0L,2:3), j= c(0:1,1L)))
str(m2)
(m3 <- as(Diagonal(2), "RsparseMatrix"))# --> dtRMatrix

---

**dtrMatrix-class**

*Triangular, dense, numeric matrices*

**Description**

The "dtrMatrix" class is the class of triangular, dense, numeric matrices in nonpacked storage. The "dtpMatrix" class is the same except in packed storage, see `pack()`.

**Objects from the Class**

Objects can be created by calls of the form `new("dtrMatrix", ...)`.

**Slots**

- **uplo**: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- **diag**: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see `triangularMatrix`.
- **x**: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.
- **Dim**: Object of class "integer". The dimensions of the matrix which must be a two-element vector of non-negative integers.

**Extends**

Class "ddenseMatrix", directly. Class "triangularMatrix", directly. Class "Matrix" and others, by class "ddenseMatrix".
Methods

Among others (such as matrix products, e.g. ?crossprod-methods),

- `norm` signature(x = "dtrMatrix", type = "character"): ..
- `rcond` signature(x = "dtrMatrix", norm = "character"): ..
- `solve` signature(a = "dtrMatrix", b = ". . ."): efficiently use a “forwardsolve” or backsolve for a lower or upper triangular matrix, respectively, see also `solve-methods`.

+, -, *, . . . , ==, >=, . . .. all the Ops group methods are available. When applied to two triangular matrices, these return a triangular matrix when easily possible.

See Also

Classes `ddenseMatrix`, `dtpMatrix`, `triangularMatrix`

Examples

```r
(m <- rbind(2:3, 0:-1))
(M <- as(m, "generalMatrix"))

(T <- as(M, "triangularMatrix")) # formally upper triangular
t2 <- as(t(M), "triangularMatrix")
stopifnot(T@uplo == "U", T2@uplo == "L", identical(T2, t(T)))

m <- matrix(0,4,4); m[upper.tri(m)] <- 1:6
t1 <- Matrix(m+diag(4))
str(t1p <- pack(t1))
t1pu <- diagN2U(t1p)
stopifnot(exprs = {
  inherits(t1 , "dtrMatrix"); validObject(t1)
  inherits(t1p, "dtpMatrix"); validObject(t1p)
  inherits(t1pu,"dtCMatrix"); validObject(t1pu)
  t1pu@x == 1:6
  all(t1pu == t1p)
  identical((t1pu - t1)@x, numeric())# sparse all-0
})
```

---

### expand-methods

Expand Matrix Factorizations

**Description**

`expand1` and `expand2` construct matrix factors from objects specifying matrix factorizations. Such objects typically do not store the factors explicitly, employing instead a compact representation to save memory.

**Usage**

```r
expand1(x, which, ...)
expand2(x, ...)
expand (x, ...)
```
Arguments

x   a matrix factorization, typically inheriting from virtual class MatrixFactorization.
which a character string indicating a matrix factor.
... further arguments passed to or from methods.

Details

Methods for expand are retained only for backwards compatibility with Matrix < 1.5-0. New
code should use expand1 and expand2, whose methods provide more control and behave more
consistently. Notably, expand2 obeys the rule that the product of the matrix factors in the returned
list should reproduce (within some tolerance) the factorized matrix, including its dimnames.
Hence if x is a matrix and y is its factorization, then

    all.equal(as(x, "matrix"), as(Reduce(`%*%`, expand2(y)), "matrix"))

should in most cases return TRUE.

Value

expand1 returns an object inheriting from virtual class Matrix, representing the factor indicated by
which, always without row and column names.
expand2 returns a list of factors, typically with names using conventional notation, as in list(L=,
U=). The first and last factors get the row and column names of the factorized matrix, which are
preserved in the Dimnames slot of x.

Methods

The following table lists methods for expand1 together with allowed values of argument which.

<table>
<thead>
<tr>
<th>class(x)</th>
<th>which</th>
</tr>
</thead>
<tbody>
<tr>
<td>Schur</td>
<td>c(&quot;Q&quot;, &quot;T&quot;, &quot;Q.&quot;&quot;)</td>
</tr>
<tr>
<td>denseLU</td>
<td>c(&quot;P1&quot;, &quot;P1.&quot;, &quot;L&quot;, &quot;U&quot;)</td>
</tr>
<tr>
<td>sparseLU</td>
<td>c(&quot;P1&quot;, &quot;P1.&quot;, &quot;P2&quot;, &quot;P2.&quot;, &quot;L&quot;, &quot;U&quot;)</td>
</tr>
<tr>
<td>sparseQR</td>
<td>c(&quot;P1&quot;, &quot;P1.&quot;, &quot;P2&quot;, &quot;P2.&quot;, &quot;Q&quot;, &quot;Q1&quot;, &quot;R&quot;, &quot;R1&quot;)</td>
</tr>
</tbody>
</table>

Methods for expand2 and expand are described below. Factor names and classes apply also to
expand1.

expand2 signature(x = "CHMsimpl") : expands the factorization \( A = P_i L_i D L_i' P_i = P_i L L' P_i \)
as list(P1, L1, D, L1, P1) (the default) or as list(P1, L, L, P1), depending on optional logical argument LDL. P1 and P1 are pMatrix, L1, L, and L are dtCMatrix, and D is a ddiMatrix.

expand2 signature(x = "CHMsuper") : as CHMsimpl, but the triangular factors are stored as
dgCMatrix.

expand2 signature(x = "p?Cholesky") : expands the factorization \( A = L_1 D L_1' = LL' \) as
list(L1, D, L1.) (the default) or as list(L, L.), depending on optional logical argument
LDL. L1, L1, L, and L are dtrMatrix or dtpMatrix, and D is a ddiMatrix.
expand2 signature(x = "pBunchKaufman"): expands the factorization \( A = UD_UU' = LD_LL' \) where \( U = \prod_{k=1}^{b_U} P_k U_k \) and \( L = \prod_{k=1}^{b_L} P_k L_k \) as list(U, DU, U.) or list(L, DL, L.), depending on x@uplo. If optional argument complete is TRUE, then an unnamed list giving the full expansion with \( 2b_U + 1 \) or \( 2b_L + 1 \) matrix factors is returned instead. \( P_k \) are represented as pMatrix, \( U_k \) and \( L_k \) are represented as dtCMatrix, and \( D_U \) and \( D_L \) are represented as dsCMatrix.

expand2 signature(x = "Schur"): expands the factorization \( A = QTQ' \) as list(Q, T, Q.). \( Q \) and \( Q. \) are x@Q and t(x@Q) modulo Dimnames, and \( T \) is x@T.

expand2 signature(x = "sparseLU"): expands the factorization \( A = P_1'LUP_2' \) as list(P1., L, U, P2.). \( P_1 \) and \( P_2 \) are pMatrix, and \( L \) and \( U \) are dtCMatrix.

expand2 signature(x = "denseLU"): expands the factorization \( A = P_1'LU \) as list(P1., L, U). \( P_1 \) is a pMatrix, and \( L \) and \( U \) are dtrMatrix if square and dgeMatrix otherwise.

expand2 signature(x = "sparseQR"): expands the factorization \( A = P_1'QRP_2' \) as list(P1., Q, R, P2.) or list(P1., Q1, R1, P2.), depending on optional logical argument complete. \( P_1 \) and \( P_2 \) are pMatrix, \( Q \) and \( Q1 \) are dgeMatrix, \( R \) is a dgCMatrix, and \( R1 \) is a dtCMatrix.

expand signature(x = "CMHfactor"): as expand2, but returning list(P, L). \( \text{expand}(x)[["P"]\] and \( \text{expand2}(x)[["P1"]\] represent the same permutation matrix \( P_1 \) but have opposite margin slots and inverted perm slots. The components of \( \text{expand}(x) \) do not preserve \( x@\text{Dimnames} \).

expand signature(x = "sparseLU"): as expand2, but returning list(P, L, U, Q). \( \text{expand}(x)[["Q"]\] and \( \text{expand2}(x)[["P2"]\] represent the same permutation matrix \( P_2 \) but have opposite margin slots and inverted perm slots. \( \text{expand}(x)[["P"]\] represents the permutation matrix \( P_1 \) rather than its transpose \( P_1' \); it is \( \text{expand2}(x)[["P1"]\] with an inverted perm slot. \( \text{expand}(x)[["L"]\] and \( \text{expand2}(x)[["Q"]\) represent the same unit lower triangular matrix \( L \), but with diag slot equal to "N" and "U", respectively. \( \text{expand}(x)[["Q"]\] and \( \text{expand}(x)[["U"]\) store the permuted first and second components of \( x@\text{Dimnames} \) in their Dimnames slots.

expand signature(x = "denseLU"): as expand2, but returning list(L, U, P). \( \text{expand}(x)[["P"]\] and \( \text{expand2}(x)[["P1"]\) are identical modulo Dimnames. The components of \( \text{expand}(x) \) do not preserve \( x@\text{Dimnames} \).

See Also

The virtual class \texttt{compMatrix} of \texttt{factorizable} matrices.

The virtual class \texttt{MatrixFactorization} of matrix factorizations.

Generic functions \texttt{Cholesky}, \texttt{BunchKaufman}, \texttt{Schur}, \texttt{lu}, and \texttt{qr} for computing factorizations.

Examples

showMethods("expand1", inherited = FALSE)
showMethods("expand2", inherited = FALSE)
set.seed(0)

(A <- Matrix(rnorm(9L, 0, 10), 3L, 3L))
(lu.A <- lu(A))
(e.lu.A <- expand2(lu.A))
stopifnot(exprs = {
  is.list(e.lu.A)
  identical(names(e.lu.A), c("P1.", "L", "U"))
  all(sapply(e.lu.A, is, "Matrix"))
})
all.equal(as(A, "matrix"), as(Reduce("%*%", e.lu.A), "matrix"))
})

## 'expand1' and 'expand2' give equivalent results modulo
dimnames and representation of permutation matrices;
see also function 'alt' in example("Cholesky-methods")
(a1 <- sapply(names(e.lu.A), expand1, x = lu.A, simplify = FALSE))
all.equal(a1, e.lu.A)

## see help("denseLU-class") and others for more examples

---

**expm-methods**

**Matrix Exponential**

### Description

Compute the exponential of a matrix.

### Usage

```r
expm(x)
```

### Arguments

- **x**
  
a matrix, typically inheriting from the `dMatrix` class.

### Details

The exponential of a matrix is defined as the infinite Taylor series
\[
\expm(A) = I + A + A^2/2! + A^3/3! + \ldots
\]
(although this is definitely not the way to compute it). The method for the `dgeMatrix` class uses Ward’s diagonal Pade’ approximation with three step preconditioning, a recommendation from Moler & Van Loan (1978) “Nineteen dubious ways…”.

### Value

The matrix exponential of `x`.

### Author(s)

This is a translation of the implementation of the corresponding Octave function contributed to the Octave project by A. Scottedward Hodel <A.S.Hodel@Eng.Auburn.EDU>. A bug in there has been fixed by Martin Maechler.

### References


for historical reference mostly:

See Also

Package expm, which provides newer (in some cases faster, more accurate) algorithms for computing the matrix exponential via its own (non-generic) function expm(). expm also implements logm(), sqrtm(), etc.

Generic function Schur.

Examples

\[(\text{m1} \leftarrow \text{Matrix}(c(1,0,1,1), \text{ncol} = 2))\]
\[(\text{e1} \leftarrow \text{expm(m1)}) \quad e \leftarrow \exp(1)\]
\[\text{stopifnot(all.equal(e@x, c(e,0,e,e), tolerance = 1e-15))}\]
\[(\text{m2} \leftarrow \text{Matrix}(c(-49, -64, 24, 31), \text{ncol} = 2))\]
\[(\text{e2} \leftarrow \text{expm(m2)})\]
\[(\text{m3} \leftarrow \text{Matrix}((\text{cbind(0, rbind(6*diag(3), 0)))) # \text{sparse!})\]
\[(\text{e3} \leftarrow \text{expm(m3)}) # \text{upper triangular}\]

Description

Read matrices stored in the Harwell-Boeing or MatrixMarket formats or write sparseMatrix objects to one of these formats.

Usage

\text{readHB}(\text{file})
\text{readMM}(\text{file})
\text{writeMM}(\text{obj, file, ...})

Arguments

\begin{itemize}
  \item \text{obj} \quad \text{a real sparse matrix}
  \item \text{file} \quad \text{for writeMM - the name of the file to be written. For readHB and readMM the name of the file to read, as a character scalar. The names of files storing matrices in the Harwell-Boeing format usually end in \text{"rua"} or \text{"rsa"}. Those storing matrices in the MatrixMarket format usually end in \text{"mtx"}. Alternatively, readHB and readMM accept connection objects.}
  \item \dots \quad \text{optional additional arguments. Currently none are used in any methods.}
\end{itemize}

Value

The readHB and readMM functions return an object that inherits from the \text{"Matrix"} class. Methods for the writeMM generic functions usually return \text{NULL} and, as a side effect, the matrix \text{obj} is written to file in the MatrixMarket format (writeMM).
Note

The Harwell-Boeing format is older and less flexible than the MatrixMarket format. The function writeHB was deprecated and has now been removed. Please use writeMM instead.

Note that these formats do not know anything about dimnames, hence these are dropped by writeMM().

A very simple way to export small sparse matrices $S$, is to use summary($S$) which returns a data.frame with columns $i$, $j$, and possibly $x$, see summary in sparseMatrix-class, and an example below.

References

https://math.nist.gov/MatrixMarket/
https://sparse.tamu.edu/

Examples

str(pores <- readMM(system.file("external/pores_1.mtx", package = "Matrix")))
str(utm <- readHB(system.file("external/utm300.rua", package = "Matrix")))
str(lundA <- readMM(system.file("external/lund_a.mtx", package = "Matrix")))
str(lundA <- readHB(system.file("external/lund_a.rsa", package = "Matrix")))
## https://math.nist.gov/MatrixMarket/data/Harwell-Boeing/counterx/counterx.htm
str(jgl <- readMM(system.file("external/jgl009.mtx", package = "Matrix")))

## NOTE: The following examples take quite some time
## ---- even on a fast internet connection:
if(FALSE) {
## The URL has been corrected, but we need an untar step:
u. <- url("https://www.cise.ufl.edu/research/sparse/RB/Boeing/msc00726.tar.gz")
str(sm <- readHB(gzcon(u.)))
}

data(KNex, package = "Matrix")
## Store as MatrixMarket (".mtx") file, here inside temporary dir./folder:
(MMfile <- file.path(tempdir(), "mmMM.mtx"))
writeMM(KNex$mm, file=MMfile)
file.info(MMfile)[,c("size", "ctime")]
## very simple export - in triplet format - to text file:
data(CAex, package = "Matrix")

s.CA <- summary(CAex)
s.CA # shows (i, j, x) [columns of a data frame]
message("writing to ", outf <- tempfile())
write.table(s.CA, file=outf, row.names=FALSE)
## and read it back -- showing off sparseMatrix():
str(dd <- read.table(outf, header=TRUE))
## has columns (i, j, x) -> we can use via do.call() as arguments to sparseMatrix():
mm <- do.call(sparseMatrix, dd)
stopifnot(all.equal(mm, CAex, tolerance=1e-15))
Multiplication by Factors from Matrix Factorizations

Description

Multiplies a matrix or vector on the left or right by a factor from a matrix factorization or its transpose.

Usage

facmul(x, factor, y, trans = FALSE, left = TRUE, ...)

Arguments

x a MatrixFactorization object.
factor a character string indicating a factor in the factorization represented by x, typically an element of names(expand2(x, ...)).
y a matrix or vector to be multiplied on the left or right by the factor or its transpose.
trans a logical indicating if the transpose of the factor should be used, rather than the factor itself.
left a logical indicating if the y should be multiplied on the left by the factor, rather than on the right.
... further arguments passed to or from methods.

Details

facmul is experimental and currently no methods are exported from Matrix.

Value

The value of op(M) %*% y or y %*% op(M), depending on left, where M is the factor (always without dimnames) and op(M) is M or t(M), depending on trans.

Examples

## Conceptually, methods for 'facmul' _would_ behave as follows ...
## Not run:
n <- 3L
x <- lu(Matrix(rnorm(n * n), n, n))
y <- rnorm(n)
L <- unname(expand2(x)[[nm <- "L"]])
stopifnot(exprs = {
  all.equal(facmul(x, nm, y, trans = FALSE, left = TRUE), L %*% y)
  all.equal(facmul(x, nm, y, trans = FALSE, left = FALSE), y %*% L)
  all.equal(facmul(x, nm, y, trans = TRUE, left = TRUE), crossprod(L, y))
  all.equal(facmul(x, nm, y, trans = TRUE, left = FALSE), tcrossprod(y, L))
})
## End(Not run)
"Low Level" Coercions and Methods

Description

"Semi-API" functions used internally by Matrix, often to bypass S4 dispatch and avoid the associated overhead. These are exported to provide this capability to expert users. Typical users should continue to rely on S4 generic functions to dispatch suitable methods, by calling, e.g., as(. , <class>) for coercions.

Usage

```
.M2kind(from, kind = "." , sparse = NA)
.M2gen(from, kind = ".")
.M2sym(from, ...)
.M2tri(from, ...)
.M2diag(from)
.M2v(from)
.M2m(from)
.M2unpacked(from)
.M2packed(from)
.M2C(from)
.M2R(from)
.M2T(from)
.M2V(from)
.m2V(from, kind = ".")

.sparse2dense(from, packed = FALSE)
.diag2dense(from, kind = "." , shape = "t" , packed = FALSE, uplo = "U")
.ind2dense(from, kind = "n")
.m2dense(from, class = ".ge", uplo = "U", diag = "N", trans = FALSE)

.dense2sparse(from, repr = "C")
.diag2sparse(from, kind = "." , shape = "t", repr = "C", uplo = "U")
.ind2sparse(from, kind = "n" , repr = ".")
.m2sparse(from, class = ".gC", uplo = "U", diag = "N", trans = FALSE)

.tCRT(x, lazy = TRUE)
.diag.dsC(x, Chx = Cholesky(x, LDL = TRUE), res.kind = "diag")
.solve.dgC.lu (a, b, tol = .Machine$double.eps, check = TRUE)
.solve.dgC.qr (a, b, order = 3L, check = TRUE)
.solve.dgC.chol(a, b, check = TRUE)
.updateCHMfactor(object, parent, mult = 0)
```
Arguments

from, x, a, b

- a Matrix, matrix, or vector.

kind

- a string ("."", ",", "n", ",", "1", "d") specifying the "kind" of the result. "," indicates that the kind of from should be preserved. "," is equivalent to "z" if from is complex and to "d" otherwise. "n" indicates that the result should inherit from nMatrix or nsparseVector (and so on).

shape

- a string ("."", "g", "s", or "t") specifying the "shape" of the result. "," indicates that the shape of from should be preserved. "g" indicates that the result should inherit from generalMatrix (and so on).

repr

- a string ("."", "C", "R", or "T") specifying the sparse representation of the result. "," is accepted only by .ind2sparse and indicates the most efficient representation, which is "C" ("R") for margin = 2 (1). "C" indicates that the result should inherit from CsparseMatrix (and so on).

packed

- a logical indicating if the result should inherit from packedMatrix rather than from unpackedMatrix. It is ignored for from inheriting from generalMatrix.

sparse

- a logical indicating if the result should inherit from sparseMatrix rather than from denseMatrix. If NA, then the result will be formally sparse if and only if from is.

uplo

- a string ("U" or "L") indicating whether the result (if symmetric or triangular) should store the upper or lower triangle of from. The elements of from in the opposite triangle are ignored.

diag

- a string ("N" or "U") indicating whether the result (if triangular) should be formally nonunit or unit triangular. In the unit triangular case, the diagonal elements of from are ignored.

trans

- a logical indicating if the result should be a 1-row matrix rather than a 1-column matrix where from is a vector but not a matrix.

class

- a string whose first three characters specify the class of the result. It should match the pattern "^[.nld](ge|sy|tr|sp|tp)" for .m2dense and "^[.nld][gst][CRT]\) for .m2sparse, where "," in the first position is equivalent to "l" for logical arguments and "," for numeric arguments.

... optional arguments passed to isSymmetric or isTriangular.

lazy

- a logical indicating if the transpose should be constructed with minimal allocation, but possibly without preserving representation.

Chx

- optionally, the Cholesky(x, ...) factorization of x. If supplied, then x is unused.

res.kind

- a string in c("trace", "sumLog", "prod", "min", "max", "range", "diag", "diagBack").

tol

- see lu-methods.

order

- see qr-methods.

check

- a logical indicating if the first argument should be tested for inheritance from dgCMatrix and coerced if necessary. Set to FALSE for speed only if it is known to already inherit from dgCMatrix.

object

- a Cholesky factorization inheriting from virtual class CHMfactor, almost always the result of a call to generic function Cholesky.

parent

- an object of class dsCMatrix or class dgCMatrix.

mult

- a numeric vector of positive length. Only the first element is used, and that must be finite.
Details

Functions with names of the form .<A>2<B> implement coercions from virtual class A to the “nearest” non-virtual subclass of virtual class B, where the virtual classes are abbreviated as follows:

M Matrix
V sparseVector
m matrix
v vector
dense denseMatrix
unpacked unpackedMatrix
packed packedMatrix
sparse CsparseMatrix, RsparseMatrix, or TsparseMatrix
C C sparseMatrix
R RsparseMatrix
T TsparseMatrix
gen generalMatrix
sym symmetricMatrix
tri triangularMatrix
diag diagonalMatrix
ind indMatrix

Abbreviations should be seen as a guide, rather than as an exact description of behaviour. Notably, .m2dense, .m2sparse, and .m2V accept vectors that are not matrices.

.tCRT(x): If lazy = TRUE, then .tCRT constructs the transpose of x using the most efficient representation, which for ‘CRT’ is ‘RCT’. If lazy = FALSE, then .tCRT preserves the representation of x, behaving as the corresponding methods for generic function t.

.diag.dsC(x): .diag.dsC computes (or uses if Chx is supplied) the Cholesky factorization of x as LDL′ in order to calculate one of several possible statistics from the diagonal entries of D. See res.kind under ‘Arguments’.

.solve.dgC.*(a, b): .solve.dgC.lu(a, b) needs a square matrix a. .solve.dgC.qr(a, b) needs a “long” matrix a, with nrow(a) >= ncol(a). .solve.dgC.chol(a, b) needs a “wide” matrix a, with nrow(a) <= ncol(a).

All three may be used to solve sparse linear systems directly. Only .solve.dgC.qr and .solve.dgC.chol be used to solve sparse least squares problems.

.updateCHMfactor(object, parent, mult): .updateCHMfactor updates object with the result of Cholesky factorizing F(parent) + mult[1] * diag(nrow(parent)), i.e., F(parent) plus mult[1] times the identity matrix, where F = identity if parent is a dsCMatrix and F = tcrossprod if parent is a dgCMatrix. The nonzero pattern of F(parent) must match that of S if object = Cholesky(S, ...).
Examples

D. <- diag(x = c(1, 1, 2, 3, 5, 8))
D.0 <- Diagonal(x = c(0, 0, 0, 3, 5, 8))
S. <- toeplitz(as.double(1:6))
C. <- new("dgCMatrix", Dim = c(3L, 4L),
p = c(0L, 1L, 1L, 1L, 3L), i = c(1L, 0L, 2L), x = c(-8, 2, 3))

stopifnot(exprs = {
  identical(.M2tri (D.), as(D., "triangularMatrix"))
  identical(.M2sym (D.), as(D., "symmetricMatrix"))
  identical(.M2diag(D.), as(D., "diagonalMatrix"))
  identical(.M2kind(C., "l"),
    as(C., "lMatrix"))
  identical(.M2kind(.sparse2dense(C.), "l"),
    as(as(C., "denseMatrix"), "lMatrix"))
  identical(.M2kind(C., "l"),
    as(C., "lMatrix"))
  identical(.sparse2dense(.M2gen(.diag2dense(D.0, ".", "t", TRUE), "C"))
    identical(.M2kind(.sparse2dense(C.), "l"),
      as(as(C., "denseMatrix"), "lMatrix"))
  identical(.M2kind(C., "l"),
    as(C., "lMatrix"))
  identical(.M2kind(.sparse2dense(C.), "l"),
    as(as(C., "denseMatrix"), "lMatrix"))
  identical(.M2kind(.sparse2dense(C.), "l"),
    as(as(C., "denseMatrix"), "lMatrix"))
  identical(.M2kind(C., "l"),
    as(C., "lMatrix"))
})

A <- tcrossprod(C.)/6 + Diagonal(3, 1/3); A[1,2] <- 3; A

## Solving sparse least squares:
X <- rbind(A, Diagonal(3)) # design matrix X (for L.S.)
Xt <- t(X) # *transposed* X (for L.S.)
(y <- drop(crossprod(Xt, c(1:3))) + c(-1,1)/1000) # small rand.err.
str(solveCh <- .solve.dgC.chol(Xt, y, check=FALSE)) # Xt *is* dgC..

stopifnot(exprs = {
  all.equal(solveCh$coef, 1:3, tol = 1e-3)# rel.err ~ 1e-4
  all.equal(solveCh$coef, drop(solve(tcrossprod(Xt), Xt %*% y)))
  all.equal(solveCh$coef, .solve.dgC.qr(X, y, check=FALSE))
})

forceSymmetric-methods

Force a Matrix to 'symmetricMatrix' Without Symmetry Checks

Description

Force a square matrix x to a symmetricMatrix, without a symmetry check as it would be applied for as(x, "symmetricMatrix").
forceSymmetric(x, uplo)

Arguments
x  any square matrix (of numbers), either “traditional” (matrix) or inheriting from Matrix.
uplo  optional string, “U” or “L” indicating which “triangle” half of x should determine the result. The default is "U" unless x already has a uplo slot (i.e., when it is symmetricMatrix, or triangularMatrix), where the default will be x@uplo.

Value
a square matrix inheriting from class symmetricMatrix.

See Also
symmpart for the symmetric part of a matrix, or the coercions as(x, <symmetricMatrix class>).

Examples

## Hilbert matrix
i <- 1:6
h6 <- 1/outer(i - 1L, i, "+")
sd <- sqrt(diag(h6))
hh <- t(h6/sd)/sd # theoretically symmetric
isSymmetric(hh, tol=0) # FALSE; hence
try( as(hh, "symmetricMatrix") ) # fails, but this works fine:
  H6 <- forceSymmetric(hh)

  ## result can be pretty surprising:
  (M <- Matrix(1:36, 6))
  forceSymmetric(M) # symmetric, hence very different in lower triangle
  (tm <- tril(M))
  forceSymmetric(tm)

Description
Utilities for formatting sparse numeric matrices in a flexible way. These functions are used by the format and print methods for sparse matrices and can be applied as well to standard R matrices. Note that all arguments but the first are optional.

formatSparseM() is the main “workhorse” of formatSpMatrix, the format method for sparse matrices.

.formatSparseSimple() is a simple helper function, also dealing with (short/empty) column names construction.
Usage

formatSparseM(x, zero.print = ".", align = c("fancy", "right"),
    m = as(x,"matrix"), asLogical=NULL, uniDiag=NULL,
    digits=NULL, cx, iN0, dn = dimnames(m))

.formatSparseSimple(m, asLogical=FALSE, digits=NULL,
    col.names, note.dropping.colnames = TRUE,
    dn=dimnames(m))

Arguments

x an R object inheriting from class sparseMatrix.
zero.print character which should be used for structural zeroes. The default "." may
    occasionally be replaced by " " (blank); using "0" would look almost like
    print()ing of non-sparse matrices.
align a string specifying how the zero.print codes should be aligned, see
    formatSpMatrix.
m (optional) a (standard R) matrix version of x.
asLogical should the matrix be formatted as a logical matrix (or rather as a numeric one);
    mostly for formatSparseM().
uniDiag logical indicating if the diagonal entries of a sparse unit triangular or unit-
    diagonal matrix should be formatted as "I" instead of "1" (to emphasize that
    the 1's are "structural").
digits significant digits to use for printing, see print.default.
cx (optional) character matrix; a formatted version of x, still with strings such as
    "0.00" for the zeros.
iN0 (optional) integer vector, specifying the location of the non-zeroes of x.
col.names, note.dropping.colnames see formatSpMatrix.
dn dimnames to be used; a list (of length two) with row and column names (or
    NULL).

Value

a character matrix like cx, where the zeros have been replaced with (padded versions of)
zero.print. As this is a dense matrix, do not use these functions for really large (really) sparse
matrices!

Author(s)

Martin Maechler

See Also

formatSpMatrix which calls formatSparseM() and is the format method for sparse matrices.
printSpMatrix which is used by the (typically implicitly called) show and print methods for
sparse matrices.
generalMatrix-class

Examples

```r
m <- suppressWarnings(matrix(c(0, 3.2, 0,0,11,0,0,0,0,-7,0), 4,9))
fm <- formatSparseM(m)
noquote(fm)
## nice, but this is nicer (with "units" vertically aligned):
print(fm, quote=FALSE, right=TRUE)
## and "the same" as :
Matrix(m)

## align = "right" is cheaper --> the "." are not aligned:
noquote(f2 <- formatSparseM(m,align="r"))
stopifnot(f2 == fm | m == 0, dim(f2) == dim(m),
         (f2 == ".") == (m == 0))
```

generalMatrix-class  Class "generalMatrix" of General Matrices

Description

Virtual class of "general" matrices; i.e., matrices that do not have a known property such as symmetric, triangular, or diagonal.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

- `factors`
- `Dim`

Dimnames: all slots inherited from `compMatrix`; see its description.

Extends

Class "compMatrix", directly. Class "Matrix", by class "compMatrix".

See Also

Classes `compMatrix`, and the non-general virtual classes: `symmetricMatrix`, `triangularMatrix`, `diagonalMatrix`.
Hilbert  

*Generate a Hilbert matrix*

**Description**

Generate the \( n \) by \( n \) symmetric Hilbert matrix. Because these matrices are ill-conditioned for moderate to large \( n \), they are often used for testing numerical linear algebra code.

**Usage**

\texttt{Hilbert(n)}

**Arguments**

\( n \)

a non-negative integer.

**Value**

the \( n \) by \( n \) symmetric Hilbert matrix as a "\texttt{dpoMatrix}" object.

**See Also**

the class \texttt{dpoMatrix}

**Examples**

\texttt{Hilbert(6)}

---

**image-methods**  

*Methods for image() in Package 'Matrix'*

**Description**

Methods for function \texttt{image} in package \texttt{Matrix}. An image of a matrix simply color codes all matrix entries and draws the \( n \times m \) matrix using an \( n \times m \) grid of (colored) rectangles.

The \texttt{Matrix} package image methods are based on \texttt{levelplot()} from package \texttt{lattice}; hence these methods return an "object" of class "\texttt{trellis}”, producing a graphic when (auto-) \texttt{print}()ed.

**Usage**

\[
## S4 method for signature 'dgTMatrix'
image(x, 
    xlim = c(1, di[2]), 
    ylim = c(di[1], 1), aspect = "iso", 
    sub = sprintf("Dimensions: %d \times %d", di[1], di[2]), 
    xlab = "Column", ylab = "Row", cuts = 15, 
    useRaster = FALSE, 
    useAbs = NULL, colorkey = !useAbs, 
    col.regions = NULL, 
    lwd = NULL, border.col = NULL, ...) 
\]
Arguments

x a Matrix object, i.e., fulfilling is(x, "Matrix").

xlim, ylim x- and y-axis limits; may be used to “zoom into” matrix. Note that x, y “feel reversed”: ylim is for the rows (= 1st index) and xlim for the columns (= 2nd index). For convenience, when the limits are integer valued, they are both extended by 0.5; also, ylim is always used decreasingly.

aspect aspect ratio specified as number (y/x) or string; see levelplot.

sub, xlab, ylab axis annotation with sensible defaults; see plot.default.

cuts number of levels the range of matrix values would be divided into.

useRaster logical indicating if raster graphics should be used (instead of the tradition rectangle vector drawing). If true, panel.levelplot.raster (from lattice package) is used, and the colorkey is also done via rasters, see also levelplot and possibly grid.raster.

Note that using raster graphics may often be faster, but can be slower, depending on the matrix dimensions and the graphics device (dimensions).

useAbs logical indicating if abs(x) should be shown; if TRUE, the former (implicit) default, the default col.regions will be grey colors (and no colorkey drawn). The default is FALSE unless the matrix has no negative entries.

colorkey logical indicating if a color key aka ‘legend’ should be produced. Default is to draw one, unless useAbs is true. You can also specify a list, see levelplot, such as list(raster=TRUE) in the case of rastering.

col.regions vector of gradually varying colors; see levelplot.

lwd (only used when useRaster is false:) non-negative number or NULL (default), specifying the line-width of the rectangles of each non-zero matrix entry (drawn by grid.rect). The default depends on the matrix dimension and the device size.

border.col color for the border of each rectangle. NA means no border is drawn. When NULL as by default, border.col <- if(lwd < .01) NA else NULL is used. Consider using an opaque color instead of NULL which corresponds to grid::get.gpar("col").

... further arguments passed to methods and levelplot, notably at for specifying (possibly non equidistant) cut values for dividing the matrix values (superseding cuts above).

Value

as all lattice graphics functions, image(<Matrix>) returns a "trellis" object, effectively the result of levelplot().

Methods

All methods currently end up calling the method for the dgTMatrix class. Use showMethods(image) to list them all.

See Also

levelplot, and print.trellis from package lattice.
Examples

```r
showMethods(image)
## And if you want to see the method definitions:
showMethods(image, includeDefs = TRUE, inherited = FALSE)

data(CAex, package = "Matrix")
image(CAex, main = "image(CAex)") -> imgC; imgC
stopifnot(!is.null(leg <- imgC$legend), is.list(leg$right)) # failed for 2 days ..
image(CAex, useAbs=TRUE, main = "image(CAex, useAbs=TRUE)"

cCA <- Cholesky(crossprod(CAex), Imult = .01)
## See ?print.trellis --- place two image() plots side by side:
print(image(cCA, main="Cholesky(crossprod(CAex), Imult = .01")
    ,
    split=(x=1,y=1,nx=2, ny=1), more=TRUE)
print(image(cCA, useAbs=TRUE),
    split=(x=2,y=1,nx=2,ny=1))
```

data(USCounties, package = "Matrix")
image(USCounties)# huge
image(sign(USCounties))## just the pattern
    # how the result looks, may depend heavily on
    # the device, screen resolution, antialiasing etc
    # e.g. x11(type="Xlib") may show very differently than cairo-based

## Drawing borders around each rectangle;
    # again, viewing depends very much on the device:
image(USCounties[1:400,1:200], lwd=.1)
## Using (xlim,ylim) has advantage : matrix dimension and (col/row) indices:
image(USCounties, c(1,200), c(1,400), lwd=.1)
image(USCounties, c(1,300), c(1,200), lwd=.5)
image(USCounties, c(1,100), c(1,200), lwd=.01)
## These 3 are all equivalent :
(I1 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE))
I2 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE, border.col=NA)
I3 <- image(USCounties, c(1,100), c(1,100), useAbs=FALSE, lwd=2, border.col=NA)
stopifnot(all.equal(I1, I2, check.environment=FALSE),
    all.equal(I2, I3, check.environment=FALSE))
## using an opaque border color
image(USCounties, c(1,100), c(1,100), useAbs=FALSE, lwd=3, border.col = adjustcolor("skyblue", 1/2))

if(interactive() || nzchar(Sys.getenv("R_MATRIX_CHECK_EXTRA"))) {
    ## Using raster graphics: For PDF this would give a 77 MB file,
    ## however, for such a large matrix, this is typically considerably
    ## *slower* (than vector graphics rectangles) in most cases :
    if(doPNG <- !dev.interactive())
        png("image-USCounties-raster.png", width=3200, height=3200)
image(USCounties, useRaster = TRUE) # should not suffer from anti-aliasing
    if(doPNG)
        dev.off()
        ## and now look at the *.png image in a viewer you can easily zoom in and out
    }#only if(doExtras)
```
Description

The class "index" is a virtual class used for indices (in signatures) for matrix indexing and subassignment of Matrix matrices.

In fact, it is currently implemented as a simple class union (setClassUnion) of "numeric", "logical" and "character".

Objects from the Class

Since it is a virtual Class, no objects may be created from it.

See Also

[-methods, and
Subassign-methods, also for examples.

Examples

showClass("index")
Operations on index matrices that result in index matrices will accordingly return an \texttt{indMatrix}. These include products of two column index matrices and (equivalently) column-indexing of a column index matrix (when dimensions are not dropped). Most other operations on \texttt{indMatrix} treat them as sparse nonzero pattern matrices (i.e., inheriting from virtual class \texttt{nsparseMatrix}). Hence vector-valued subsets of \texttt{indMatrix}, such as those given by \texttt{diag}, are always of type "\texttt{logical}".

**Objects from the Class**

Objects can be created explicitly with calls of the form \texttt{new("indMatrix", ...)}, but they are more commonly created by coercing 1-based integer index vectors, with calls of the form \texttt{as(., "indMatrix")}; see ‘Methods’ below.

**Slots**

- \texttt{margin}: an integer, either 1 or 2, specifying whether the matrix is a row (1) or column (2) index.
- \texttt{perm}: a 1-based integer index vector, i.e., a vector of length \texttt{Dim[margin]} with elements taken from \texttt{1:Dim[1+margin%%2]}.
- \texttt{Dim,Dimnames}: inherited from virtual superclass \texttt{Matrix}.

**Extends**

Classes \texttt{"sparseMatrix"} and \texttt{"generalMatrix"}, directly.

**Methods**

- \texttt{%% signature(x = "indMatrix", y = "Matrix")} and others listed by \texttt{showMethods("%%", classes = "indMatrix")}: matrix products implemented where appropriate as indexing operations.
- \texttt{coerce signature(from = "numeric", to = "indMatrix")}: supporting typical \texttt{indMatrix} construction from a vector of positive integers. Row indexing is assumed.
- \texttt{coerce signature(from = "list", to = "indMatrix")}: supporting \texttt{indMatrix} construction for row and column indexing, including index vectors of length 0 and index vectors whose maximum is less than the number of rows or columns being indexed.
- \texttt{coerce signature(from = "indMatrix", to = "matrix")}: coercion to a traditional \texttt{matrix} of \texttt{logical} type, with \texttt{FALSE} and \texttt{TRUE} in place of 0 and 1.
- \texttt{t signature(x = "indMatrix")}: the transpose, which is an \texttt{indMatrix} with identical \texttt{perm} but opposite \texttt{margin}.
- \texttt{rowSums, rowMeans, colSums, colMeans signature(x = "indMatrix")}: row and column sums and means.
- \texttt{rbind2, cbind2 signature(x = "indMatrix", y = "indMatrix")}: row-wise catenation of two row index matrices with equal numbers of columns and column-wise catenation of two column index matrices with equal numbers of rows.
- \texttt{kronecker signature(X = "indMatrix", Y = "indMatrix")}: Kronecker product of two row index matrices or two column index matrices, giving the row or column index matrix corresponding to their “interaction”.
Author(s)

Fabian Scheipl and Uni Muenchen, building on the existing class \texttt{pMatrix} after a nice hike’s conversation with Martin Maechler. Methods for \texttt{crossprod(x, y)} and \texttt{kronecker(x, y)} with both arguments inheriting from \texttt{indMatrix} were made considerably faster thanks to a suggestion by Boris Vaillant. Diverse tweaks by Martin Maechler and Mikael Jagan, notably the latter’s implementation of \texttt{margin}, prior to which the \texttt{indMatrix} class was designated only for row index matrices.

See Also

Subclass \texttt{pMatrix} of permutation matrices, a special case of index matrices; virtual class \texttt{nMatrix} of nonzero pattern matrices, and its subclasses.

Examples

```r
p1 <- as(c(2,3,1), "pMatrix")
(sm1 <- as(rep(c(2,3,1), e=3), "indMatrix"))
stopifnot(all(sm1 == p1[rep(1:3, each=3),]))

## row-indexing of a \texttt{pMatrix} turns it into an \texttt{indMatrix}:
class(p1[rep(1:3, each=3),])

set.seed(12) # so we know '10' is in sample
## random index matrix for 30 observations and 10 unique values:
(s10 <- as(sample(10, 30, replace=TRUE),"indMatrix"))

## Sample rows of a numeric matrix :
(mm <- matrix(1:10, nrow=10, ncol=3))
s10 %*% mm

set.seed(27)
IM1 <- as(sample(1:20, 100, replace=TRUE), "indMatrix")
IM2 <- as(sample(1:18, 100, replace=TRUE), "indMatrix")
(c12 <- crossprod(IM1,IM2))
# same as cross-tabulation of the two index vectors:
stopifnot(all(c12 - unclass(table(IM1@perm, IM2@perm)) == 0))

# 3 observations, 4 implied values, first does not occur in sample:
as(2:4, "indMatrix")
# 3 observations, 5 values, first and last do not occur in sample:
as(list(2:4, 5), "indMatrix")

as(sm1, "nMatrix")
s10[1:7, 1:4] # gives an "ngTMatrix" (most economic!)
s10[1:4, ] # preserves "indMatrix"-class

I1 <- as(c(5:1,6:4,7:3), "indMatrix")
I2 <- as(7:1, "pMatrix")
(I12 <- rbind(I1, I2))
stopifnot(is(I12, "indMatrix"),
          identical(I12, rbind(I1, I2)),
          colSums(I12) == c(2L,2:4,4:2))
```

```
invertPerm and signPerm compute the inverse and sign of a length-n permutation vector. isPerm tests if a length-n integer vector is a valid permutation vector. asPerm coerces a length-m transposition vector to a length-n permutation vector, where m ≤ n.

**Usage**

invertPerm(p, off = 1L, ioff = 1L)
signPerm(p, off = 1L)
isPerm(p, off = 1L)
asPerm(pivot, off = 1L, ioff = 1L, n = length(pivot))

invPerm(p, zero.p = FALSE, zero.res = FALSE)

**Arguments**

- **p** an integer vector of length n.
- **pivot** an integer vector of length m.
- **off** an integer offset, indicating that p is a permutation of \( \text{off}+0:(n-1) \) or that pivot contains m values sampled with replacement from \( \text{off}+0:(n-1) \).
- **ioff** an integer offset, indicating that the result should be a permutation of \( \text{ioff}+0:(n-1) \).
- **n** a integer greater than or equal to m, indicating the length of the result. Transpositions are applied to a permutation vector vector initialized as seq_len(n).
- **zero.p** a logical. Equivalent to off=0 if TRUE and off=1 if FALSE.
- **zero.res** a logical. Equivalent to ioff=0 if TRUE and ioff=1 if FALSE.

**Details**

invertPerm(p, off, ioff=1) is equivalent to order(p) or sort.list(p) for all values of off. For the default value off=1, it returns the value of p after p[p] <- seq_along(p).

invPerm is a simple wrapper around invertPerm, retained for backwards compatibility.

**Value**

By default, i.e., with off=1 and ioff=1:

invertPerm(p) returns an integer vector of length length(p) such that p[invertPerm(p)] and invertPerm(p)[p] are both seq_along(p), i.e., the identity permutation.
signPerm(p) returns 1 if p is an even permutation and -1 otherwise (i.e., if p is odd).
isPerm(p) returns TRUE if p is a permutation of seq_along(p) and FALSE otherwise.
asPerm(pivot) returns the result of transposing elements i and pivot[i] of a permutation vector initialized as seq_len(n), for i in seq_along(pivot).
See Also

Class `pMatrix` of permutation matrices.

Examples

```r
p <- sample(10L) # a random permutation vector
ip <- invertPerm(p)
s <- signPerm(p)

## 'p' and 'ip' are indeed inverses:
stopifnot(exprs = {
  isPerm(p)
  isPerm(ip)
  identical(s, 1L) || identical(s, -1L)
  identical(s, signPerm(ip))
  identical(p[ip], 1:10)
  identical(ip[p], 1:10)
  identical(invertPerm(ip), p)
})

## Product of transpositions (1 2)(2 1)(4 3)(6 8)(10 1) = (3 4)(6 8)(1 10)
pivot <- c(2L, 1L, 3L, 3L, 5L, 8L, 7L, 8L, 9L, 1L)
q <- asPerm(pivot)
stopifnot(exprs = {
  identical(q, c(10L, 2L, 4L, 3L, 5L, 8L, 7L, 6L, 9L, 1L))
  identical(q[1L], seq_len(10L)) # because the permutation is odd:
    signPerm(q) == -1L
})

invPerm # a less general version of 'invertPerm'
```

is.na-methods

Methods for generic functions `anyNA()`, `is.na()`, `is.nan()`, `is.infinite()`, and `is.finite()`, for objects inheriting from virtual class `Matrix` or `sparseVector`.

Usage

```r
## S4 method for signature 'denseMatrix'
is.na(x)
## S4 method for signature 'sparseMatrix'
is.na(x)
## S4 method for signature 'diagonalMatrix'
is.na(x)
## S4 method for signature 'indMatrix'
is.na(x)
## S4 method for signature 'sparseVector'
is.na(x)
## ... 
## and likewise for anyNA, is.na, is.nan, is.infinite, is.finite
```
Arguments

x  
an R object, here a sparse or dense matrix or vector.

Value

For is.*(), an nMatrix or nSparseVector matching the dimensions of x and specifying the positions in x of (some subset of) NA, NaN, Inf, and -Inf. For anyNA(), TRUE if x contains NA or NaN and FALSE otherwise.

See Also

NA, NaN, Inf

Examples

(M <- Matrix(1:6, nrow = 4, ncol = 3, 
dimnames = list(letters[1:4], LETTERS[1:3])))
stopifnot(!anyNA(M), !any(is.na(M)))

M[2:3, 2] <- NA
(inM <- is.na(M))
stopifnot(anyNA(M), sum(inM) == 2)

(A <- spMatrix(nrow = 10, ncol = 20, 
i = c(1, 3:8), j = c(2, 9, 6:10), x = 7 * (1:7)))
stopifnot(!anyNA(A), !any(is.na(A)))

(inA <- is.na(A))
stopifnot(anyNA(A), sum(inA) == 1 + 1 + 5)

Description

Are the Dimnames dn NULL-like?

is.null.DN(dn) is less strict than is.null(dn), because it is also true (TRUE) when the dimnames dn are "like" NULL, or list(NULL, NULL), as they can easily be for the traditional R matrices (matrix) which have no formal class definition, and hence much freedom in how their dimnames look like.

Usage

is.null.DN(dn)

Arguments

dn  
dimnames() of a matrix-like R object.

Value

logical TRUE or FALSE.
Note

This function is really to be used on "traditional" matrices rather than those inheriting from \texttt{Matrix}, as the latter will always have \texttt{dimnames list(NULL, NULL)} exactly, in such a case.

Author(s)

Martin Maechler

See Also

\texttt{is.null, dimnames, matrix}.

Examples

\begin{verbatim}
> m1 <- m2 <- m3 <- m4 <- m <-
>   matrix(round(100 * rnorm(6)), 2, 3)
> dimnames(m1) <- list(NULL, NULL)
> dimnames(m2) <- list(NULL, character())
> dimnames(m3) <- rev(dimnames(m2))
> dimnames(m4) <- rep(list(character()), 2)

> m4 # prints absolutely identically to m

> c.o <- capture.output
> cm <- c.o(m)
> stopifnot(exprs = {
>   m == m1; m == m2; m == m3; m == m4
>   identical(cm, c.o(m1)); identical(cm, c.o(m2))
>   identical(cm, c.o(m3)); identical(cm, c.o(m4))
> })

> hasNoDimnames <- function(.) is.null.DN(dimnames(.))
> stopifnot(exprs = {
>   hasNoDimnames(m)
>   hasNoDimnames(m1); hasNoDimnames(m2)
>   hasNoDimnames(m3); hasNoDimnames(m4)
>   hasNoDimnames(Matrix(m) -> M)
>   hasNoDimnames(as(M, "sparseMatrix"))
> })
\end{verbatim}

Description

\texttt{isSymmetric} tests whether its argument is a symmetric square matrix, by default tolerating some numerical fuzz and requiring symmetric \texttt{[dD]imnames} in addition to symmetry in the mathematical sense. \texttt{isSymmetric} is a generic function in \texttt{base}, which has a \texttt{method} for traditional matrices of implicit \texttt{class "matrix"}. Methods are defined here for various proper and virtual classes in \texttt{Matrix}, so that \texttt{isSymmetric} works for all objects inheriting from virtual class "\texttt{Matrix}".
## isSymmetric-methods

### Usage

```r
## S4 method for signature 'denseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'CsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'RsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'TsparseMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'diagonalMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'indMatrix'
isSymmetric(object, checkDN = TRUE, ...)
## S4 method for signature 'dgeMatrix'
isSymmetric(object, checkDN = TRUE, tol = 100 * .Machine$double.eps, tol1 = 8 * tol, ...)
## S4 method for signature 'dgCMatrix'
isSymmetric(object, checkDN = TRUE, tol = 100 * .Machine$double.eps, ...)
```

### Arguments

- `object`: a "Matrix".
- `checkDN`: a logical indicating whether symmetry of the Dimnames slot of object should be checked.
- `tol, tol1`: numerical tolerances allowing approximate symmetry of numeric (rather than logical) matrices. See also `isSymmetric.matrix`.
- `...`: further arguments passed to methods (typically methods for `all.equal`).

### Details

The Dimnames slot of object, say `dn`, is considered to be symmetric if and only if

- `dn[[1]]` and `dn[[2]]` are identical or one is NULL; 
- `ndn <- names(dn)` is NULL or `ndn[1]` and `ndn[2]` are identical or one is the empty string "".

Hence `list(a=nms, a=nms)` is considered to be symmetric, and so too are `list(a=nms, NULL)` and `list(NULL, a=nms)`.

Note that this definition is looser than that employed by `isSymmetric.matrix`, which requires `dn[1]` and `dn[2]` to be identical, where `dn` is the dimnames attribute of a traditional matrix.

### Value

A logical, either TRUE or FALSE (never NA).

### See Also

`forceSymmetric`; `symmpart` and `skewpart`; virtual class "symmetricMatrix" and its subclasses.

### Examples

```r
isSymmetric(Diagonal(4)) # TRUE of course
M <- Matrix(c(1,2,2,1), 2,2)
isSymmetric(M) # TRUE (*and* of formal class "dsyMatrix")
```
isTriangular-methods

isSymmetric(as(M, "generalMatrix")) # still symmetric, even if not "formally"
isSymmetric(triu(M)) # FALSE

## Look at implementations:
showMethods("isSymmetric", includeDefs = TRUE) # includes S3 generic from base

isTriangular-methods  Test whether a Matrix is Triangular or Diagonal

Description

isTriangular and isDiagonal test whether their argument is a triangular or diagonal matrix, respectively. Unlike the analogous isSymmetric, these two functions are generically from Matrix rather than base. Hence Matrix defines methods for traditional matrices of implicit class "matrix" in addition to matrices inheriting from virtual class "Matrix".

By our definition, triangular and diagonal matrices are square, i.e., they have the same number of rows and columns.

Usage

isTriangular(object, upper = NA, ...)  
isDiagonal(object)

Arguments

object an R object, typically a matrix.
upper a logical, either TRUE or FALSE, in which case TRUE is returned only for upper or lower triangular object; or otherwise NA (the default), in which case TRUE is returned for any triangular object.
...

Value

A logical, either TRUE or FALSE (never NA).

If object is triangular and upper is NA, then isTriangular returns TRUE with an attribute kind, either "U" or "L", indicating that object is upper or lower triangular, respectively. Users should not rely on how kind is determined for diagonal matrices, which are both upper and lower triangular.

See Also

isSymmetric; virtual classes "triangularMatrix" and "diagonalMatrix" and their subclasses.

Examples

isTriangular(Diagonal(4))  
## is TRUE: a diagonal matrix is also (both upper and lower) triangular
(M <- Matrix(c(1,2,0,1), 2,2))
isTriangular(M) # TRUE (and of formal class "dtrMatrix")
isTriangular(as(M, "generalMatrix")) # still triangular, even if not "formally"
isTriangular(crossprod(M)) # FALSE
KhatriRao

Khatri-Rao Matrix Product

Description

Computes Khatri-Rao products for any kind of matrices. The Khatri-Rao product is a column-wise Kronecker product. Originally introduced by Khatri and Rao (1968), it has many different applications, see Liu and Trenkler (2008) for a survey. Notably, it is used in higher-dimensional tensor decompositions, see Bader and Kolda (2008).

Usage

KhatriRao(X, Y = X, FUN = "*", sparseY = TRUE, make.dimnames = FALSE)

Arguments

X, Y matrices of with the same number of columns.
FUN the (name of the) function to be used for the column-wise Kronecker products, see `kronecker`, defaulting to the usual multiplication.
sparseY logical specifying if Y should be coerced and treated as `sparseMatrix`. Set this to FALSE, e.g., to distinguish structural zeros from zero entries.
make.dimnames logical indicating if the result should inherit `dimnames` from X and Y in a simple way.

Value

a "CsparseMatrix", say R, the Khatri-Rao product of X \((n \times k)\) and Y \((m \times k)\), is of dimension \((n \cdot m) \times k\), where the j-th column, \(R[,j]\) is the kronecker product \(\text{kronecker}(X[,j], Y[,j])\).

Note

The current implementation is efficient for large sparse matrices.

Author(s)

Original by Michael Cysouw, Univ. Marburg; minor tweaks, bug fixes etc, by Martin Maechler.

References


KhatriRao

See Also

kronecker.

Examples

```r
## Example with very small matrices:
m <- matrix(1:12, 3, 4)
d <- diag(1:4)
KhatriRao(m, d)
KhatriRao(d, m)
dimnames(m) <- list(LETTERS[1:3], letters[1:4])
KhatriRao(m, d, make.dimnames=TRUE)
KhatriRao(d, m, make.dimnames=TRUE)
dimnames(d) <- list(NULL, paste0("D", 1:4))
KhatriRao(m, d, make.dimnames=TRUE)
KhatriRao(d, m, make.dimnames=TRUE)
dimnames(d) <- list(paste0("D", 10*1:4), paste0("d", 1:4))
(Kmd <- KhatriRao(m, d, make.dimnames=TRUE))
(Kdm <- KhatriRao(d, m, make.dimnames=TRUE))

nm <- as(m, "nsparseMatrix")
nd <- as(d, "nsparseMatrix")
KhatriRao(nm, nd, make.dimnames=TRUE)
KhatriRao(nd, nm, make.dimnames=TRUE)

stopifnot(dim(KhatriRao(m, d)) == c(nrow(m)*nrow(d), ncol(d)))
## border cases / checks:
zm <- nm; zm[] <- FALSE  # all FALSE matrix
stopifnot(all(K1 <- KhatriRao(nd, zm) == 0), identical(dim(K1), c(12L, 4L)),
          all(K2 <- KhatriRao(zm, nd) == 0), identical(dim(K2), c(12L, 4L)))
d0 <- d; d0[] <- 0; m0 <- Matrix(d0[-1,])
stopifnot(all(K3 <- KhatriRao(d0, m) == 0), identical(dim(K3), dim(Kdm)),
          all(K4 <- KhatriRao(m, d0) == 0), identical(dim(K4), dim(Kmd)),
          all(KhatriRao(d0, d0) == 0), all(KhatriRao(m0, d0) == 0),
          all(KhatriRao(d0, m0) == 0), all(KhatriRao(m0, m0) == 0),
          identical(dimnames(KhatriRao(m, d0, make.dimnames=TRUE)), dimnames(Kmd)))

## a matrix with "structural" and non-structural zeros:
m01 <- new("dgCMatrix", i = c(0L, 2L, 0L, 1L), p = c(0L, 0L, 0L, 2L, 4L),
          Dim = 3:4, x = c(1, 0, 1, 0, 1))
D4 <- Diagonal(4, x=1:4)  # "as" d
DU <- Diagonal(4)  # unit-diagonal: uplo="U"
(K5 <- KhatriRao( d0, m01))
K5D <- KhatriRao(D4, m01, sparseY=FALSE)
K5DD <- KhatriRao(D4, m01, sparseY=FALSE)
(K6 <- KhatriRao(diag(3), t(m01)))
K6D <- KhatriRao(Diagonal(3), t(m01))
K6d <- KhatriRao(diag(3), t(m01), sparseY=FALSE)
K6Dd <- KhatriRao(Diagonal(3), t(m01), sparseY=FALSE)
stopifnot(exprs = {
  all(K5 == K5d)
  identical(cbind(c(7L, 10L), c(3L, 4L)),
           which(K5 != 0, arr.ind = TRUE, useNames=FALSE))
  identical(K5d, K5DD)
})
```
identical(K6, K6D)
all(K6 == K6d)
identical(cbind(3:4, 1L),
    which(K6 != 0, arr.ind = TRUE, useNames=FALSE))
identical(K6d, K6Dd)
)}

---

**KNex**

**Koenker-Ng Example Sparse Model Matrix and Response Vector**

**Description**

A model matrix \( mm \) and corresponding response vector \( y \) used in an example by Koenker and Ng. The matrix \( mm \) is a sparse matrix with 1850 rows and 712 columns but only 8758 non-zero entries. It is a "dgCMatrix" object. The vector \( y \) is just numeric of length 1850.

**Usage**

```r
data(KNex)
```

**References**


**Examples**

```r
data(KNex, package = "Matrix")
class(KNex$mm)
dim(KNex$mm)
image(KNex$mm)
str(KNex)

system.time(# a fraction of a second
    sparse.sol <- with(KNex, solve(crossprod(mm), crossprod(mm, y))))

head(round(sparse.sol,3))

### Compare with QR-based solution ("more accurate, but slightly slower"):

```r

system.time(
    sp.sol2 <- with(KNex, qr.coef(qr(mm), y))
)

all.equal(sparse.sol, sp.sol2, tolerance = 1e-13) # TRUE
```
**kronecker-methods**  
*Methods for Function 'kronecker()' in Package 'Matrix'*

**Description**

Computes Kronecker products for objects inheriting from "Matrix".

In order to preserve sparseness, we treat 0 * NA as 0, not as NA as usually in R (and as used for the base function kronecker).

**Methods**

- **kronecker** signature(X = "Matrix", Y = "ANY")
- **kronecker** signature(X = "ANY", Y = "Matrix")
- **kronecker** signature(X = "diagonalMatrix", Y = "ANY")
- **kronecker** signature(X = "sparseMatrix", Y = "ANY")
- **kronecker** signature(X = "TsparseMatrix", Y = "TsparseMatrix")
- **kronecker** signature(X = "dgTMatrix", Y = "dgTMatrix")
- **kronecker** signature(X = "dtTMatrix", Y = "dtTMatrix")
- **kronecker** signature(X = "indMatrix", Y = "indMatrix")

**Examples**

```r
(t1 <- spMatrix(5,4, x= c(3,2,-7,11), i= 1:4, j=4:1)) # 5 x 4  
(t2 <- kronecker(Diagonal(3, 2:4), t1)) # 15 x 12

## should also work with special-cased logical matrices
l3 <- upper.tri(matrix(,3,3))  
M <- Matrix(l3)  
(N <- as(M, "nsparseMatrix")) # "ntCMatrix" (upper triangular)
N2 <- as(N, "generalMatrix") # (lost "t"riangularity)
MM <- kronecker(M,M)  
NN <- kronecker(N,N) # "dtTMatrix" i.e. did keep
NN2 <- kronecker(N2,N2)  
stopifnot(identical(NN,MM),  
          is(NN2, "sparseMatrix"), all(NN2 == NN),
          is(NN, "triangularMatrix"))
```

**ldenseMatrix-class**  
*Virtual Class "ldenseMatrix" of Dense Logical Matrices*

**Description**

ldenseMatrix is the virtual class of all dense logical (S4) matrices. It extends both denseMatrix and lMatrix directly.

**Slots**

- x: logical vector containing the entries of the matrix.
- Dim, Dimnames: see Matrix.
ldiMatrix-class

Extends

Class "lMatrix", directly. Class "denseMatrix", directly. Class "Matrix", by class "lMatrix". Class "Matrix", by class "denseMatrix".

Methods

as.vector signature(x = "ldenseMatrix", mode = "missing"): ...

which signature(x = "ndenseMatrix"), semantically equivalent to base function which(x, arr.ind); for details, see the lMatrix class documentation.

See Also

Class lgeMatrix and the other subclasses.

Examples

showClass("ldenseMatrix")

as(diag(3) > 0, "ldenseMatrix")

ldiMatrix-class

Class “ldiMatrix” of Diagonal Logical Matrices

Description

The class "ldiMatrix" of logical diagonal matrices.

Objects from the Class

Objects can be created by calls of the form new("ldiMatrix", ...) but typically rather via Diagonal.

Slots

x: "logical" vector.

diag: "character" string, either "U" or "N", see ddiMatrix.

Dim,Dimnames: matrix dimension and dimnames, see the Matrix class description.

Extends

Class "diagonalMatrix" and class "lMatrix", directly.

Class "sparseMatrix", by class "diagonalMatrix".

See Also

Classes ddiMatrix and diagonalMatrix; function Diagonal.
**Examples**

```r
(lM <- Diagonal(x = c(TRUE, FALSE, FALSE)))
str(lM)#> gory details (slots)
crossprod(lM) # numeric
(nM <- as(lM, "nMatrix"))
crossprod(nM) # pattern sparse
```

---

**Description**

This is the class of general dense logical matrices.

**Slots**

- **x**: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.
- **Dim, Dimnames**: The dimension (a length-2 "integer") and corresponding names (or NULL), see the `Matrix` class.
- **factors**: Object of class "list". A named list of factorizations that have been computed for the matrix.

**Extends**

Class "ldenseMatrix", directly. Class "lMatrix", by class "ldenseMatrix". Class "denseMatrix", by class "ldenseMatrix". Class "Matrix", by class "ldenseMatrix".

**Methods**

Currently, mainly `t()` and coercion methods (for `as(.)`); use, e.g., `showMethods(class="lgeMatrix")` for details.

**See Also**

Non-general logical dense matrix classes such as `ltrMatrix`, or `lsyMatrix`; sparse logical classes such as `lgCMatrix`.

**Examples**

```r
showClass("lgeMatrix")
str(new("lgeMatrix"))
set.seed(1)
(lM <- Matrix(matrix(rnorm(28), 4, 7) > 0))# a simple random lgeMatrix
set.seed(11)
(lC <- Matrix(matrix(rnorm(28), 4, 7) > 0))# a simple random lgCMatrix
as(lM, "CsparseMatrix")
```
lsparseMatrix-classes  Sparse logical matrices

Description

The lsparseMatrix class is a virtual class of logical sparse matrices, i.e., sparse matrices with entries TRUE, FALSE, or NA.

These can be stored in the "triplet" form (class TsparseMatrix, subclasses lgTMatrix, lsTMatrix, and ltTMatrix) or in compressed column-oriented form (class CsparseMatrix, subclasses lgCMatrix, lsCMatrix, and ltCMatrix) or—rarely—in compressed row-oriented form (class RsparseMatrix, subclasses lgRMatrix, lsRMatrix, and ltRMatrix). The second letter in the name of these non-virtual classes indicates general, symmetric, or triangular.

Details

Note that triplet stored (TsparseMatrix) matrices such as lgTMatrix may contain duplicated pairs of indices \((i, j)\) as for the corresponding numeric class dgTMatrix where for such pairs, the corresponding \(x\) slot entries are added. For logical matrices, the \(x\) entries corresponding to duplicated index pairs \((i, j)\) are “added” as well if the addition is defined as logical or, i.e., “\(TRUE + TRUE \rightarrow TRUE\)” and “\(TRUE + FALSE \rightarrow TRUE\)”.

Note the use of asUniqueT() for getting an internally unique representation without duplicated \((i, j)\) entries.

Objects from the Class

Objects can be created by calls of the form new("lgCMatrix", ...) and so on. More frequently objects are created by coercion of a numeric sparse matrix to the logical form, e.g. in an expression \(x != 0\).

The logical form is also used in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence any numeric sparse matrices can be treated as logical sparse matrices.

Slots

- \(x\): Object of class "logical", i.e., either TRUE, NA, or FALSE.
- uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.
- diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N" for non-unit. The implicit diagonal elements are not explicitly stored when diag is "U". Present in the triangular classes only.
- \(p\): Object of class "integer" of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.
- \(i\): Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.
- \(j\): Object of class "integer" of length nnzero (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed row-oriented forms only.
lsyMatrix-class

Symmetric Dense Logical Matrices

Description

The "lsyMatrix" class is the class of symmetric, dense logical matrices in non-packed storage and "lspMatrix" is the class of these in packed storage. In the packed form, only the upper triangle or the lower triangle is stored.
Objects from the Class

Objects can be created by calls of the form `new("lsyMatrix", ...)`.

Slots

- **uplo**: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- **x**: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.
- **Dim, Dimnames**: The dimension (a length-2 "integer") and corresponding names (or NULL), see the `Matrix` class.
- **factors**: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Both extend classes "ldenseMatrix" and "symmetricMatrix", directly; further, class "Matrix" and others, indirectly. Use `showClass("lsyMatrix")`, e.g., for details.

Methods

Currently, mainly `t()` and coercion methods (for `as()`; use, e.g., `showMethods(class="lsyMatrix")` for details.

See Also

`lgeMatrix, Matrix, t`

Examples

```r
(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
str(M2)
# can
(sM <- M2 | t(M2)) # lge
as(sM, "symmetricMatrix")
str(sM <- as(sM, "packedMatrix")) # packed symmetric
```

**ltrMatrix-class**

Triangular Dense Logical Matrices

**Description**

The "ltrMatrix" class is the class of triangular, dense, logical matrices in nonpacked storage. The "ltpMatrix" class is the same except in packed storage.
Slots

- `x`: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.
- `uplo`: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- `diag`: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see `triangularMatrix`.
- `Dim`, `Dimnames`: The dimension (a length-2 "integer") and corresponding names (or NULL), see the `Matrix` class.
- `factors`: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

Both extend classes "ldenseMatrix" and "triangularMatrix", directly; further, class "Matrix", "lMatrix" and others, indirectly. Use `showClass("ltrMatrix")`, e.g., for details.

Methods

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="ltrMatrix")` for details.

See Also

Classes `lgeMatrix`, `Matrix`; function `t`

Examples

```r
showClass("ltrMatrix")

str(new("ltpMatrix"))
(lutr <- as(upper.tri(matrix(, 4, 4)), "ldenseMatrix"))
str(lutp <- pack(lutr)) # packed matrix: only 10 = 4*(4+1)/2 entries
!lutp # the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(lutp, pack(!lutp)))
```

Description

Computes the pivoted LU factorization of an $m \times n$ real matrix $A$, which has the general form

$$P_1 A P_2 = LU$$

or (equivalently)

$$A = P_1' L U P_2'$$

where $P_1$ is an $m \times m$ permutation matrix, $P_2$ is an $n \times n$ permutation matrix, $L$ is an $m \times \min(m, n)$ unit lower trapezoidal matrix, and $U$ is a $\min(m, n) \times n$ upper trapezoidal matrix.
Methods for `denseMatrix` are built on LAPACK routine `dgetrf`, which does not permute columns, so that \( P_2 \) is an identity matrix.

Methods for `sparseMatrix` are built on CSparse routine `cs_lu`, which requires \( m = n \), so that \( L \) and \( U \) are triangular matrices.

### Usage

```r
lu(x, ...)  
## S4 method for signature 'dgeMatrix'
lu(x, warnSing = TRUE, ...)  
## S4 method for signature 'dgCMatrix'
lu(x, errSing = TRUE, order = NA_integer_,
    tol = 1, ...)  
## S4 method for signature 'dsyMatrix'
lu(x, cache = TRUE, ...)  
## S4 method for signature 'dsCMatrix'
lu(x, cache = TRUE, ...)  
## S4 method for signature 'matrix'
lu(x, ...)
```

### Arguments

- **x**: a finite matrix or `Matrix` to be factorized, which must be square if sparse.
- **warnSing**: a logical indicating if a warning should be signaled for singular \( x \). Used only by methods for dense matrices.
- **errSing**: a logical indicating if an error should be signaled for singular \( x \). Used only by methods for sparse matrices.
- **order**: an integer in 0:3 passed to CSparse routine `cs_sqr`, indicating a strategy for choosing the column permutation \( P_2 \). 0 means no column permutation. 1, 2, and 3 indicate a fill-reducing ordering of \( A + A', \tilde{A}' \tilde{A}, \) and \( A' A \), where \( \tilde{A} \) is \( A \) with “dense” rows removed. NA (the default) is equivalent to 2 if \( \text{tol} = 1 \) and 1 otherwise. Do not set to 0 unless you know that the column order of \( A \) is already sensible.
- **tol**: a number. The original pivot element is used if its absolute value exceeds \( \text{tol} \times a \), where \( a \) is the maximum in absolute value of the other possible pivot elements. Set \( \text{tol} < 1 \) only if you know what you are doing.
- **cache**: a logical indicating if the result should be cached in \( x@factors["LU"] \). Note that caching is experimental and that only methods for classes extending `compMatrix` will have this argument.
- **...**: further arguments passed to or from methods.

### Details

What happens when \( x \) is determined to be near-singular differs by method. The method for class `dgeMatrix` completes the factorization, warning if `warnSing = TRUE` and in any case returning a valid `denseLU` object. Users of this method can detect singular \( x \) with a suitable warning handler; see `tryCatch`. In contrast, the method for class `dgCMatrix` abandons further computation, throwing an error if `errSing = TRUE` and otherwise returning NA. Users of this method can detect singular \( x \) with an error handler or by setting `errSing = FALSE` and testing for a formal result with `is(.,'sparseLU')`.
Value

An object representing the factorization, inheriting from virtual class `LU`. The specific class is `denseLU` unless `x` inherits from virtual class `sparseMatrix`, in which case it is `sparseLU`.

References

The LAPACK source code, including documentation; see [https://netlib.org/lapack/double/dgetrf.f](https://netlib.org/lapack/double/dgetrf.f).


See Also

Classes `denseLU` and `sparseLU` and their methods.

Classes `dgeMatrix` and `dgCMatrix`.

Generic functions `expand1` and `expand2`, for constructing matrix factors from the result.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, and `qr`, for computing other factorizations.

Examples

```r
showMethods("lu", inherited = FALSE)
set.seed(0)

## ---- Dense ----------------------------------------------------------
(A1 <- Matrix(rnorm(9L), 3L, 3L))
(lu.A1 <- lu(A1))
(A2 <- round(10 * A1[, -3L]))
(lu.A2 <- lu(A2))

## A ~ P1' L U in floating point
str(e.lu.A2 <- expand2(lu.A2), max.level = 2L)
stopifnot(all.equal(A2, Reduce("%*%", e.lu.A2)))

## ---- Sparse ---------------------------------------------------------
A3 <- as(readMM(system.file("external/pores_1.mtx", package = "Matrix")), "CsparseMatrix")
(lu.A3 <- lu(A3))

## A ~ P1' L U P2' in floating point
str(e.lu.A3 <- expand2(lu.A3), max.level = 2L)
stopifnot(all.equal(A3, Reduce("%*%", e.lu.A3)))
```
Description

From an R object coercible to "TsparseMatrix", typically a (sparse) matrix, produce its triplet representation which may collapse to a “Duplet” in the case of binary aka pattern, such as "nMatrix" objects.

Usage

mat2triplet(x, uniqT = FALSE)

Arguments

x
any R object for which as(x, "TsparseMatrix") works; typically a matrix of one of the Matrix package matrices.

uniqT
logical indicating if the triplet representation should be ‘unique’ in the sense of asUniqueT(byrow=FALSE).

Value

A list, typically with three components,

i vector of row indices for all non-zero entries of x
i vector of columns indices for all non-zero entries of x
x vector of all non-zero entries of x; exists only when as(x, "TsparseMatrix") is not a "nsparseMatrix".

Note that the order of the entries is determined by the coercion to "TsparseMatrix" and hence typically with increasing j (and increasing i within ties of j).

Note

The mat2triplet() utility was created to be a more efficient and more predictable substitute for summary(<sparseMatrix>). UseRs have wrongly expected the latter to return a data frame with columns i and j which however is wrong for a "diagonalMatrix".

See Also

The summary() method for "sparseMatrix", summary,sparseMatrix-method. mat2triplet() is conceptually the inverse function of spMatrix and (one case of) sparseMatrix.

Examples

mat2triplet # simple definition

i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
(Ax <- sparseMatrix(i, j, x = x)) ## 8 x 10 "dgCMatrix"
str(trA <- mat2triplet(Ax))
stopifnot(i == sort(trA$i), sort(j) == trA$j, x == sort(trA$x))
D <- Diagonal(x=4:2)
summary(D)
str(mat2triplet(D))

**Description**

The basic matrix product, `%*%` is implemented for all our Matrix and also for sparseVector classes, fully analogously to R’s base matrix and vector objects.

The functions `crossprod` and `tcrossprod` are matrix products or “cross products”, ideally implemented efficiently without computing `t(.)`’s unnecessarily. They also return symmetricMatrix classed matrices when easily detectable, e.g., in `crossprod(m)`, the one argument case.

tcrossprod() takes the cross-product of the transpose of a matrix. `tcrossprod(x)` is formally equivalent to, but faster than, the call `x %*% t(x)`, and so is `tcrossprod(x, y)` instead of `x %*% t(y)`.

Boolean matrix products are computed via either `%&%` or `boolArith = TRUE`.

**Usage**

```r
## S4 method for signature 'CsparseMatrix,diagonalMatrix'
x %*% y
## S4 method for signature 'CsparseMatrix,diagonalMatrix'
crossprod(x, y = NULL, boolArith = NA, ...)
  ## .... and for many more signatures
## S4 method for signature 'TsparseMatrix,missing'
tcrossprod(x, y = NULL, boolArith = NA, ...)
  ## .... and for many more signatures
```

**Arguments**

- `x` a matrix-like object
- `y` a matrix-like object, or for `[t]crossprod()` `NULL` (by default); the latter case is formally equivalent to `y = x`.
- `boolArith` `logical`, i.e., `NA`, `TRUE`, or `FALSE`. If true the result is (coerced to) a pattern matrix, i.e., "nMatrix", unless there are `NA` entries and the result will be a "lMatrix". If false the result is (coerced to) numeric. When `NA`, currently the default, the result is a pattern matrix when `x` and `y` are "nsparseMatrix" and numeric otherwise.
- `...` potentially more arguments passed to and from methods.

**Details**

For some classes in the Matrix package, such as `dgCMat`, it is much faster to calculate the cross-product of the transpose directly instead of calculating the transpose first and then its cross-product. `boolArith = TRUE` for regular (“non cross”) matrix products, `%*%` cannot be specified. Instead, we provide the `%&%` operator for `boolArith` matrix products.
Value

A Matrix object, in the one argument case of an appropriate symmetric matrix class, i.e., inheriting from symmetricMatrix.

Methods

%*% signature(x = "dgeMatrix", y = "dgeMatrix"): Matrix multiplication; ditto for several other signature combinations, see showMethods("%*%", class = "dgeMatrix").
%*% signature(x = "dtrMatrix", y = "matrix") and other signatures (use showMethods("%*%", class="dtrMatrix"): matrix multiplication. Multiplication of (matching) triangular matrices now should remain triangular (in the sense of class triangularMatrix).
crossprod signature(x = "dgeMatrix", y = "dgeMatrix"): ditto for several other signatures, use showMethods("crossprod", class = "dgeMatrix"), matrix crossproduct, an efficient version of t(x) %*% y.
crossprod signature(x = "CsparseMatrix", y = "missing") returns t(x) %*% x as an dsCMatrix object.
crossprod signature(x = "TsparseMatrix", y = "missing") returns t(x) %*% x as an dsCMatrix object.
crossprod,tcrossprod signature(x = "dtrMatrix", y = "matrix") and other signatures, see "%*%" above.

Note

boolArith = TRUE, FALSE or NA has been newly introduced for Matrix 1.2.0 (March 2015). Its implementation has still not been tested extensively. Notably the behaviour for sparse matrices with x slots containing extra zeros had not been documented previously, see the %&% help page.
Currently, boolArith = TRUE is implemented via CsparseMatrix coercions which may be quite inefficient for dense matrices. Contributions for efficiency improvements are welcome.

See Also
tcrossprod in R’s base, and crossprod and %*%. Matrix package %&% for boolean matrix product methods.

Examples

```r
## A random sparse "incidence" matrix :
m <- matrix(0, 400, 500)
set.seed(12)
m[runif(314, 0, length(m))] <- 1
mm <- as(m, "CsparseMatrix")
object.size(m) / object.size(mm) # smaller by a factor of > 200

## tcrossprod() is very fast:
system.time(tCmm <- tcrossprod(mm))# 0 (PIII, 933 MHz)
系统.time(cm <- crossprod(t(m))) # 0.16
system.time(cm. <- tcrossprod(m)) # 0.02
stopifnot(cm == as(tCmm, "matrix"))

## show sparse sub matrix
tCmm[1:16, 1:30]
```
Construct a Classed Matrix

**Description**

Construct a Matrix of a class that inherits from Matrix.

**Usage**

```r
Matrix(data=NA, nrow=1, ncol=1, byrow=FALSE, dimnames=NULL, sparse = NULL, doDiag = TRUE, forceCheck = FALSE)
```

**Arguments**

- `data` an optional numeric data vector or matrix.
- `nrow` when `data` is not a matrix, the desired number of rows
- `ncol` when `data` is not a matrix, the desired number of columns
- `byrow` logical. If FALSE (the default) the matrix is filled by columns, otherwise the matrix is filled by rows.
- `dimnames` a `dimnames` attribute for the matrix: a list of two character components. They are set if not `NULL` (as per default).
- `sparse` logical or `NULL`, specifying if the result should be sparse or not. By default, it is made sparse when more than half of the entries are 0.
- `doDiag` logical indicating if a `diagonalMatrix` object should be returned when the resulting matrix is diagonal (*mathematically*). As class `diagonalMatrix` extends `sparseMatrix`, this is a natural default for all values of `sparse`. Otherwise, if `doDiag` is false, a dense or sparse (depending on `sparse`) symmetric matrix will be returned.
- `forceCheck` logical indicating if the checks for structure should even happen when `data` is already a "Matrix" object.

**Details**

If either of `nrow` or `ncol` is not given, an attempt is made to infer it from the length of `data` and the other parameter. Further, `Matrix()` makes efforts to keep `logical` matrices logical, i.e., inheriting from class `lMatrix`, and to determine specially structured matrices such as symmetric, triangular or diagonal ones. Note that a `symmetric` matrix also needs symmetric `dimnames`, e.g., by specifying `dimnames = list(NULL,NULL)`, see the examples.

Most of the time, the function works via a traditional (full) `matrix`. However, `Matrix(0, nrow,ncol)` directly constructs an “empty” `sparseMatrix`, as does `Matrix(FALSE, *)`.

Although it is sometime possible to mix unclassed matrices (created with `matrix`) with ones of class "Matrix", it is much safer to always use carefully constructed ones of class "Matrix".

**Value**

Returns matrix of a class that inherits from "Matrix". Only if `data` is not a `matrix` and does not already inherit from class `Matrix` are the arguments `nrow`, `ncol` and `byrow` made use of.
See Also

The classes `Matrix`, `symmetricMatrix`, `triangularMatrix`, and `diagonalMatrix`; further, `matrix`.

Special matrices can be constructed, e.g., via `sparseMatrix` (sparse), `bdia` (block-diagonal), `bandSparse` (banded sparse), or `Diagonal`.

Examples

```r
Matrix(0, 3, 2) # 3 by 2 matrix of zeros -> sparse
Matrix(0, 3, 2, sparse=FALSE)# -> 'dense'

## 4 cases - 3 different results :
Matrix(0, 2, 2) # diagonal !
Matrix(0, 2, 2, sparse=FALSE)# (ditto)
Matrix(0, 2, 2, doDiag=FALSE)# -> sparse symm. "dsCMatrix"
Matrix(0, 2, 2, sparse=FALSE, doDiag=FALSE)# -> dense symm. "dsyMatrix"

Matrix(0:6, 3, 2) # a 3 by 2 matrix (+ integer warning)
Matrix(0:6 + 1, nrow=3)

## logical ones:
Matrix(diag(4) > 0) # -> "ldiMatrix" with diag = "U"
Matrix(diag(4) > 0, sparse=TRUE) # (ditto)
Matrix(diag(4) >= 0) # -> "lsyMatrix" (of all 'TRUE')

## triangular
l3 <- upper.tri(matrix(,3,3))
(M <- Matrix(l3)) # -> "ltCMatrix"
Matrix(! l3) # -> "ltrMatrix"
as(l3, "CsparseMatrix")# "lgCMatrix"

Matrix(1:9, nrow=3,
      dimnames = list(c("a", "b", "c"), c("A", "B", "C")))
(I3 <- Matrix(diag(3)))# identity, i.e., unit "diagonalMatrix"
str(I3) # note 'diag = "U"' and the empty 'x' slot

(A <- cbind(a=c(2,1), b=1:2))# symmetric *apart* from dimnames
Matrix(A) # hence 'dgeMatrix'
(As <- Matrix(A, dimnames = list(NULL,NULL)))# -> symmetric
forceSymmetric(A)# also symmetric, w/ symm. dimnames
stopifnot(is(As, "symmetricMatrix"),
          is(Matrix(0, 3,3), "sparseMatrix"),
          is(Matrix(FALSE, 1,1), "sparseMatrix"))
```

Matrix-class

Virtual Class "Matrix" of Matrices

Description

The `Matrix` class is a class contained by all actual classes in the `Matrix` package. It is a “virtual” class.
**Slots**

- **Dim**: an integer vector of length 2 giving the dimensions of the matrix.
- **Dimnames**: a list of length 2. Each element must be NULL or a character vector of length equal to the corresponding element of Dim.

**Methods**

- **determinant** signature(x = "Matrix", logarithm = "missing"): and
- **determinant** signature(x = "Matrix", logarithm = "logical"): compute the (log) determinant of x. The method chosen depends on the actual Matrix class of x. Note that det also works for all our matrices, calling the appropriate determinant() method. The Matrix::det is an exact copy of base::det, but in the correct namespace, and hence calling the S4-aware version of determinant().
- **diff** signature(x = "Matrix"): As diff() for traditional matrices, i.e., applying diff() to each column.
- **dim** signature(x = "Matrix"): extract matrix dimensions dim.
- **dim<-** signature(x = "Matrix", value = "ANY"): where value is integer of length 2. Allows to reshape Matrix objects, but only when prod(value) == prod(dim(x)).
- **dimnames** signature(x = "Matrix"): extract dimnames.
- **dimnames<-** signature(x = "Matrix", value = "list"): set the dimnames to a list of length 2, see dimnames<-.
- **length** signature(x = "Matrix"): simply defined as prod(dim(x)) (and hence of mode "double").
- **show** signature(object = "Matrix"): show method for printing. For printing sparse matrices, see printSpMatrix.
- **image** signature(object = "Matrix"): draws an image of the matrix entries, using levelplot() from package lattice.
- **head** signature(object = "Matrix"): return only the "head", i.e., the first few rows.
- **tail** signature(object = "Matrix"): return only the "tail", i.e., the last few rows of the respective matrix.

- **as.matrix**, **as.array** signature(x = "Matrix"): the same as as(x, "matrix"); see also the note below.
- **as.vector** signature(x = "Matrix", mode = "missing"): as.vector(m) should be identical to as.vector(as(m, "matrix")), implemented more efficiently for some subclasses.
- **as(x, "vector"), as(x, "numeric")** etc. similarly.
- **coerce** signature(from = "ANY", to = "Matrix"): This relies on a correct as.matrix() method for from.

There are many more methods that (conceptually should) work for all "Matrix" objects, e.g., colSums, rowMeans. Even base functions may work automatically (if they first call as.matrix() on their principal argument), e.g., apply, eigen, svd or kappa all do work via coercion to a “traditional” (dense) matrix.

**Note**

Loading the Matrix namespace “overloads” as.matrix and as.array in the base namespace by the equivalent of function(x) as(x, "matrix"). Consequently, as.matrix(m) or as.array(m) will properly work when m inherits from the "Matrix" class — also for functions in package base and other packages. E.g., apply or outer can therefore be applied to "Matrix" matrices.
Author(s)
Douglas Bates <bates@stat.wisc.edu> and Martin Maechler

See Also
the classes `dgeMatrix`, `dgCMatrix`, and function `Matrix` for construction (and examples).
Methods, e.g., for `kronecker`.

Examples

```r
slotNames("Matrix")

cl <- getClass("Matrix")
names(cl@subclasses) # more than 40 ..

showClass("Matrix") #> output with slots and all subclasses

(M <- Matrix(c(0,1,0,0), 6, 4))
dim(M)
diag(M)
cm <- M[1:4,] + 10*Diagonal(4)
diff(M)
## can reshape it even :
dim(M) <- c(2, 12)
M
stopifnot(identical(M, Matrix(c(0,1,0,0), 2,12)),
all.equal(det(cm),
    determinant(as(cm,"matrix"), log=FALSE)$modulus,
    check.attributes=FALSE))
```

Virtual Classes Not Yet Really Implemented and Used

Description
`iMatrix` is the virtual class of all integer (S4) matrices. It extends the `Matrix` class directly.
`zMatrix` is the virtual class of all `complex` (S4) matrices. It extends the `Matrix` class directly.

Examples

```r
showClass("iMatrix")
showClass("zMatrix")
```
MatrixClass

The Matrix (Super-) Class of a Class

Description

Return the (maybe super-)class of class cl from package Matrix, returning character(0) if there is none.

Usage

MatrixClass(cl, cld = getClassDef(cl), ...Matrix = TRUE,
         dropVirtual = TRUE, ...)

Arguments

cl string, class name

cld its class definition

...Matrix logical indicating if the result must be of pattern "[dlniz]..Matrix" where
the first letter "[dlniz]" denotes the content kind.
dropVirtual logical indicating if virtual classes are included or not.

... further arguments are passed to .selectSuperClasses().

Value

a character string

Author(s)

Martin Maechler, 24 Mar 2009

See Also

Matrix, the mother of all Matrix classes.

Examples

mkA <- setClass("A", contains="dgCMatrix")
(A <- mkA())
stopifnot(identical(
    MatrixClass("A"),
    "dgCMatrix"))
MatrixFactorization-class

Virtual Class "MatrixFactorization" of Matrix Factorizations

Description

MatrixFactorization is the virtual class of factorizations of $m \times n$ matrices $A$, having the general form

$$P_1 A P_2 = A_1 \cdots A_p$$

or (equivalently)

$$A = P'_1 A_1 \cdots A_p P'_2$$

where $P_1$ and $P_2$ are permutation matrices. Factorizations requiring symmetric $A$ have the constraint $P_2 = P'_1$, and factorizations without row or column pivoting have the constraints $P_1 = I_m$ and $P_2 = I_n$, where $I_m$ and $I_n$ are the $m \times m$ and $n \times n$ identity matrices.

CholeskyFactorization, BunchKaufmanFactorization, SchurFactorization, LU, and QR are the virtual subclasses of MatrixFactorization containing all Cholesky, Bunch-Kaufman, Schur, LU, and QR factorizations, respectively.

Slots

- Dim: an integer vector of length 2 giving the dimensions of the factorized matrix.
- Dimnames: a list of length 2 preserving the dimnames of the factorized matrix. Each element must be NULL or a character vector of length equal to the corresponding element of Dim.

Methods

determinant signature(x = "MatrixFactorization", logarithm = "missing"): sets logarithm = TRUE and recalls the generic function.
dim signature(x = "MatrixFactorization"): returns x@Dim.
dimnames signature(x = "MatrixFactorization"): returns x@Dimnames.
dimnames<- signature(x = "MatrixFactorization", value = "NULL"): returns x with x@Dimnames set to list(NULL, NULL).
dimnames<- signature(x = "MatrixFactorization", value = "list"): returns x with x@Dimnames set to value.
length signature(x = "MatrixFactorization"): returns prod(x@Dim).
show signature(object = "MatrixFactorization"): prints the internal representation of the factorization using str.
solve signature(a = "MatrixFactorization", b = .): see solve-methods.
unname signature(obj = "MatrixFactorization"): returns obj with obj@Dimnames set to list(NULL, NULL).
**ndenseMatrix-class**

**See Also**

The virtual class `compMatrix` of factorizable matrices.

Classes extending CholeskyFactorization, namely `Cholesky`, `pCholesky`, and `CHMfactor`.

Classes extending BunchKaufmanFactorization, namely `BunchKaufman` and `pBunchKaufman`.

Classes extending SchurFactorization, namely `Schur`.

Classes extending LU, namely `denseLU` and `sparseLU`.

Classes extending QR, namely `sparseQR`.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, `lu`, and `qr` for computing factorizations.

Generic functions `expand1` and `expand2` for constructing matrix factors from `MatrixFactorization` objects.

**Examples**

```r
showClass("MatrixFactorization")
```

---

**ndenseMatrix-class**  Virtual Class “ndenseMatrix” of Dense Logical Matrices

**Description**

`ndenseMatrix` is the virtual class of all dense logical (S4) matrices. It extends both `denseMatrix` and `lMatrix` directly.

**Slots**

x: logical vector containing the entries of the matrix.

Dim, Dimnames: see `Matrix`.

**Extends**

Class "nMatrix", directly. Class "denseMatrix", directly. Class "Matrix", by class "nMatrix". Class "Matrix", by class "denseMatrix".

**Methods**

```r
%*% signature(x = "nsparsityMatrix", y = "ndenseMatrix"): ...
%*% signature(x = "ndenseMatrix", y = "nsparsityMatrix"): ...
crossprod signature(x = "nsparsityMatrix", y = "ndenseMatrix"): ...
crossprod signature(x = "ndenseMatrix", y = "nsparsityMatrix"): ...
as.vector signature(x = "ndenseMatrix", mode = "missing"): ...
diag signature(x = "ndenseMatrix"): extracts the diagonal as for all matrices, see the generic diag().
which signature(x = "ndenseMatrix"). semantically equivalent to base function which(x, arr.ind); for details, see the `lMatrix` class documentation.
```

**See Also**

Class `ngeMatrix` and the other subclasses.
Examples

```
showClass("ndenseMatrix")

as(diag(3) > 0, "ndenseMatrix") # -> "nge"
```

---

### Description

Compute the nearest positive definite matrix to an approximate one, typically a correlation or variance-covariance matrix.

### Usage

```r
nearPD(x, corr = FALSE, keepDiag = FALSE, base.matrix = FALSE, 
do2eigen = TRUE, doSym = FALSE, 
doDykstra = TRUE, only.values = FALSE, 
ensureSymmetry = !isSymmetric(x), 
eig.tol = 1e-06, conv.tol = 1e-07, posd.tol = 1e-08, 
maxit = 100, conv.norm.type = "I", trace = FALSE)
```

### Arguments

- **x**: numeric $n \times n$ approximately positive definite matrix, typically an approximation to a correlation or covariance matrix. If x is not symmetric (and ensureSymmetry is not false), `symmpart(x)` is used.
- **corr**: logical indicating if the matrix should be a correlation matrix.
- **keepDiag**: logical, generalizing corr: if TRUE, the resulting matrix should have the same diagonal (diag(x)) as the input matrix.
- **base.matrix**: logical indicating if the resulting mat component should be a **base matrix** or (by default) a Matrix of class dpoMatrix.
- **do2eigen**: logical indicating if a posdefify() eigen step should be applied to the result of the Higham algorithm.
- **doSym**: logical indicating if $X \leftarrow (X + t(X))/2$ should be done, after $X \leftarrow tcrossprod(Qd, Q)$; some doubt if this is necessary.
- **doDykstra**: logical indicating if Dykstra’s correction should be used; true by default. If false, the algorithm is basically the direct fixpoint iteration $Y_k = P_U(P_S(Y_{k-1}))$.
- **only.values**: logical; if TRUE, the result is just the vector of eigenvalues of the approximating matrix.
- **ensureSymmetry**: logical; by default, symmpart(x) is used whenever isSymmetric(x) is not true. The user can explicitly set this to TRUE or FALSE, saving the symmetry test. **Beware** however that setting it FALSE for an asymmetric input x, is typically nonsense!
- **eig.tol**: defines relative positiveness of eigenvalues compared to largest one, $\lambda_1$. Eigenvalues $\lambda_k$ are treated as if zero when $\lambda_k/\lambda_1 \leq eig.tol$.
- **conv.tol**: convergence tolerance for Higham algorithm.
nearPD

posd.tol tolerance for enforcing positive definiteness (in the final posdefify step when do2eigen is TRUE).
maxit maximum number of iterations allowed.
conv.norm.type convergence norm type (norm(*, type)) used for Higham algorithm. The default is "I" (infinity), for reasons of speed (and back compatibility); using "F" is more in line with Higham’s proposal.
trace logical or integer specifying if convergence monitoring should be traced.

Details

This implements the algorithm of Higham (2002), and then (if do2eigen is true) forces positive definiteness using code from posdefify. The algorithm of Knol and ten Berge (1989) (not implemented here) is more general in that it allows constraints to (1) fix some rows (and columns) of the matrix and (2) force the smallest eigenvalue to have a certain value.

Note that setting corr = TRUE just sets diag(.) <- 1 within the algorithm.

Higham (2002) uses Dykstra’s correction, but the version by Jens Oehlschlägel did not use it (accidentally), and still gave reasonable results; this simplification, now only used if doDykstra = FALSE, was active in nearPD() up to Matrix version 0.999375-40.

Value

If only.values = TRUE, a numeric vector of eigenvalues of the approximating matrix; Otherwise, as by default, an S3 object of class “nearPD”, basically a list with components

mat a matrix of class dpoMatrix, the computed positive-definite matrix.
eigenvalues numeric vector of eigenvalues of mat.
corr logical, just the argument corr.
normF the Frobenius norm (norm(x-X, "F")) of the difference between the original and the resulting matrix.
iterations number of iterations needed.
converged logical indicating if iterations converged.

Author(s)

Jens Oehlschlägel donated a first version. Subsequent changes by the Matrix package authors.

References


See Also

A first version of this (with non-optional corr=TRUE) has been available as nearcor(); and more simple versions with a similar purpose posdefify(), both from package sfsmisc.
Examples

```r
## Higham(2002), p.334f - simple example
A <- matrix(1, 3, 3); A[1,3] <- A[3,1] <- 0
n.A <- nearPD(A, corr=TRUE, do2eigen=FALSE)
set.seed(27)
m <- matrix(round(rnorm(25),2), 5, 5)
m <- m + t(m)
diag(m) <- pmax(0, diag(m)) + 1
(m <- round(cov2cor(m), 2))
str(near.m <- nearPD(m, trace = TRUE))
round(near.m$mat, 2)
norm(m - near.m$mat) # 1.102 / 1.08

if(requireNamespace("sfsmisc")) {
  m2 <- sfsmisc::posdefify(m) # a simpler approach
  norm(m - m2) # 1.185, i.e., slightly "less near"
}
round(nearPD(m, only.values=TRUE), 9)
```

## A longer example, extended from Jens’ original, showing the effects of some of the options:

```r
pr <- Matrix(c(1, 0.477, 0.644, 0.478, 0.651, 0.826,
               0.477, 1, 0.516, 0.682, 0.75,
               0.644, 0.516, 1, 0.599, 0.581, 0.742,
               0.478, 0.233, 0.599, 1, 0.741, 0.8,
               0.651, 0.682, 0.581, 0.741, 1, 0.798,
               0.826, 0.75, 0.742, 0.8, 0.798, 1),
nrow = 6, ncol = 6)
nc. <- nearPD(pr, conv.tol = 1e-7) # default
cr. <- nearPD(pr, conv.tol = 1e-7, corr = TRUE)
cr.1 <- nearPD(pr, conv.tol = 1e-15)
str(ncr)# still 2 iterations
cr.1 <- nearPD(pr, conv.tol = 1e-15, corr = TRUE)
cr.1 $ iterations # 27 / 30 !

ncF <- nearPD(pr, conv.tol = 1e-15, conv.norm = "F")
stopifnot(all.equal(ncr, ncF))# norm type does not matter at all in this example
```

## But indeed, the 'corr = TRUE' constraint did ensure a better solution;
## cov2cor() does not just fix it up equivalently:
```
norm(pr - cov2cor(ncr$mat)) # = 0.09994
norm(pr - ncr.1$mat) # = 0.08746 / 0.08805
```
### 3) a real data example from a 'systemfit' model (3 eq.):

```r
(load(system.file("external", "symW.rda", package="Matrix"))) # "symW"
dim(symW) # 24 x 24
class(symW)# "dsCMatrix": sparse symmetric
if(dev.interactive()) image(symW)
EV <- eigen(symW, only=TRUE)$values
summary(EV) ## looking more closely {EV sorted decreasingly}:
tail(EV)# all 6 are negative
EV2 <- eigen(sWpos <- nearPD(symW)$mat, only=TRUE)$values
stopifnot(EV2 > 0)
if(requireNamespace("sfsmisc")) {
  plot(pmax(1e-3,EV), EV2, type="o", log="xy", xaxt="n", yaxt="n")
  for(side in 1:2) sfsmisc::eaxis(side)
} else
  plot(pmax(1e-3,EV), EV2, type="o", log="xy")
abline(0, 1, col="red3", lty=2)
```

---

**ngeMatrix-class**

**Class "ngeMatrix" of General Dense Nonzero-pattern Matrices**

**Description**

This is the class of general dense nonzero-pattern matrices, see \texttt{nMatrix}.  

**Slots**

- \texttt{x}: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

- \texttt{Dim,Dimnames}: The dimension (a length-2 "integer") and corresponding names (or NULL), see the \texttt{Matrix} class.

- \texttt{factors}: Object of class "list". A named list of factorizations that have been computed for the matrix.

**Extends**

Class "\texttt{ndenseMatrix}". directly. Class "\texttt{lMatrix}". by class "\texttt{ndenseMatrix}". Class "\texttt{denseMatrix}". by class "\texttt{ndenseMatrix}". Class "\texttt{Matrix}". by class "\texttt{ndenseMatrix}". Class "\texttt{Matrix}". by class "\texttt{ndenseMatrix}".

**Methods**

Currently, mainly \texttt{t() and coercion methods (for as(.)): use, e.g., showMethods(class="ngeMatrix") for details.}

**See Also**

Non-general logical dense matrix classes such as \texttt{ntrMatrix}, or \texttt{nsyMatrix}; \texttt{sparse} logical classes such as \texttt{ngCMatrix}.

**Examples**

```r
showClass("ngeMatrix")
```
Class "nMatrix" of Non-zero Pattern Matrices

Description

The nMatrix class is the virtual “mother” class of all non-zero pattern (or simply pattern) matrices in the Matrix package.

Slots

Common to all matrix object in the package:

Dim: Object of class “integer” - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

Dimnames: list of length two: each component containing NULL or a character vector length equal the corresponding Dim element.

Methods

coerce signature(from = "matrix", to = "nMatrix"): Note that these coercions (must) coerce NAs to non-zero, hence conceptually TRUE. This is particularly important when sparseMatrix objects are coerced to "nMatrix" and hence to nsparseMatrix.

Additional methods contain group methods, such as

Ops signature(e1 = "nMatrix", e2 = "...."),....

Arith signature(e1 = "nMatrix", e2 = "...."),....

Compare signature(e1 = "nMatrix", e2 = "...."),....

Logic signature(e1 = "nMatrix", e2 = "...."),....

Summary signature(x = "nMatrix", "...."),....

See Also

The classes lMatrix, nsparseMatrix, and the mother class, Matrix.

Examples

getClass("nMatrix")

L3 <- Matrix(upper.tri(diag(3)))
L3 # an "ltCMatrix"
as(L3, "nMatrix") # -> ntC*

## similar, not using Matrix()
as(upper.tri(diag(3)), "nMatrix")# currently "ngTMatrix"
nnzero-methods

The Number of Non-Zero Values of a Matrix

Description

Returns the number of non-zero values of a numeric-like R object, and in particular an object x inheriting from class `Matrix`.

Usage

`nnzero(x, na.counted = NA)`

Arguments

- `x`: an R object, typically inheriting from class `Matrix` or `numeric`.
- `na.counted`: a `logical` describing how `NA`s should be counted. There are three possible settings for `na.counted`:
  - `TRUE`: `NA`s are counted as non-zero (since “they are not zero”).
  - `NA` (default): the result will be `NA` if there are `NA`’s in `x` (since “`NA`’s are not known, i.e., may be zero”).
  - `FALSE`: `NA`s are omitted from `x` before the non-zero entries are counted.

For sparse matrices, you may often want to use `na.counted = TRUE`.

Value

the number of non zero entries in `x` (typically `integer`).

Note that for a `symmetric` sparse matrix `S` (i.e., inheriting from class `symmetricMatrix`), `nnzero(S)` is typically twice the `length(S@x)`.

Methods

- `signature(x = "ANY")`: the default method for non-`Matrix` class objects, simply counts the number 0s in `x`, counting `NA`’s depending on the `na.counted` argument, see above.
- `signature(x = "denseMatrix")`: conceptually the same as for traditional `matrix` objects, care has to be taken for "`symmetricMatrix`" objects.
- `signature(x = "diagonalMatrix")`, and `signature(x = "indMatrix")`: fast simple methods for these special "`sparseMatrix`" classes.
- `signature(x = "sparseMatrix")`: typically, the most interesting method, also carefully taking "`symmetricMatrix`" objects into account.

See Also

The `Matrix` class also has a `length` method; typically, `length(M)` is much larger than `nnzero(M)` for a sparse matrix `M`, and the latter is a better indication of the `size` of `M`.

drop0, `zapsmall`. 
Examples

```r
m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[3,1:4] <- m[1:3,6] <- 0
(mT <- as(m, "TsparseMatrix"))
nzero(mT)
(S <- crossprod(mT))
nzero(S)
str(S) # slots are smaller than nnzero()
stopifnot(nnzero(S) == sum(as.matrix(S) != 0))# failed earlier
```

```r
data(KNex, package = "Matrix")
M <- KNex$mm
class(M)
dim(M)
length(M); stopifnot(length(M) == prod(dim(M)))
nzero(M) # more relevant than length
## the above are also visible from
str(M)
```

---

### norm-methods

#### Matrix Norms

**Description**

Computes a matrix norm of `x`, using Lapack for dense matrices. The norm can be the one ("O", or "1") norm, the infinity ("I") norm, the Frobenius ("F") norm, the maximum modulus ("M") among elements of a matrix, or the spectral norm or 2-norm ("2"), as determined by the value of `type`.

**Usage**

```r
norm(x, type, ...)
```

**Arguments**

- `x` a real or complex matrix.
- `type` A character indicating the type of norm desired.
  - "0", "o" or "1" specifies the one norm, (maximum absolute column sum);
  - "I" or "i" specifies the infinity norm (maximum absolute row sum);
  - "F" or "f" specifies the Frobenius norm (the Euclidean norm of `x` treated as if it were a vector);
  - "M" or "m" specifies the maximum modulus of all the elements in `x`; and
  - "2" specifies the “spectral norm” aka “2-norm”, which is the largest singular value (`svd`) of `x`.

The default is "0". Only the first character of `type[1]` is used.

- `...` further arguments passed to or from other methods.

**Details**

For dense matrices, the methods eventually call the Lapack functions `dlange`, `dlansy`, `dlantr`, `zlange`, `zlansy`, and `zlantr`.
Value

A numeric value of class "norm", representing the quantity chosen according to type.

References


See Also

onenormest(), an approximate randomized estimate of the 1-norm condition number, efficient for large sparse matrices.

The norm() function from R’s base package.

Examples

x <- Hilbert(9)
norm(x)# = "O" = "1"
stopifnot(identical(norm(x), norm(x, "1")))
norm(x, "I")# the same, because 'x' is symmetric

allnorms <- function(x) {
    do2 <- getRversion() >= "4.0.0" || !anyNA(x)
    vapply(c("1", "I", "F", "M", if(do2) "2"), norm, 0, x = x)
}
allnorms(x)
allnorms(Hilbert(10))
i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
A <- sparseMatrix(i, j, x = x) ## 8 x 10 "dgCMatrix"
(sA <- sparseMatrix(i, j, x = x, symmetric = TRUE)) ## 8 x 10 "dgCMatrix"
(tA <- sparseMatrix(i, j, x = x, triangular= TRUE))## 8 x 10 "dgCMatrix"
(allnorms(A) -> nA)
allnorms(sA)
allnorms(tA)
stopifnot(all.equal(nA, allnorms(as(A, "matrix"))),
            all.equal(nA, allnorms(tA)))# because tA == rbind(A, 0, 0)
A. <- A; A.[1,3] <- NA
stopifnot(is.na(allnorms(A.))) # gave error

Description

The nsparseMatrix class is a virtual class of sparse “pattern” matrices, i.e., binary matrices conceptually with TRUE/FALSE entries. Only the positions of the elements that are TRUE are stored.

These can be stored in the “triplet” form (TsparseMatrix, subclasses ngTMatrix, nsTMatrix, and ntTMatrix which really contain pairs, not triplets) or in compressed column-oriented form (class CsparseMatrix, subclasses ngCMatrix, nsCMatrix, and ntCMatrix) or—rarely—in compressed row-oriented form (class RsparseMatrix, subclasses ngRMatrix, nsRMatrix, and ntRMatrix).

The second letter in the name of these non-virtual classes indicates general, symmetric, or triangular.
Objects from the Class

Objects can be created by calls of the form `new("ngCMatrix", ...)` and so on. More frequently objects are created by coercion of a numeric sparse matrix to the pattern form for use in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence numeric sparse matrices can be treated as sparse pattern matrices.

Slots

- **uplo**: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.
- **diag**: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N" for non-unit. The implicit diagonal elements are not explicitly stored when `diag` is "U". Present in the triangular classes only.
- **p**: Object of class "integer" of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.
- **i**: Object of class "integer" of length `nnzero` (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.
- **j**: Object of class "integer" of length `nnzero` (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed row-oriented forms only.
- **Dim**: Object of class "integer" - the dimensions of the matrix.

Methods

- **coerce** signature `from = "dgCMatrix", to = "ngCMatrix"`, and many similar ones; typically you should coerce to "nsparseMatrix" (or "nMatrix"). Note that coercion to a sparse pattern matrix records all the potential non-zero entries, i.e., explicit ("non-structural") zeroes are coerced to TRUE, not FALSE, see the example.
- **t** signature `x = "ngCMatrix")`: returns the transpose of `x`
- **which** signature `x = "lsparseMatrix")`. semantically equivalent to base function `which(x, arr.ind)`; for details, see the `lMatrix` class documentation.

See Also

the class `dgCMatrix`

Examples

```r
(m <- Matrix(c(0,0,2:0), 3,5, dimnames=list(LETTERS[1:3],NULL)))
## `extract the nonzero-pattern of (m) into an nMatrix'

nm <- as(m, "nsparseMatrix") ## -> will be a "ngCMatrix"
str(nm) # no 'x' slot

nnm <- !nm # no longer sparse
## consistency check:
stopifnot(xor(as( nnm, "matrix"),
            as(nnm, "matrix")))
```
## low-level way of adding "non-structural zeros" :

```r
nnm <- as(nnm, "lsparseMatrix") # "lgCMatrix"
nnm$x[2:4] <- c(FALSE, NA, NA)
nnm
as(nnm, "nMatrix") # NAs *and* non-structural 0 |---› ‘TRUE’
```

data(KNex, package = "Matrix")
nmm <- as(KNex$mm, "nMatrix")
str(xlx <- crossprod(nmm))# "nsCMatrix"
stopifnot(isSymmetric(xlx))
image(xlx, main = paste("crossprod(nmm) : Sparse", class(xlx)))

---

### nsyMatrix-class

**Symmetric Dense Nonzero-Pattern Matrices**

#### Description

The "nsyMatrix" class is the class of symmetric, dense nonzero-pattern matrices in non-packed storage and "nspMatrix" is the class of these in packed storage. Only the upper triangle or the lower triangle is stored.

#### Objects from the Class

Objects can be created by calls of the form `new("nsyMatrix", ...)`. 

#### Slots

- **uplo**: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- **x**: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.
- **Dim,Dimnames**: The dimension (a length-2 "integer") and corresponding names (or NULL), see the `Matrix` class.
- **factors**: Object of class "list". A named list of factorizations that have been computed for the matrix.

#### Extends

"nsyMatrix" extends class "ngeMatrix", directly, whereas "nspMatrix" extends class "ndenseMatrix", directly.

Both extend class "symmetricMatrix", directly, and class "Matrix" and others, indirectly, use `showClass("nsyMatrix")`, e.g., for details.

#### Methods

Currently, mainly `t()` and coercion methods (for `as(.);` use, e.g., `showMethods(class="nsyMatrix")` for details.

#### See Also

`ngeMatrix, Matrix, t`
Examples

(s0 <- new("nsyMatrix"))
(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
(sM <- M2 & t(M2)) # -> "lge"
(class(sM <- as(sM, "nMatrix")) # -> "nge"
    (sM <- as(sM, "symmetricMatrix")) # -> "nsy"
str(sM <- as(sM, "packedMatrix")) # -> "nsp", i.e., packed symmetric

ntrMatrix-class Triangular Dense Logical Matrices

Description

The "ntrMatrix" class is the class of triangular, dense, logical matrices in nonpacked storage. The "ntpMatrix" class is the same except in packed storage.

Slots

x: Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

uplo: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

diag: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see triangularMatrix.

Dim,Dimnames: The dimension (a length-2 "integer") and corresponding names (or NULL), see the Matrix class.

factors: Object of class "list". A named list of factorizations that have been computed for the matrix.

Extends

"ntrMatrix" extends class "ngeMatrix", directly, whereas "ntpMatrix" extends class "ndenseMatrix", directly.
Both extend Class "triangularMatrix", directly, and class "denseMatrix", "lMatrix" and others, indirectly, use showClass("nsyMatrix"), e.g., for details.

Methods

Currently, mainly t() and coercion methods (for as(.); use, e.g., showMethods(class="ntrMatrix") for details.

See Also

Classes ngeMatrix, Matrix; function t
Examples

```
showClass("ntnMatrix")

str(new("ntnMatrix"))
(nutr <- as(upper.tri(matrix(, 4, 4)), "ndenseMatrix"))
str(nutp <- pack(nutr)) # packed matrix: only 10 = 4*(4+1)/2 entries
!nutp # the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(nutp, pack(!nutp)))
```

Description

The class "number" is a virtual class, currently used for vectors of eigen values which can be "numeric" or "complex".

It is a simple class union (`setClassUnion`) of "numeric" and "complex".

Objects from the Class

Since it is a virtual Class, no objects may be created from it.

Examples

```
showClass("number")
stopifnot(is(1i, "number"), is(pi, "number"), is(1:3, "number") )
```

pack

**Representation of Packed and Unpacked Dense Matrices**

Description

`pack()` coerces dense symmetric and dense triangular matrices from unpacked format (storing the full matrix) to packed format (storing only one of the upper and lower triangles). `unpack()` performs the reverse coercion. The two formats are formalized by the virtual classes "packedMatrix" and "unpackedMatrix".

Usage

```
pack(x, ...)
## S4 method for signature 'dgeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'lgeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'ngeMatrix'
pack(x, symmetric = NA, upperTri = NA, ...)
## S4 method for signature 'matrix'
pack(x, symmetric = NA, upperTri = NA, ...)
```

unpack(x, ...)

```
Arguments

- **x**: A dense symmetric or dense triangular matrix.
  
  For **pack()**: typically an "unpackedMatrix" or a standard "matrix", though "packedMatrix" are allowed and returned unchanged.

  For **unpack()**: typically a "packedMatrix", though "unpackedMatrix" are allowed and returned unchanged.

- **symmetric**: logical (including NA) optionally indicating whether x is symmetric (or triangular).

- **upperTri**: (for triangular x only) logical (including NA) indicating whether x is upper (or lower) triangular.

- **...**: further arguments passed to or from other methods.

Details

package checks matrices **not** inheriting from one of the virtual classes "symmetricMatrix" "triangularMatrix" for symmetry (via `isSymmetric()`) then for upper and lower triangularity (via `isTriangular()`) in order to identify a suitable coercion. Setting one or both of **symmetric** and **upperTri** to TRUE or FALSE rather than NA allows skipping of irrelevant tests for large matrices known to be symmetric or (upper or lower) triangular.

Users should **not** assume that **pack()** and **unpack()** are inverse operations. Specifically, `y <- unpack(pack(x))` may not reproduce an "unpackedMatrix" x in the sense of `identical()`. See the examples.

Value

- **For pack()**: a "packedMatrix" giving the condensed representation of x.
- **For unpack()**: an "unpackedMatrix" giving the full storage representation of x.

Examples

```r
showMethods("pack")
(s <- crossprod(matrix(sample(15), 5,3))) # traditional symmetric matrix
(sp <- pack(s))
(mt <- as.matrix(tt <- tril(s))
(pt <- pack(mt))
stopifnot(identical(pt, pack(tt)),
dim(s ) == dim(sp), all(s == sp),
dim(mt) == dim(pt), all(mt == pt), all(mt == tt))

showMethods("unpack")
(cp4 <- chol(Hilbert(4))) # is triangular
tp4 <- pack(cp4) # [t]riangular [p]acked
str(tp4)
(unpack(tp4))
stopifnot(identical(tp4, pack(unpack(tp4))))

z1 <- new("dsyMatrix", Dim = c(2L, 2L), x = as.double(1:4), uplo = "U")
z2 <- unpack(pack(z1))
stopifnot(!identical(z1, z2), # _not_ identical
all(z1 == z2)) # but mathematically equal
cbind(z1@x, z2@x) # (unused!) lower triangle is "lost" in translation
```
Virtual Class "packedMatrix" of Packed Dense Matrices

Description

Class "packedMatrix" is the virtual class of dense symmetric or triangular matrices in "packed" format, storing only the choose(n+1,2) == n*(n+1)/2 elements of the upper or lower triangle of an n-by-n matrix. It is used to define common methods for efficient subsetting, transposing, etc. of its proper subclasses: currently "[dln]spMatrix" (packed symmetric), "[dln]tpMatrix" (packed triangular), and subclasses of these, such as "dppMatrix", "pCholesky", and "pBunchKaufman".

Slots

uplo: "character"; either "U", for upper triangular, and "L", for lower.
Dim, Dimnames: as all Matrix objects.

Extends


Methods

pack signature(x = "packedMatrix"): ...
unpack signature(x = "packedMatrix"): ...
isSymmetric signature(object = "packedMatrix"): ...
isTriangular signature(object = "packedMatrix"): ...
isDiagonal signature(object = "packedMatrix"): ...
t signature(x = "packedMatrix"): ...
diag signature(x = "packedMatrix"): ...
diag<- signature(x = "packedMatrix"): ...

Author(s)

Mikael Jagan

See Also

pack and unpack; its virtual "complement" unpackedMatrix"; its proper subclasses "dspMatrix", "ltpMatrix", etc.

Examples

showClass("packedMatrix")
showMethods(classes = "packedMatrix")
The `pMatrix` class is the class of permutation matrices, stored as 1-based integer permutation vectors. A permutation matrix is a square matrix whose rows and columns are all standard unit vectors. It follows that permutation matrices are a special case of index matrices (hence `pMatrix` is defined as a direct subclass of `indMatrix`).

Multiplying a matrix on the left by a permutation matrix is equivalent to permuting its rows. Analogously, multiplying a matrix on the right by a permutation matrix is equivalent to permuting its columns. Indeed, such products are implemented in `Matrix` as indexing operations; see 'Details' below.

**Details**

By definition, a permutation matrix is both a row index matrix and a column index matrix. However, the `perm` slot of a `pMatrix` cannot be used interchangeably as a row index vector and column index vector. If `margin=1`, then `perm` is a row index vector, and the corresponding column index vector can be computed as `invPerm(perm)`, i.e., by inverting the permutation. Analogously, if `margin=2`, then `perm` and `invPerm(perm)` are column and row index vectors, respectively.

Given an `n`-by-`n` row permutation matrix `P` with `perm` slot `p` and a matrix `M` with conformable dimensions, we have

\[
PM = P \%\% M = M[p, ]
\]
\[
MP = M \%\% P = M[, i(p)]
\]
\[
P'M = \text{crossprod}(P, M) = M[i(p), ]
\]
\[
MP' = \text{tcrossprod}(M, P) = M[, p]
\]
\[
P'P = \text{crossprod}(P) = \text{Diagonal}(n)
\]
\[
PP' = \text{tcrossprod}(P) = \text{Diagonal}(n)
\]

where `i := invPerm`.

**Objects from the Class**

Objects can be created explicitly with calls of the form `new("pMatrix", ...),` but they are more commonly created by coercing 1-based integer index vectors, with calls of the form `as(. , "pMatrix");` see 'Methods' below.

**Slots**

- `margin,perm` inherited from superclass `indMatrix`. Here, `perm` is an integer vector of length `Dim[1]` and a permutation of `1:Dim[1]`.
- `Dim,Dimnames` inherited from virtual superclass `Matrix`.

**Extends**

Class "indMatrix", directly.
Methods

\%\% signature(x = "pMatrix", y = "Matrix") and others listed by showMethods("\%\%", classes = "pMatrix"): matrix products implemented where appropriate as indexing operations.

coerce signature(from = "numeric", to = "pMatrix"): supporting typical pMatrix construction from a vector of positive integers, specifically a permutation of 1:n. Row permutation is assumed.

t signature(x = "pMatrix"): the transpose, which is a pMatrix with identical perm but opposite margin. Coincides with the inverse, as permutation matrices are orthogonal.

solve signature(a = "pMatrix", b = "missing"): the inverse permutation matrix, which is a pMatrix with identical perm but opposite margin. Coincides with the transpose, as permutation matrices are orthogonal. See showMethods("solve", classes = "pMatrix") for more signatures.

determinant signature(x = "pMatrix", logarithm = "logical"): always returning 1 or -1, as permutation matrices are orthogonal. In fact, the result is exactly the sign of the permutation.

See Also

Superclass \texttt{indMatrix} of index matrices, for many inherited methods; \texttt{invPerm}, for computing inverse permutation vectors.

Examples

\begin{verbatim}
(pm1 <- as(as.integer(c(2,3,1)), "pMatrix"))
t(pm1) # is the same as solve(pm1)

pm1 %*% t(pm1) # check that the transpose is the inverse
stopifnot(all(diag(3) == as(pm1 %*% t(pm1), "matrix")), is.logical(as(pm1, "matrix")))

set.seed(11)
## random permutation matrix :
(p10 <- as(sample(10),"pMatrix"))

## Permute rows / columns of a numeric matrix :
(mm <- round(array(rnorm(3 * 3), c(3, 3)), 2))

## row-indexing of a <pMatrix> keeps it as an <indMatrix>:

\end{verbatim}
Description

Format and print sparse matrices flexibly. These are the “workhorses” used by the `format`, `show` and `print` methods for sparse matrices. If `x` is large, `printSpMatrix2(x)` calls `printSpMatrix()` twice, namely, for the first and the last few rows, suppressing those in between, and also suppresses columns when `x` is too wide.

`printSpMatrix()` basically prints the result of `formatSpMatrix()`.

Usage

```r
formatSpMatrix(x, digits = NULL, maxp = 1e9,
    cld = getClassDef(class(x)), zero.print = ".",
    col.names, note.dropping.colnames = TRUE, uniDiag = TRUE,
    align = c("fancy", "right"))
```

```r
printSpMatrix(x, digits = NULL, maxp = max(100L, getOption("max.print")),
    cld = getClassDef(class(x)),
    zero.print = ".", col.names, note.dropping.colnames = TRUE,
    uniDiag = TRUE, col.trailer = "",
    align = c("fancy", "right"))
```

```r
printSpMatrix2(x, digits = NULL, maxp = max(100L, getOption("max.print")),
    zero.print = ".", col.names, note.dropping.colnames = TRUE,
    uniDiag = TRUE, suppRows = NULL, suppCols = NULL,
    col.trailer = if(suppCols) "......" else "",
    align = c("fancy", "right"),
    width = getOption("width"), fitWidth = TRUE)
```

Arguments

- **x**: an R object inheriting from class `sparseMatrix`.
- **digits**: significant digits to use for printing, see `print.default`, the default, `NULL`, corresponds to using `getOption("digits")`.
- **maxp**: integer, default from `options(max.print)`, influences how many entries of large matrices are printed at all. Typically should not be smaller than around 1000; values smaller than 100 are silently “rounded up” to 100.
- **cld**: the class definition of `x`; must be equivalent to `getClassDef(class(x))` and exists mainly for possible speedup.
- **zero.print**: character which should be printed for structural zeroes. The default "." may occasionally be replaced by " " (blank); using "0" would look almost like `print()`ing of non-sparse matrices.
- **col.names**: logical or string specifying if and how column names of `x` should be printed, possibly abbreviated. The default is taken from `options("sparse.colnames")` if that is set, otherwise `FALSE` unless there are less than ten columns. When `TRUE` the full column names are printed.
  - When `col.names` is a string beginning with "abb" or "sub" and ending with an integer `n` (i.e., of the form "abb...<n>"), the column names are `abbreviate()`d or `substring()`ed to (target) length `n`, see the examples.
- **note.dropping.colnames**: logical specifying, when `col.names` is `FALSE` if the dropping of the column names should be noted, `TRUE` by default.
uniDiag  logical indicating if the diagonal entries of a sparse unit triangular or unit-diagonal matrix should be formatted as "I" instead of "1" (to emphasize that the 1's are "structural").

col.trailer a string to be appended to the right of each column; this is typically made use of by `show(<sparseMatrix>)` only, when suppressing columns.

suppRows, suppCols 
logicals or NULL, for `printSpMatrix2()` specifying if rows or columns should be suppressed in printing. If NULL, sensible defaults are determined from `dim(x)` and `options(c("width", "max.print"))`. Setting both to FALSE may be a very bad idea.

align a string specifying how the zero.print codes should be aligned, i.e., padded as strings. The default, "fancy", takes some effort to align the typical zero.print = "." with the position of 0, i.e., the first decimal (one left of decimal point) of the numbers printed, whereas align = "right" just makes use of `print(*, right = TRUE)`.

width number, a positive integer, indicating the approximately desired (line) width of the output, see also `fitWidth`.

fitWidth logical indicating if some effort should be made to match the desired width or temporarily enlarge that if deemed necessary.

Details

formatSpMatrix: If x is large, only the first rows making up the approximately first maxp entries is used, otherwise all of x. `.formatSparseSimple()` is applied to (a dense version of) the matrix. Then, `formatSparseM` is used, unless in trivial cases or for sparse matrices without x slot.

Value

formatSpMatrix() 
returns a character matrix with possibly empty column names, depending on col.names etc, see above.

printSpMatrix*() 
return x invisibly, see `invisible`.

Author(s)

Martin Maechler

See Also

the virtual class `sparseMatrix` and the classes extending it; maybe `sparseMatrix` or `spMatrix` as simple constructors of such matrices.

The underlying utilities `formatSparseM` and `.formatSparseSimple()` (on the same page).

Examples

```R
f1 <- gl(5, 3, labels = LETTERS[1:5])
X <- as(f1, "sparseMatrix")
X ## <==> show(X) <==> print(X)
t(X) ## shows column names, since only 5 columns
```
qr-methods

Methods for QR Factorization

Description

Computes the pivoted QR factorization of an \(m \times n\) real matrix \(A\), which has the general form

\[ P_1 AP_2 = QR \]

or (equivalently)

\[ A = P_1'QRP_2' \]

where \(P_1\) and \(P_2\) are permutation matrices, \(Q = \prod_{j=1}^{n} H_j\) is an \(m \times m\) orthogonal matrix equal to the product of \(n\) Householder matrices \(H_j\), and \(R\) is an \(m \times n\) upper trapezoidal matrix.

denseMatrix use the default method implemented in base, namely qr.default. It is built on LINPACK routine dqrde and LAPACK routine dgeqp3, which do not pivot rows, so that \(P_1\) is an identity matrix.

Methods for sparseMatrix are built on CSparse routines cs_sqr and cs_qr, which require \(m \geq n\).

Usage

\(\text{qr}(x, \ldots)\)

## S4 method for signature 'dgCMatrix'
\(\text{qr}(x, \text{order} = 3L, \ldots)\)

Arguments

\(x\) a finite matrix or Matrix to be factorized, satisfying \(\text{ncol}(x) \geq n\text{col}(x)\) if sparse.

\(\text{order}\) an integer in \(0:3\) passed to CSparse routine cs_sqr, indicating a strategy for choosing the column permutation \(P_2\). \(0\) means no column permutation. \(1, 2,\) and \(3\) indicate a fill-reducing ordering of \(A + A', A'A,\) and \(A'A\), where \(A'\) is \(A\) with “dense” rows removed. Do not set to \(0\) unless you know that the column order of \(A\) is already sensible.

\(\ldots\) further arguments passed to or from methods.
Details

If \( x \) is sparse and structurally rank deficient, having structural rank \( r < n \), then \( x \) is augmented with \( (n - r) \) rows of (partly non-structural) zeros, such that the augmented matrix has structural rank \( n \). This augmented matrix is factorized as described above:

\[
P_1 A P_2 = P_1 \begin{bmatrix} A_0 \\ 0 \end{bmatrix} P_2 = QR
\]

where \( A_0 \) denotes the original, user-supplied \( (m - (n - r)) \times n \) matrix.

Value

An object representing the factorization, inheriting from virtual S4 class `QR` or S3 class `qr`. The specific class is `qr` unless \( x \) inherits from virtual class `sparseMatrix`, in which case it is `sparseQR`.

References


See Also

Class `sparseQR` and its methods.

Class `dgCMatrix`.

Generic function `qr` from `base`, whose default method `qr.default` "defines" the S3 class `qr` of dense QR factorizations.

Generic functions `expand1` and `expand2`, for constructing matrix factors from the result.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, and `lu`, for computing other factorizations.

Examples

```r
showMethods("qr", inherited = FALSE)
## Rank deficient: columns 3 \{b2\} and 6 \{c3\} are "extra"
M <- as(cbind(a1 = 1,
              b1 = rep(c(1, 0), each = 3L),
              b2 = rep(c(0, 1), each = 3L),
              c1 = rep(c(1, 0, 0), 2L),
              c2 = rep(c(0, 1, 0), 2L),
              c3 = rep(c(0, 0, 1), 2L)),
              "CsparseMatrix")
rownames(M) <- paste0("r", seq_len(nrow(M)))
b <- 1:6
eps <- .Machine$double.eps
## .... [1] full rank ..................................................
## ===> a least squares solution of A x = b exists
## and is unique _in exact arithmetic_
(A1 <- M[, -c(3L, 6L)])
(qr.A1 <- qr(A1))
```
stopifnot(exprs = {
  rankMatrix(A1) == ncol(A1)
  ( d1 <- abs(diag(qr.A1@R)); sum(d1 < max(d1) * eps) == 0L )
  rcond(crossprod(A1)) >= eps
  all.equal(qr.coef(qr.A1, b), drop(solve(crossprod(A1), crossprod(A1, b))))
  all.equal(qr.fitted(qr.A1, b) + qr.resid(qr.A1, b), b)
})

## .... [2] numerically rank deficient with full structural rank .......
## ==> a least squares solution of A x = b does not
## exist or is not unique _in exact arithmetic_

(A2 <- M)
(qr.A2 <- qr(A2))

stopifnot(exprs = {
  rankMatrix(A2) == ncol(A2) - 2L
  ( d2 <- abs(diag(qr.A2@R)); sum(d2 < max(d2) * eps) == 2L )
  rcond(crossprod(A2)) < eps

  all.equal(qr.coef(qr.A2, b); drop(solve(crossprod(A2), crossprod(A2, b))))
  tryCatch({ qr.coef(qr.A2, b); TRUE }, condition = function(x) FALSE)
  all.equal(qr.fitted(qr.A2, b) + qr.resid(qr.A2, b), b)
})

## ... [3] numerically and structurally rank deficient ...............
## ==> factorization of _augmented_ matrix with
## full structural rank proceeds as in [2]
## NB: implementation details are subject to change; see (*) below

A3 <- M
A3[, c(3L, 6L)] <- 0
A3
(qr.A3 <- qr(A3)) # with a warning ... "additional 2 row(s) of zeros"

stopifnot(exprs = {
  ## sparseQR object preserves the unaugmented dimensions (*)
  dim(qr.A3 ) == dim(A3)
  dim(qr.A3@V) == dim(A3) + c(2L, 0L)
  dim(qr.A3@R) == dim(A3) + c(2L, 0L)

  ## The augmented matrix remains numerically rank deficient
  rankMatrix(A3) == ncol(A3) - 2L
  ( d3 <- abs(diag(qr.A3@R)); sum(d3 < max(d3) * eps) == 2L )
  rcond(crossprod(A3)) < eps
})

## Auxiliary functions accept and return a vector or matrix
## with dimensions corresponding to the unaugmented matrix (*),
## in all cases with a warning

qr.coef (qr.A3, b)
qr.fitted(qr.A3, b)
qr.resid (qr.A3, b)
## By disabling column pivoting, one gets the "vanilla" factorization
## $A = Q^\top R$, where $Q^\top := P_1^{-1} Q$ is orthogonal because $P_1$ and $Q$ are

(qr.A1.pp <- qr(A1, order = 0L)) # partial pivoting

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

stopifnot(exprs = {
  length(qr.A1@q) == ncol(A1)
  length(qr.A1.pp@q) == 0L # indicating no column pivoting
  ae2(A1[, qr.A1@q + 1L], qr.Q(qr.A1) %*% qr.R(qr.A1))
})

---

### Description

Compute 'the' matrix rank, a well-defined functional in theory(*), somewhat ambiguous in practice. We provide several methods, the default corresponding to Matlab's definition.

(*) The rank of a $n \times m$ matrix $A$, $rk(A)$, is the maximal number of linearly independent columns (or rows); hence $rk(A) \leq \min(n,m)$.

### Usage

```r
rankMatrix(x, tol = NULL, 
           method = c("tolNorm2", "qr.R", "qrLINPACK", "qr", 
                       "useGrad", "maybeGrad"), 
           sval = svd(x, 0, 0)$d, warn.t = TRUE, warn.qr = TRUE)
```

```r
qr2rankMatrix(qr, tol = NULL, isBqr = is.qr(qr), do.warn = TRUE)
```

### Arguments

- **x**: numeric matrix, of dimension $n \times m$, say.
- **tol**: nonnegative number specifying a (relative, "scalefree") tolerance for testing of "practically zero" with specific meaning depending on method; by default, $\max(\dim(x)) \times .Machine$double$.eps$ is according to Matlab's default (for its only method which is our method="tolNorm2").
- **method**: a character string specifying the computational method for the rank, can be abbreviated:
  - "tolNorm2": the number of singular values $\geq tol \times \text{max(sval)}$;
  - "qrLINPACK": for a dense matrix, this is the rank of $\text{qr}(x, tol, \text{LAPACK}=\text{FALSE})$ (which is $\text{qr}(\ldots)\%\%\text{rank}$);
    This ("\text{qr*}", dense) version used to be the recommended way to compute a matrix rank for a while in the past.
    For sparse $x$, this is equivalent to "qr.R".
  - "qr.R"
"qr.R": this is the rank of triangular matrix \( R \), where qr() uses LAPACK or a "sparseQR" method (see qr-methods) to compute the decomposition \( QR \).

The rank of \( R \) is then defined as the number of "non-zero" diagonal entries \( d_i \) of \( R \), and "non-zero"s fulfill \( |d_i| \geq \text{tol} \cdot \max(|d_i|) \).

"qr": for back compatibility; for dense \( x \), it corresponds to "qrLINPACK", whereas for sparse \( x \), it uses "qr.R".

For all the "qr*" methods, singular values sval are not used, which may be crucially important for a large sparse matrix \( x \), as in that case, when sval is not specified, the default, computing svd() currently coerces \( x \) to a dense matrix.

"useGrad": considering the “gradient" of the (decreasing) singular values, the index of the smallest gap.

"maybeGrad": choosing method "useGrad" only when that seems reasonable; otherwise using "tolNorm2".

sval numeric vector of non-increasing singular values of \( x \); typically unspecified and computed from \( x \) when needed, i.e., unless method = "qr".

warn.t logical indicating if rankMatrix() should warn when it needs \( t(x) \) instead of \( x \). Currently, for method = "qr" only, gives a warning by default because the caller often could have passed \( t(x) \) directly, more efficiently.

warn.qr in the \( QR \) cases (i.e., if method starts with "qr"), rankMatrix() calls qr2rankMatrix(\ldots, do.warn = warn.qr), see below.

qr an R object resulting from qr(x,\ldots), i.e., typically inheriting from class "qr" or "sparseQR".

isBqr logical indicating if qr is resulting from base qr(). (Otherwise, it is typically from Matrix package sparse qr.)

do.warn logical; if true, warn about non-finite diagonal entries in the \( R \) matrix of the \( QR \) decomposition. Do not change lightly!

Details
qr2rankMatrix() is typically called from rankMatrix() for the "qr*" methods, but can be used directly - much more efficiently in case the qr-decomposition is available anyway.

Value

If \( x \) is a matrix of all \( 0 \) (or of zero dimension), the rank is zero; otherwise, typically a positive integer in \( 1:\text{min}(|\text{dim}(x)|) \) with attributes detailing the method used.

There are rare cases where the sparse \( QR \) decomposition “fails" in so far as the diagonal entries of \( R \), the \( d_i \) (see above), end with non-finite, typically NaN entries. Then, a warning is signalled (unless warn.qr / do.warn is not true) and NA (specifically, NA_integer_) is returned.

Note

For large sparse matrices \( x \), unless you can specify sval yourself, currently method = "qr" may be the only feasible one, as the others need sval and call svd() which currently coerces \( x \) to a denseMatrix which may be very slow or impossible, depending on the matrix dimensions.

Note that in the case of sparse \( x \), method = "qr", all non-strictly zero diagonal entries \( d_i \) where counted, up to including Matrix version 1.1-0, i.e., that method implicitly used tol = 0, see also the set.seed(42) example below.
Author(s)

Martin Maechler; for the "*Grad" methods building on suggestions by Ravi Varadhan.

See Also

qr, svd.

Examples

```r
rankMatrix(cbind(1, 0, 1:3)) # 2
```

```r
(meths <- eval(formals(rankMatrix)$method))
```

```r
## a "border" case:
H12 <- Hilbert(12)
rankMatrix(H12, tol = 1e-20) # 12; but 11 with default method & tol.
sapply(meths, function(.m.) rankMatrix(H12, method = .m.))
## tolNorm2 qr.R qrLINPACK qr useGrad maybeGrad
## 11 11 12 12 11 11
## # The meaning of 'tol' for method="qrLINPACK" and *dense* x is not entirely "scale free"
rMQL <- function(ex, M) rankMatrix(M, method="qrLINPACK", tol = 10^-ex)
rMQR <- function(ex, M) rankMatrix(M, method="qr.R", tol = 10^-ex)
sapply(5:15, rMQL, M = H12) # result is platform dependent
## 7 7 8 10 10 11 11 12 12 12 12 (x86_64)
sapply(5:15, rMQL, M = 1000 * H12) # not identical unfortunately
## 7 7 8 10 11 11 12 12 12 12
sapply(5:15, rMQR, M = H12)
## 5 6 7 8 8 9 9 10 10 11 11
sapply(5:15, rMQR, M = 1000 * H12) # the *same*
```

```r
## "sparse" case:
M15 <- kronecker(diag(x=c(100,1,10)), Hilbert(5))
sapply(meths, function(.m.) rankMatrix(M15, method = .m.))
#---> all 15, but 'useGrad' has 14.
sapply(meths, function(.m.) rankMatrix(M15, method = .m., tol = 1e-7)) # all 14
```

```r
## "large" sparse
n <- 250000; p <- 33; nnz <- 10000
L <- sparseMatrix(i = sample.int(n, nnz, replace=TRUE),
                   j = sample.int(p, nnz, replace=TRUE),
                   x = rnorm(nnz))
(st1 <- system.time(r1 <- rankMatrix(L)))) # warning+ ~1.5 sec (2013)
(st2 <- system.time(r2 <- rankMatrix(L, method = "qr"))) # considerably faster!
r1[[1]] == print(r2[[1]]) ## -->> ( 33 TRUE )
```

```r
## another sparse-"qr" one, which `\`failed\' till 2013-11-23:
set.seed(42)
f1 <- factor(sample(50, 1000, replace=TRUE))
f2 <- factor(sample(50, 1000, replace=TRUE))
f3 <- factor(sample(50, 1000, replace=TRUE))
D <- t(do.call(rbind, lapply(list(f1,f2,f3), as, 'sparseMatrix')))
dim(D); nnzero(D) ## 1000 x 150 // 3000 non-zeros (= 2%)
stopifnot(rankMatrix(D, method="qr") == 148,
          rankMatrix(crossprod(D),method="qr") == 148)
```
## zero matrix has rank 0:
stopifnot(sapply(meths, function(.m.)
    rankMatrix(matrix(0, 2, 2), method = .m.)) == 0)

---

### rcond-methods

**Estimate the Reciprocal Condition Number**

#### Description

Estimate the reciprocal of the condition number of a matrix.

This is a generic function with several methods, as seen by `showMethods(rcond)`.

#### Usage

```r
rcond(x, norm, ...)
```

#### Arguments

- **x**: an `R` object that inherits from the `Matrix` class.
- **norm**: character string indicating the type of norm to be used in the estimate. The default is "O" for the 1-norm ("O" is equivalent to "1"). For sparse matrices, when `useInv=TRUE`, `norm` can be any of the kinds allowed for `norm`; otherwise, the other possible value is "I" for the infinity norm, see also `norm`.
- **useInv**: logical (or "Matrix" containing `solve(x)`). If not false, compute the reciprocal condition number as $1/(\|x\| \cdot \|x^{-1}\|)$, where $x^{-1}$ is the inverse of $x$, `solve(x)`. This may be an efficient alternative (only) in situations where `solve(x)` is fast (or known), e.g., for (very) sparse or triangular matrices. Note that the result may differ depending on `useInv`, as per default, when it is false, an approximation is computed.
- **...**: further arguments passed to or from other methods.

#### Value

An estimate of the reciprocal condition number of `x`.

#### BACKGROUND

The condition number of a regular (square) matrix is the product of the `norm` of the matrix and the norm of its inverse (or pseudo-inverse).

More generally, the condition number is defined (also for non-square matrices $A$) as

$$
\kappa(A) = \max_{\|v\|=1} \frac{\|Av\|}{\min_{\|v\|=1} \|Av\|}.
$$

Whenever `x` is not a square matrix, in our method definitions, this is typically computed via `rcond(qr.R(qr(X)), ...)` where $X$ is `x` or `t(x)`.
The condition number takes on values between 1 and infinity, inclusive, and can be viewed as a factor by which errors in solving linear systems with this matrix as coefficient matrix could be magnified.

rcond() computes the reciprocal condition number \( 1/\kappa \) with values in \([0, 1]\) and can be viewed as a scaled measure of how close a matrix is to being rank deficient (aka “singular”).

Condition numbers are usually estimated, since exact computation is costly in terms of floating-point operations. An (over) estimate of reciprocal condition number is given, since by doing so overflow is avoided. Matrices are well-conditioned if the reciprocal condition number is near 1 and ill-conditioned if it is near zero.

**References**


**See Also**

`norm`, `kappa()` from package base computes an approximate condition number of a “traditional” matrix, even non-square ones, with respect to the \( p = 2 \) (Euclidean) norm. `solve`.

`condest`, a newer approximate estimate of the (1-norm) condition number, particularly efficient for large sparse matrices.

**Examples**

```r
x <- Matrix(rnorm(9), 3, 3)
rcond(x)
## typically "the same" (with more computational effort):
1 / (norm(x) * norm(solve(x)))
rcond(Hilbert(9)) # should be about 9.1e-13

## For non-square matrices:
rcond(x1 <- cbind(1,1:10)) # 0.05278
rcond(x2 <- cbind(x1, 2:11)) # practically 0, since x2 does not have full rank

## sparse
(S1 <- Matrix(rbind(0:1,0, diag(3:-2))))
rcond(S1)
m1 <- as(S1, "denseMatrix")
all.equal(rcond(S1), rcond(m1))

## wide and sparse
rcond(Matrix(cbind(0, diag(2:-1))))

## Large sparse example
m <- Matrix(c(3,0:2, 2,2)
M <- bdiag(kronecker(Diagonal(2), m), kronecker(m,m))
36*(1M <- solve(M)) # still sparse
MM <- kronecker(Diagonal(10), kronecker(Diagonal(5),kronecker(m,M)))
dim(M3 <- kronecker(bdiag(M,M),MM)) # 12'800 ^ 2
if(interactive()) ## takes about 2 seconds if you have >= 8 GB RAM
  system.time(r <- rcond(M3))
## whereas this is *fast* even though it computes solve(M3)
  system.time(r. <- rcond(M3, useInv=TRUE))
if(interactive()) ## the values are not the same
c(r, r.) # 0.05555 0.013888
```
## for all 4 norms available for sparseMatrix :
cbind(rr <- sapply(c("1","I","F","M"),
    function(N) rcond(M3, norm=N, useInv=TRUE))

### rep2abI

**Replicate Vectors into 'abIndex' Result**

**Description**

rep2abI(x, times) conceptually computes `rep.int(x, times)` but with an `abIndex` class result.

**Usage**

`rep2abI(x, times)`

**Arguments**

- `x` numeric vector
- `times` integer (valued) scalar: the number of repetitions

**Value**

a vector of class `abIndex`

**See Also**

`rep.int()`, the base function; `abIseq, abIndex`.

**Examples**

```r
(ab <- rep2abI(2:7, 4))
stopifnot(identical(as(ab, "numeric"),
    rep(2:7, 4)))
```

### replValue-class

**Virtual Class "replValue" - Simple Class for Subassignment Values**

**Description**

The class "replValue" is a virtual class used for values in signatures for sub-assignment of `Matrix` matrices.

In fact, it is a simple class union (setClassUnion) of "numeric" and "logical" (and maybe "complex" in the future).

**Objects from the Class**

Since it is a virtual Class, no objects may be created from it.
See Also

Subassign-methods, also for examples.

Examples

showClass("replValue")

iseq <- c(iseq(2, 100), iseq(20, -2))
iseq@rleD # is "rleDiff"

iseq[1:2]  # is a "replValue"

iseq[is diff(1:10)]  # is a "rleDiff"
rsparsematrix

Random Sparse Matrix

Description

Generate a random sparse matrix efficiently. The default has rounded gaussian non-zero entries, and \texttt{rand.x} = \texttt{NULL} generates random pattern matrices, i.e., inheriting from \texttt{nsparseMatrix}.

Usage

\begin{verbatim}
rsparsematrix(nrow, ncol, density, nnz = round(density * maxE),
           symmetric = FALSE,
           rand.x = function(n) signif(rnorm(n), 2), ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{nrow, ncol} number of rows and columns, i.e., the matrix dimension (\texttt{dim}).
  \item \texttt{density} optional number in \([0, 1]\), the density is the proportion of non-zero entries among all matrix entries. If specified it determines the default for \texttt{nnz}, otherwise \texttt{nnz} needs to be specified.
  \item \texttt{nnz} number of non-zero entries, for a sparse matrix typically considerably smaller than \texttt{nrow*ncol}. Must be specified if \texttt{density} is not.
  \item \texttt{symmetric} logical indicating if result should be a matrix of class \texttt{symmetricMatrix}. Note that in the symmetric case, \texttt{nnz} denotes the number of non zero entries of the upper (or lower) part of the matrix, including the diagonal.
  \item \texttt{rand.x} \texttt{NULL} or the random number generator for the \texttt{x} slot, a \texttt{function} such that \texttt{rand.x(n)} generates a numeric vector of length \texttt{n}. Typical examples are \texttt{rand.x = rnorm}, or \texttt{rand.x = runif}; the default is nice for didactical purposes.
  \item ... optionally further arguments passed to \texttt{sparseMatrix()}, notably \texttt{repr}.
\end{itemize}

Details

The algorithm first samples “encoded” \((i, j)\)s without replacement, via one dimensional indices, if not symmetric \texttt{sample.int(nrow*ncol, nnz)}, then—if \texttt{rand.x} is \texttt{NULL}—gets \texttt{x <- rand.x(nnz)} and calls \texttt{sparseMatrix(i=i, j=j, x=x, ...)}. When \texttt{rand.x=NULL}, \texttt{sparseMatrix(i=i, j=j, ...)} will return a pattern matrix (i.e., inheriting from \texttt{nsparseMatrix}).

Value

a \texttt{sparseMatrix}, say \(M\) of dimension \((nrow, ncol)\), i.e., with \texttt{dim(M) == c(nrow, ncol)}, if \texttt{symmetric} is not true, with \texttt{nzM <- nnzero(M)} fulfilling \texttt{nzM <= nnz} and typically, \texttt{nzM == nnz}.

Author(s)

Martin Maechler
Examples

set.seed(17)# to be reproducible
M <- rsparsematrix(8, 12, nnz = 30) # small example, not very sparse
M
M1 <- rsparsematrix(1000, 20, nnz = 123, rand.x = runif)
summary(M1)

## a random *symmetric* Matrix
(S9 <- rsparsematrix(9, 9, nnz = 10, symmetric=TRUE)) # dsCMatrix
nnzero(S9)# ~ 20: as 'nnz' only counts one "triangle"

## a random pattern aka boolean Matrix (no 'x' slot):
(n7 <- rsparsematrix(5, 12, nnz = 10, rand.x = NULL))

## a [T]riplet representation sparseMatrix:
T2 <- rsparsematrix(40, 12, nnz = 99, repr = "T")
head(T2)

RsparseMatrix-class  Class "RsparseMatrix" of Sparse Matrices in Row-compressed Form

Description

The "RsparseMatrix" class is the virtual class of all sparse matrices coded in sorted compressed row-oriented form. Since it is a virtual class, no objects may be created from it. See showClass("RsparseMatrix") for its subclasses.

Slots

j: Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

p: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

Dim, Dimnames: inherited from the superclass, see sparseMatrix.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

Originally, few methods were defined on purpose, as we rather use the CsparseMatrix in Matrix. Then, more methods were added but beware that these typically do not return "RsparseMatrix" results, but rather Csparse* or Tsparse* ones; e.g., R[i, j] <- v for an "RsparseMatrix" R works, but after the assignment, R is a (triplet) "TsparseMatrix".

t signature(x = "RsparseMatrix"): ...

coerce signature(from = "RsparseMatrix", to = "CsparseMatrix"): ...

coerce signature(from = "RsparseMatrix", to = "TsparseMatrix"): ...
**See Also**

its superclass, `sparseMatrix`, and, e.g., class `dgRMatrix` for the links to other classes.

**Examples**

```r
showClass("RsparseMatrix")
```

---

**Description**

Schur is the class of Schur factorizations of \( n \times n \) real matrices \( A \), having the general form

\[
A = QTQ'
\]

where \( Q \) is an orthogonal matrix and \( T \) is a block upper triangular matrix with 1 \( \times \) 1 or 2 \( \times \) 2 diagonal blocks specifying the real and complex conjugate eigenvalues of \( A \). The column vectors of \( Q \) are the Schur vectors of \( A \), and \( T \) is the Schur form of \( A \).

The Schur factorization generalizes the spectral decomposition of normal matrices \( A \), whose Schur form is block diagonal, to arbitrary square matrices.

**Details**

The matrix \( A \) and its Schur form \( T \) are *similar* and thus have the same spectrum. The eigenvalues are computed trivially as the eigenvalues of the diagonal blocks of \( T \).

**Slots**

- `Dim`, `Dimnames` inherited from virtual class `MatrixFactorization`.
- `Q` an orthogonal matrix, inheriting from virtual class `Matrix`.
- `T` a block upper triangular matrix, inheriting from virtual class `Matrix`. The diagonal blocks have dimensions 1-by-1 or 2-by-2.
- `EValues` a numeric or complex vector containing the eigenvalues of the diagonal blocks of \( T \), which are the eigenvalues of \( T \) and consequently of the factorized matrix.

**Extends**

Class `SchurFactorization`, directly. Class `MatrixFactorization`, by class `SchurFactorization`, distance 2.

**Instantiation**

Objects can be generated directly by calls of the form `new("Schur", ...)` but they are more typically obtained as the value of `Schur(x)` for \( x \) inheriting from `Matrix` (often `dgeMatrix`).

**Methods**

- `determinant` signature(from = "Schur", logarithm = "logical"): computes the determinant of the factorized matrix \( A \) or its logarithm.
- `expand1` signature(x = "Schur"): see `expand1-methods`.
- `expand2` signature(x = "Schur"): see `expand2-methods`.
- `solve` signature(a = "Schur", b = .): see `solve-methods`. 
Schur-methods

References

The LAPACK source code, including documentation; see https://netlib.org/lapack doubledgees.f.


See Also

Class dgeMatrix.

Generic functions Schur, expand1 and expand2.

Examples

showClass("Schur")
set.seed(0)

n <- 4L
(A <- Matrix(rnorm(n * n), n, n))

## With dimnames, to see that they are propagated :
dimnames(A) <- list(paste0("r", seq_len(n)),
                     paste0("c", seq_len(n)))

(sch.A <- Schur(A))
str(e.sch.A <- expand2(sch.A), max.level = 2L)

## A ~ Q T Q' in floating point
stopifnot(exprs = {
  identical(names(e.sch.A), c("Q", "T", "Q.'"))
  all.equal(A, with(e.sch.A, Q %*% T %*% Q.))
})

## Factorization handled as factorized matrix
b <- rnorm(n)
stopifnot(all.equal(det(A), det(sch.A)),
          all.equal(solve(A, b), solve(sch.A, b)))

## One of the non-general cases:
Schur(Diagonal(6L))

---

Schur-methods  Methods for Schur Factorization

Description

Computes the Schur factorization of an \( n \times n \) real matrix \( A \), which has the general form

\[
A = QTQ'
\]

where \( Q \) is an orthogonal matrix and \( T \) is a block upper triangular matrix with \( 1 \times 1 \) and \( 2 \times 2 \) diagonal blocks specifying the real and complex conjugate eigenvalues of \( A \). The column vectors of \( Q \) are the Schur vectors of \( A \), and \( T \) is the Schur form of \( A \).

Methods are built on LAPACK routine dgees.
Usage

Schur(x, vectors = TRUE, ...)  

Arguments  

- **x** a finite square matrix or Matrix to be factorized.  
- **vectors** a logical. If TRUE (the default), then Schur vectors are computed in addition to the Schur form.  
- **...** further arguments passed to or from methods.  

Value  

An object representing the factorization, inheriting from virtual class SchurFactorization if vectors = TRUE. Currently, the specific class is always Schur in that case.  

An exception is if x is a traditional matrix, in which case the result is a named list containing Q, T, and EValues slots of the Schur object.  

If vectors = FALSE, then the result is the same named list but without Q.  

References  

The LAPACK source code, including documentation; see https://netlib.org/lapack/double/dgees.f.  


See Also  

- Class Schur and its methods.  
- Class dgeMatrix.  
- Generic functions expand1 and expand2, for constructing matrix factors from the result.  
- Generic functions Cholesky, BunchKaufman, lu, and qr, for computing other factorizations.  

Examples  

showMethods("Schur", inherited = FALSE)  
set.seed(0)  
Schur(Hilbert(9L)) # real eigenvalues  
(A <- Matrix(round(rnorm(25L, sd = 100)), 5L, 5L))  
(sch.A <- Schur(A)) # complex eigenvalues  
## A ~ Q T Q' in floating point  
str(e.sch.A <- expand2(sch.A), max.level = 2L)  
stopifnot(all.equal(A, Reduce("%*%", e.sch.A)))  
(e1 <- eigen(sch.A@T, only.values = TRUE)$values)  
(e2 <- eigen(A, only.values = TRUE)$values)  
(e3 <- sch.A@EValues)  
stopifnot(exprs = {  
  all.equal(e1, e2, tolerance = 1e-13)  
  all.equal(e3, e1, tolerance = 1e-13)  
  all.equal(e3, e2, tolerance = 1e-13)  
})
```r
all.equal(e1, e3[order(Mod(e3), decreasing = TRUE)], tolerance = 1e-13)
identical(Schur(A, vectors = FALSE),
  list(T = sch.A@T, EValues = e3))
identical(Schur(as(A, "matrix")),
  list(Q = as(sch.A@Q, "matrix"),
       T = as(sch.A@T, "matrix"), EValues = e3))
```

 solve-methods

Methods in Package Matrix for Function solve

Description

Methods for generic function solve for solving linear systems of equations, i.e., for \( X \) in \( A X = B \), where \( A \) is a square matrix and \( X \) and \( B \) are matrices with dimensions consistent with \( A \).

Usage

```r
solve(a, b, ...)
```

## S4 method for signature 'dgeMatrix,ANY'
solve(a, b, tol = .Machine$double.eps, ...)

## S4 method for signature 'dgCMatrix,missing'
solve(a, b, sparse = TRUE, ...)

## S4 method for signature 'dgCMatrix,matrix'
solve(a, b, sparse = FALSE, ...)

## S4 method for signature 'dgCMatrix,denseMatrix'
solve(a, b, sparse = FALSE, ...)

## S4 method for signature 'dgCMatrix,sparseMatrix'
solve(a, b, sparse = TRUE, ...)

## S4 method for signature 'denseLU,dgeMatrix'
solve(a, b, ...)

## S4 method for signature 'BunchKaufman,dgeMatrix'
solve(a, b, ...)

## S4 method for signature 'Cholesky,dgeMatrix'
solve(a, b, ...)

## S4 method for signature 'sparseLU,dgCMatrix'
solve(a, b, tol = .Machine$double.eps, ...)

## S4 method for signature 'sparseQR,dgCMatrix'
solve(a, b, ...)

## S4 method for signature 'CHMfactor,dgCMatrix'
solve(a, b, system = c("A", "LDLt", "LD", "DLt", "L", "Lt", "D", "P", "Pt"), ...)

Arguments

- `a` a finite square matrix or Matrix containing the coefficients of the linear system, or otherwise a MatrixFactorization, in which case methods behave (by default) as if the factorized matrix were specified.
b

a vector, `sparseVector`, matrix, or `Matrix` satisfying `NROW(b) == nrow(a)`, giving the right-hand side(s) of the linear system. Vectors `b` are treated as `length(b)`-by-1 matrices. If `b` is missing, then methods take `b` to be an identity matrix.

tol

a non-negative number. For a inheriting from `denseMatrix`, an error is signaled if the reciprocal one-norm condition number (see `rcond`) of `a` is less than `tol`, indicating that `a` is near-singular. For a of class `sparseLU`, an error is signaled if the ratio `min(d)/max(d)` is less than `tol`, where `d = abs(diag(a@U))`. (Interpret with care, as this ratio is a cheap heuristic and not in general equal to or even proportional to the reciprocal one-norm condition number.) Setting `tol = 0` disables the test.

sparse

a logical indicating if the result should be formally sparse, i.e., if the result should inherit from virtual class `sparseMatrix`. Only methods for sparse `a` and missing or matrix `b` have this argument. Methods for missing or sparse `b` use `sparse = TRUE` by default. Methods for dense `b` use `sparse = FALSE` by default.

system

a string specifying a linear system to be solved. Only methods for a inheriting from `CHMfactor` have this argument. See ‘Details’.

... further arguments passed to or from methods.

Details

Methods for general and symmetric matrices compute a triangular factorization (LU, Bunch-Kaufman, or Cholesky) and call the method for the corresponding factorization class. The factorization is sparse if `a` is. Methods for sparse, symmetric matrices attempt a Cholesky factorization and perform an LU factorization only if that fails (typically because `a` is not positive definite).

Triangular, diagonal, and permutation matrices do not require factorization (they are already “factors”), hence methods for those are implemented directly. For triangular `a`, solutions are obtained by forward or backward substitution; for diagonal `a`, they are obtained by scaling the rows of `b`; and for permutations `a`, they are obtained by permuting the rows of `b`.

Methods for dense `a` are built on 14 LAPACK routines: class `d..Matrix`, where `..=(ge|tr|tp|sy|sp|po|pp)`, uses routines `d..tri` and `d..trs` for missing and non-missing `b`, respectively. A corollary is that these methods always give a dense result.

Methods for sparse `a` are built on CSparse routines `cs_lsolve`, `cs_usolve`, and `cs_spsolve` and CHOLMOD routines `cholmod_solve` and `cholmod_spsolve`. By default, these methods give a vector result if `b` is a vector, a sparse matrix result if `b` is missing or a sparse matrix, and a dense matrix result if `b` is a dense matrix. One can override this behaviour by setting the `sparse` argument, where available, but that should be done with care. Note that a sparse result may be sparse only in the formal sense and not at all in the mathematical sense, depending on the nonzero patterns of `a` and `b`. Furthermore, whereas dense results are fully preallocated, sparse results must be “grown” in a loop over the columns of `b`.

Methods for a of class `sparseQR` are simple wrappers around `qr.coef`, giving the least squares solution in overdetermined cases.

Methods for a inheriting from `CHMfactor` can solve systems other than the default one $AX = B$. The correspondence between its `system` argument the system actually solved is outlined in the table below. See `CHMfactor-class` for a definition of notation.

<table>
<thead>
<tr>
<th>system</th>
<th>isLDL(a)=TRUE</th>
<th>isLDL(a)=FALSE</th>
</tr>
</thead>
<tbody>
<tr>
<td>&quot;A&quot;</td>
<td>$AX = B$</td>
<td>$AX = B$</td>
</tr>
<tr>
<td>&quot;LDLt&quot;</td>
<td>$L_1 D L_1^t X = B$</td>
<td>$LL^t X = B$</td>
</tr>
<tr>
<td>&quot;LD&quot;</td>
<td>$L_1 DX = B$</td>
<td>$LX = B$</td>
</tr>
</tbody>
</table>
### Sparse Design / Model Matrices

```
"DLt"  DL_1'X = B  L'X = B
"L"    L_1X = B    LX = B
"Lt"   L_1'X = B   L'X = B
"D"    DX = B     X = B
"P"    X = P_1B    X = P'B
"Pt"   X = P_1'B   X = P'B
```

#### See Also

Virtual class `MatrixFactorization` and its subclasses.

Generic functions `Cholesky`, `BunchKaufman`, `Schur`, `lu`, and `qr` for computing factorizations.

Generic function `solve` from `base`.

Function `qr.coef` from `base` for computing least squares solutions of overdetermined linear systems.

#### Examples

```r
## A close to symmetric example with "quite sparse" inverse:
n1 <- 7; n2 <- 3
dd <- data.frame(a = gl(n1,n2), b = gl(n2,1,n1*n2))# balanced 2-way
X <- sparse.model.matrix(~ -1+ a + b, dd)# no intercept --> even sparser
XXt <- tcrossprod(X)
diag(XXt) <- rep(c(0,0,1,0), length.out = nrow(XXt))
n <- nrow(ZZ <- kronecker(XXt, Diagonal(x=c(4,1))))
image(a <- 2*Diagonal(n) + ZZ %*% Diagonal(x=c(10, rep(1, n-1))))
isSymmetric(a) # FALSE
image(drop0(skewpart(a)))
image(ia0 <- solve(a, tol = 0)) # checker board, dense [but really, a is singular!]
try(solve(a, sparse=TRUE))##-> error [ TODO: assertError ]
ia. <- solve(a, sparse=TRUE, tol = 1e-19)##-> *no* error
if(R.version$arch == "x86_64")
## Fails on 32-bit [Fedora 19, R 3.0.2] from Matrix 1.1-0 on [FIXME ??] only
stopifnot(all.equal(as.matrix(ia.), as.matrix(ia0)))
a <- a + Diagonal(n)
idad <- solve(a)
ias <- solve(a, sparse=FALSE)
stopifnot(all.equal(as(iad,"denseMatrix"), ias, tolerance=1e-14))
I. <- iad %*% a
I0 <- drop0(zapsmall(I.)); image(I0)
.I <- a %*% iad
.I0 <- drop0(zapsmall(.I))
stopifnot( all.equal(as(I0, "diagonalMatrix"), Diagonal(n)),
           all.equal(as(.I0,"diagonalMatrix"), Diagonal(n)) )
```
Description

Construct a sparse model or “design” matrix, from a formula and data frame (sparse.model.matrix) or a single factor (fac2sparse).

The fac2[Ss]parse() functions are utilities, also used internally in the principal user level function sparse.model.matrix().

Usage

sparse.model.matrix(object, data = environment(object),
  contrasts.arg = NULL, xlev = NULL, transpose = FALSE,
  drop.unused.levels = FALSE, row.names = TRUE,
  sep = "", verbose = FALSE, ...)

fac2sparse(from, to = c("d", "1", "n"),
  drop.unused.levels = TRUE, repr = c("C", "R", "T"), giveCsparse)

fac2Sparse(from, to = c("d", "1", "n"),
  drop.unused.levels = TRUE, repr = c("C", "R", "T"), giveCsparse,
  factorPatt12, contrasts.arg = NULL)

Arguments

- **object**: an object of an appropriate class. For the default method, a model formula or terms object.
- **data**: a data frame created with `model.frame`. If another sort of object, `model.frame` is called first.
- **contrasts.arg**: for `sparse.model.matrix()`: A list, whose entries are contrasts suitable for input to the `contrasts` replacement function and whose names are the names of columns of data containing factors.
  
  for `fac2Sparse()`: character string or NULL or (coercable to) "sparseMatrix", specifying the contrasts to be applied to the factor levels.
- **xlev**: to be used as argument of `model.frame` if data has no "terms" attribute.
- **transpose**: logical indicating if the transpose should be returned; if the transposed is used anyway, setting `transpose = TRUE` is more efficient.
- **drop.unused.levels**: should factors have unused levels dropped? The default for sparse.model.matrix has been changed to FALSE, 2010-07, for compatibility with R’s standard (dense) model.matrix().
- **row.names**: logical indicating if row names should be used.
- **sep**: character string passed to `paste()` when constructing column names from the variable name and its levels.
- **verbose**: logical or integer indicating if (and how much) progress output should be printed.
- **...**: further arguments passed to or from other methods.
- **from**: (for fac2sparse()) a factor.
- **to**: a character indicating the “kind” of sparse matrix to be returned. The default, "d" is for double.
- **giveCsparse**: deprecated, replaced with repr; logical indicating if the result must be a CsparseMatrix.
repr

character string, one of "C", "T", or "R", specifying the sparse representation to be used for the result, i.e., one from the super classes CsparseMatrix, TsparseMatrix, or RsparseMatrix.

factorPatt12

logical vector, say fp, of length two; when fp[1] is true, return “contrasted” t(X); when fp[2] is true, the original (“dummy”) t(X), i.e, the result of fac2sparse().

Value

a sparse matrix, extending CsparseMatrix (for fac2sparse() if repr = "C" as per default; a TsparseMatrix or RsparseMatrix, otherwise).

For fac2Sparse(), a list of length two, both components with the corresponding transposed model matrix, where the corresponding factorPatt12 is true.

fac2sparse(), the basic workhorse of sparse.model.matrix(), returns the transpose (t) of the model matrix.

Note

model.Matrix(sparse = TRUE) from package MatrixModels may be nowadays be preferable to sparse.model.matrix, as model.Matrix returns an object of class modelMatrix with additional slots assign and contrasts relating to the model variables.

Author(s)

Doug Bates and Martin Maechler, with initial suggestions from Tim Hesterberg.

See Also

model.matrix in package stats, part of base R.
model.Matrix in package MatrixModels; see ‘Note’.

as(f, "sparseMatrix") (see coerce(from = "factor", ..) in the class doc sparseMatrix) produces the transposed sparse model matrix for a single factor f (and no contrasts).

Examples

dd <- data.frame(a = gl(3,4), b = gl(4,1,12))# balanced 2-way
options("contrasts") # the default: "contr.treatment"
sparse.model.matrix(~ a + b, dd)
sparse.model.matrix(~ -1+ a + b, dd)# no intercept --> even sparser
sparse.model.matrix(~ a + b, dd, contrasts = list(a="contr.sum"))
sparse.model.matrix(~ a + b, dd, contrasts = list(b="contr.SAS"))

## Sparse method is equivalent to the traditional one:
stopifnot(all(sparse.model.matrix(~ a + b, dd) ==
  Matrix(model.matrix(~ a + b, dd), sparse=TRUE)),
  all(sparse.model.matrix(~0 + a + b, dd) ==
  Matrix(model.matrix(~0 + a + b, dd), sparse=TRUE)))

(ff <- gl(3,4,, c("X","Y", "Z")))
fac2sparse(ff) # 3 x 12 sparse Matrix of class "dgCMatrix"

##
## X 1 1 1 1 . . . . . .
## Y . . . 1 1 1 1 . . . .
## Z . . . . . . 1 1 1 1 . . .
sparseLU-class

Sparse LU Factorizations

Description

sparseLU is the class of sparse, row- and column-pivoted LU factorizations of \( n \times n \) real matrices \( A \), having the general form

\[
P_1 A P_2 = LU
\]

or (equivalently)

\[
A = P'_1 L U P'_2
\]

where \( P_1 \) and \( P_2 \) are permutation matrices, \( L \) is a unit lower triangular matrix, and \( U \) is an upper triangular matrix.

Slots

\( \text{Dim, Dimnames} \) inherited from virtual class MatrixFactorization.

\( L \) an object of class dtCMatrix, the unit lower triangular \( L \) factor.

\( U \) an object of class dtCMatrix, the upper triangular \( U \) factor.

\( p, q \) 0-based integer vectors of length \( \text{Dim[1]} \), specifying the permutations applied to the rows and columns of the factorized matrix. \( q \) of length 0 is valid and equivalent to the identity permutation, implying no column pivoting. Using \( \text{R} \) syntax, the matrix \( P_1 A P_2 \) is precisely \( A[p+1, q+1] \) (\( A[p+1, ] \) when \( q \) has length 0).

Extends

Class \( \text{LU} \), directly. Class MatrixFactorization, by class \( \text{LU} \), distance 2.

Instantiation

Objects can be generated directly by calls of the form \( \text{new("sparseLU",...)} \), but they are more typically obtained as the value of \( \text{lu(x)} \) for \( x \) inheriting from \( \text{sparseMatrix} \) (often \( \text{dgCMatrix} \)).
sparseLU-class

Methods

determinant signature(from = "sparseLU", logarithm = "logical"): computes the determinant of the factorized matrix $A$ or its logarithm.

expand signature(x = "sparseLU"): see expand-methods.

expand1 signature(x = "sparseLU"): see expand1-methods.

expand2 signature(x = "sparseLU"): see expand2-methods.

solve signature(a = "sparseLU", b = .): see solve-methods.

References


See Also

Class denseLU for dense LU factorizations.

Class dgCMatrix.

Generic functions lu, expand1 and expand2.

Examples

showClass("sparseLU")
set.seed(2)

A <- as(readMM(system.file("external", "pores_1.mtx", package = "Matrix")), "CsparseMatrix")
(n <- A@Dim[1L])

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(n)), 
paste0("c", seq_len(n)))

(lu.A <- lu(A))
str(e.lu.A <- expand2(lu.A), max.level = 2L)

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)

ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## $A \sim P_1 \cdot L \cdot U \cdot P_2'$ in floating point
stopifnot(exprs = {
  identical(names(e.lu.A), c("P1.", "L", "U", "P2."))
  identical(e.lu.A[["P1."]],
    new("pMatrix", Dim = c(n, n), Dimnames = c(dn[1L], list(NULL)),
      margin = 1L, perm = invertPerm(lu.A@p, 0L, 1L)))
  identical(e.lu.A[["P2."]],
    new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
      margin = 2L, perm = invertPerm(lu.A@q, 0L, 1L)))
  identical(e.lu.A[["L"]], lu.A@L)
  identical(e.lu.A[["U"]], lu.A@U)
  ae1(A, with(e.lu.A, P1. %*% L %*% U %*% P2.))
  ae2(A[lu.A@p + 1L, lu.A@q + 1L], with(e.lu.A, L %*% U))
})
## Factorization handled as factorized matrix

```r
b <- rnorm(n)
stopifnot(identical(det(A), det(lu.A)),
          identical(solve(A, b), solve(lu.A, b)))
```

### sparseMatrix

**General Sparse Matrix Construction from Nonzero Entries**

**Description**

User-friendly construction of sparse matrices (inheriting from virtual class `CsparseMatrix`, `RsparseMatrix`, or `TsparseMatrix`) from the positions and values of their nonzero entries.

This interface is recommended over direct construction via calls such as `new("..[CRT]Matrix", ...)`.

**Usage**

```r
sparseMatrix(i, j, p, x, dims, dimnames,
             symmetric = FALSE, triangular = FALSE, index1 = TRUE,
             repr = c("C", "R", "T"), giveCsparse,
             check = TRUE, use.last.ij = FALSE)
```

**Arguments**

- `i, j` integer vectors of equal length specifying the positions (row and column indices) of the nonzero (or non-`TRUE`) entries of the matrix. Note that, when `x` is non-missing, the `x_k` corresponding to repeated pairs `(i_k, j_k)` are added, for consistency with the definition of class `TsparseMatrix`, unless `use.last.ij` is `TRUE`, in which case only the last such `x_k` is used.

- `p` integer vector of pointers, one for each column (or row), to the initial (zero-based) index of elements in the column (or row). Exactly one of `i`, `j`, and `p` must be missing.

- `x` optional, typically nonzero values for the matrix entries. If specified, then the length must equal that of `i` (or `j`) or equal 1, in which case `x` is recycled as necessary. If missing, then the result is a nonzero pattern matrix, i.e., inheriting from class `nsparseMatrix`.

- `dims` optional length-2 integer vector of matrix dimensions. If missing, then `!index1+c(max(i),max(j))` is used.

- `dimnames` optional list of `dimnames`; if missing, then `NULL` ones are used.

- `symmetric` logical indicating if the resulting matrix should be symmetric. In that case, `(i, j, p)` should specify only one triangle (upper or lower).

- `triangular` logical indicating if the resulting matrix should be triangular. In that case, `(i, j, p)` should specify only one triangle (upper or lower).

- `index1` logical. If `TRUE` (the default), then `i` and `j` are interpreted as 1-based indices, following the R convention. That is, counting of rows and columns starts at 1. If `FALSE`, then they are interpreted as 0-based indices.
sparseMatrix

repr character string, one of "C", "R", and "T", specifying the representation of the sparse matrix result, i.e., specifying one of the virtual classes CsparseMatrix, RsparseMatrix, and TsparseMatrix.

giveCsparse (deprecated, replaced by repr) logical indicating if the result should inherit from CsparseMatrix or TsparseMatrix. Note that operations involving CsparseMatrix are very often (but not always) more efficient.

check logical indicating whether to check that the result is formally valid before returning. Do not set to FALSE unless you know what you are doing!

use.last.ij logical indicating if, in the case of repeated (duplicated) pairs \((i_k, j_k)\), only the last pair should be used. FALSE (the default) is consistent with the definition of class TsparseMatrix.

Details

Exactly one of the arguments \(i, j\) and \(p\) must be missing.

In typical usage, \(p\) is missing, \(i\) and \(j\) are vectors of positive integers and \(x\) is a numeric vector. These three vectors, which must have the same length, form the triplet representation of the sparse matrix.

If \(i\) or \(j\) is missing then \(p\) must be a non-decreasing integer vector whose first element is zero. It provides the compressed, or “pointer” representation of the row or column indices, whichever is missing. The expanded form of \(p\), \(\text{rep(seq_along(dp),dp)}\) where \(dp \leftarrow \text{diff}(p)\), is used as the \((1\text{-based})\) row or column indices.

You cannot set both singular and triangular to true; rather use Diagonal() (or its alternatives, see there).

The values of \(i, j, p\) and index1 are used to create 1-based index vectors \(i\) and \(j\) from which a TsparseMatrix is constructed, with numerical values given by \(x\), if non-missing. Note that in that case, when some pairs \((i_k, j_k)\) are repeated (aka “duplicated”), the corresponding \(x_k\) are added, in consistency with the definition of the TsparseMatrix class, unless use.last.ij is set to true.

By default, when \(\text{repr} = "C"\), the CsparseMatrix derived from this triplet form is returned, where \(\text{repr} = "R"\) now allows to directly get an RsparseMatrix and \(\text{repr} = "T"\) leaves the result as TsparseMatrix.

The reason for returning a CsparseMatrix object instead of the triplet format by default is that the compressed column form is easier to work with when performing matrix operations. In particular, if there are no zeros in \(x\) then a CsparseMatrix is a unique representation of the sparse matrix.

Value

A sparse matrix, by default in compressed sparse column format and (formally) without symmetric or triangular structure, i.e., by default inheriting from both CsparseMatrix and generalMatrix.

Note

You do need to use index1 = FALSE (or add + 1 to \(i\) and \(j\)) if you want use the 0-based \(i\) (and \(j\)) slots from existing sparse matrices.

See Also

Matrix(*, sparse=TRUE) for the constructor of such matrices from a dense matrix. That is easier in small sample, but much less efficient (or impossible) for large matrices, where something like sparseMatrix() is needed. Further bdiag and Diagonal for (block-)diagonal and bandSparse for banded sparse matrix constructors.
Random sparse matrices via \texttt{rsparsematrix()}.  

The standard \texttt{R xtabs(*, sparse=TRUE)}, for sparse tables and \texttt{sparse.model.matrix()} for building sparse model matrices.  

Consider \texttt{CsparseMatrix} and similar class definition help files.  

\section*{Examples}

## simple example
\begin{verbatim}
i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
(A <- sparseMatrix(i, j, x = x)) # 8 x 10 "dgCMatrix"
summary(A)
\end{verbatim}

\begin{verbatim}
str(A) # note that *internally* 0-based row indices are used
\end{verbatim}

## dims can be larger than the maximum row or column
\begin{verbatim}
(AA <- sparseMatrix(c(1,3:8), c(2,9,6:10), x = 7 * (1:7), dims = c(10,20)))
summary(AA)
\end{verbatim}

## i, j and x can be in an arbitrary order, as long as they are consistent
\begin{verbatim}
set.seed(1); (perm <- sample(1:7))
(A1 <- sparseMatrix(i[perm], j[perm], x = x[perm]))
stopifnot(identical(A, A1))
\end{verbatim}

## The slots are 0-index based, so
\begin{verbatim}
try( sparseMatrix(i=A@i, p=A@p, x= seq_along(A@x)) )
\end{verbatim}

## fails and you should say so: 1-indexing is FALSE:
\begin{verbatim}
sparseMatrix(i=A@i, p=A@p, x= seq_along(A@x), index1 = FALSE)
\end{verbatim}

## the \{(i,j)\} pairs can be repeated, in which case the x's are summed
\begin{verbatim}
(args <- data.frame(i = c(i, 1), j = c(j, 2), x = c(x, 2)))
(Aa <- do.call(sparseMatrix, args))
\end{verbatim}

## explicitly ask for elimination of such duplicates, so
\begin{verbatim}
# that the last one is used:
(A. <- do.call(sparseMatrix, c(args, list(use.last.ij = TRUE))))
stopifnot(Aa[1,2] == 9, # 2+7 == 9
A.[1,2] == 2) # 2 was *after* 7
\end{verbatim}

## for a pattern matrix, of course there is no "summing":
\begin{verbatim}
(nA <- do.call(sparseMatrix, args[c("i","j")]))
\end{verbatim}

\begin{verbatim}
str(m)
\end{verbatim}

\begin{verbatim}
sparseMatrix(x = 2.72, i=1:3, j=2:4) # recycling x
\end{verbatim}

\begin{verbatim}
sparseMatrix(x = TRUE, i=1:3, j=2:4) # recycling x, |--> "lgCMatrix"
\end{verbatim}

## no 'x' --> pattern matrix:
\begin{verbatim}
(n <- sparseMatrix(i=1:6, j=rev(2:7)))# -> ngCMatrix
## Virtual Class "sparseMatrix" — Mother of Sparse Matrices

### Description

Virtual Mother Class of All Sparse Matrices

### Slots

- **Dim**: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.
- **Dimnames**: a list of length two - inherited from class Matrix, see Matrix.

### Extends

Class "Matrix", directly.

### Methods

- **show** (object = "sparseMatrix") : The `show` method for sparse matrices prints "structural" zeroes as "." using `printSpMatrix()` which allows further customization.
- **print** signature(x = "sparseMatrix"). ....

The `print` method for sparse matrices by default is the same as `show()` but can be called with extra optional arguments, see `printSpMatrix()`.
format signature(x = "sparseMatrix").

The format method for sparse matrices, see formatSpMatrix() for details such as the extra optional arguments.

summary (object = "sparseMatrix", uniqT=FALSE): Returns an object of S3 class "sparseSummary" which is basically a data.frame with columns (i,j,x) (or just (i,j) for nsparsesMatrix class objects) with the stored (typically non-zero) entries. The print method resembles Matlab’s way of printing sparse matrices, and also the MatrixMarket format, see writeMM.

cbind2 (x = *, y = *): several methods for binding matrices together, column-wise, see the basic cbind and rbind functions.

Note that the result will typically be sparse, even when one argument is dense and larger than the sparse one.

rbind2 (x = *, y = *): binding matrices together row-wise, see cbind2 above.

determinant (x = "sparseMatrix", logarithm=TRUE): determinant() methods for sparse matrices typically work via Cholesky or lu decompositions.

diag (x = "sparseMatrix"): extracts the diagonal of a sparse matrix.

dim<- signature(x = "sparseMatrix", value = "ANY"): allows to reshape a sparse matrix to a sparse matrix with the same entries but different dimensions. value must be of length two and fulfill prod(value) == prod(dim(x)).

coerce signature(from = "factor", to = "sparseMatrix"): Coercion of a factor to "sparseMatrix" produces the matrix of indicator rows stored as an object of class "dgCMatrix". To obtain columns representing the interaction of the factor and a numeric covariate, replace the "x" slot of the result by the numeric covariate then take the transpose. Missing values (NA) from the factor are translated to columns of all 0s.

See also colSums, norm, ... for methods with separate help pages.

Note

In method selection for multiplication operations (i.e. %*% and the two-argument form of crossprod) the sparseMatrix class takes precedence in the sense that if one operand is a sparse matrix and the other is any type of dense matrix then the dense matrix is coerced to a dgeMatrix and the appropriate sparse matrix method is used.

See Also

sparseMatrix, and its references, such as xtabs(*, sparse=TRUE), or sparse.model.matrix(), for constructing sparse matrices.

T2graph for conversion of "graph" objects (package graph) to and from sparse matrices.

Examples

showClass("sparseMatrix") ## and look at the help() of its subclasses
M <- Matrix(0, 10000, 100)
M[1,1] <- M[2,3] <- 3.14
M ## show(.) method suppresses printing of the majority of rows

data(CAex, package = "Matrix")

# 72 x 72 matrix

determinant(CAex) # works via sparse lu(.)

## factor -> t( <sparse design matrix> ) :
sparseQR-class

(\texttt{fact <- gl(5, 3, 30, labels = LETTERS[1:5])})
(\texttt{Xt <- as(fact, "sparseMatrix")}) \# indicator rows

## missing values --> all-0 columns:
\texttt{f.mis <- fact}
\texttt{i.mis <- c(3:5, 17)}
\texttt{is.na(f.mis) <- i.mis}
\texttt{Xt != (X. <- as(f.mis, "sparseMatrix")) \# differ only in columns 3:5,17}
\texttt{stopifnot(all(X.[,i.mis] == 0), all(Xt[-i.mis] == X.[,-i.mis]))}

sparseQR-class \quad \textit{Sparse QR Factorizations}

\textbf{Description}

\texttt{sparseQR} is the class of sparse, row- and column-pivoted QR factorizations of \( m \times n \) (\( m \geq n \)) real matrices, having the general form

\[
P_1 A P_2 = QR = \begin{bmatrix} Q_1 & Q_2 \end{bmatrix} \begin{bmatrix} R_1 \\ 0 \end{bmatrix} = Q_1 R_1
\]

or (equivalently)

\[
A = P'_1 Q R P'_2 = P'_1 \begin{bmatrix} Q_1 & Q_2 \end{bmatrix} \begin{bmatrix} R_1 \\ 0 \end{bmatrix} P'_2 = P'_1 Q_1 R_1 P'_2
\]

where \( P_1 \) and \( P_2 \) are permutation matrices, \( Q = \prod_{j=1}^{n} H_j \) is an \( m \times m \) orthogonal matrix (\( Q_1 \) contains the first \( n \) column vectors) equal to the product of \( n \) Householder matrices \( H_j \), and \( R \) is an \( m \times n \) upper trapezoidal matrix (\( R_1 \) contains the first \( n \) row vectors and is upper \textit{triangular}).

\textbf{Usage}

\texttt{qrR(qr, complete = FALSE, backPermute = TRUE, row.names = TRUE)}

\textbf{Arguments}

\texttt{qr} \quad an object of class \texttt{sparseQR}, almost always the result of a call to generic function \texttt{qr} with sparse \texttt{x}.

\texttt{complete} \quad a logical indicating if \( R \) should be returned instead of \( R_1 \).

\texttt{backPermute} \quad a logical indicating if \( R \) or \( R_1 \) should be multiplied on the right by \( P'_2 \).

\texttt{row.names} \quad a logical indicating if \texttt{dimnames(qr)[1]} should be propagated unpermuted to the result. If \texttt{complete} = \texttt{FALSE}, then only the first \( n \) names are kept.

\textbf{Details}

The method for \texttt{qr.Q} does not return \( Q \) but rather the (also orthogonal) product \( P'_1 Q \). This behaviour is algebraically consistent with the \texttt{base} implementation (see \texttt{qr}), which can be seen by noting that \texttt{qr.default} in \texttt{base} does not pivot rows, constraining \( P_1 \) to be an identity matrix. It follows that \texttt{qr.Q(qr.default(x))} also returns \( P'_1 Q \).

Similarly, the methods for \texttt{qr.qy} and \texttt{qr.qty} multiply on the left by \( P'_1 Q \) and \( Q' P_1 \) rather than \( Q \) and \( Q' \).
It is wrong to expect the values of qr.Q (or qr.R, qr.qy, qr.qty) computed from “equivalent” sparse and dense factorizations (say, qr(x) and qr(as(x, "matrix")) for x of class dgCMatrix) to compare equal. The underlying factorization algorithms are quite different, notably as they employ different pivoting strategies, and in general the factorization is not unique even for fixed $P_1$ and $P_2$.

On the other hand, the values of qr.X, qr.coef, qr.fitted, and qr.resid are well-defined, and in those cases the sparse and dense computations should compare equal (within some tolerance).

The method for qr.R is a simple wrapper around qrR, but not back-permuting by default and never giving row names. It did not support backPermute = TRUE until Matrix 1.6-0, hence code needing the back-permuted result should call qrR if Matrix >= 1.6-0 is not known.

Slots

- Dim, Dimnames inherited from virtual class MatrixFactorization.

- beta a numeric vector of length Dim[2], used to construct Householder matrices; see V below.

- V an object of class dgCMatix with Dim[2] columns. The number of rows nrow(V) is at least Dim[1] and at most Dim[1]+Dim[2]. V is lower trapezoidal, and its column vectors generate the Householder matrices $H_j$ that compose the orthogonal $Q$ factor. Specifically, $H_j$ is constructed as $\text{diag}(\text{Dim}[1]) - \beta[j] \times \text{tcrossprod}(V[, j])$.

- R an object of class dgCMatix with nrow(V) rows and Dim[2] columns. R is the upper trapezoidal $R$ factor.

- p, q 0-based integer vectors of length nrow(V) and Dim[2], respectively, specifying the permutations applied to the rows and columns of the factorized matrix. q of length 0 is valid and equivalent to the identity permutation, implying no column pivoting. Using R syntax, the matrix $P_1A P_2'$ is precisely $A[p+1, q+1]$ ($A[p+1,]$ when q has length 0).

Extends

Class QR, directly. Class MatrixFactorization, by class QR, distance 2.

Instantiation

Objects can be generated directly by calls of the form new("sparseQR", ...), but they are more typically obtained as the value of qr(x) for x inheriting from sparseMatrix (often dgCMatrix).

Methods

determinant signature(from = "sparseQR", logarithm = "logical"): computes the determinant of the factorized matrix $A$ or its logarithm.

expand1 signature(x = "sparseQR"): see expand1-methods.

expand2 signature(x = "sparseQR"): see expand2-methods.

qr.Q signature(qr = "sparseQR"): returns as a dgeMatrix either $P_1'Q$ or $P_1'Q_1$, depending on optional argument complete. The default is FALSE, indicating $P_1'Q_1$.

qr.R signature(qr = "sparseQR"): qrR returns $R$, $R_1$, $RP2'$, or $R_1P2'$, depending on optional arguments complete and backPermute. The default in both cases is FALSE, indicating $R_1$, for compatibility with base. The class of the result in that case is dtCMatix. In the other three cases, it is dgCMatix.

qr.X signature(qr = "sparseQR"): returns $A$ as a dgeMatrix, by default. If $m > n$ and optional argument ncol is greater than $n$, then the result is augmented with $P_1'Q J$, where $J$ is composed of columns $(n+1)$ through ncol of the $m \times m$ identity matrix.
qr.coef signature(qr = "sparseQR", y = .): returns as a dgeMatrix or vector the result of multiplying y on the left by $P_2R_1^{-1}Q_1'P_1$.

qr.fitted signature(qr = "sparseQR", y = .): returns as a dgeMatrix or vector the result of multiplying y on the left by $P_1'Q_1'Q_2'P_1$.

qr.resid signature(qr = "sparseQR", y = .): returns as a dgeMatrix or vector the result of multiplying y on the left by $P_2R_2^{-1}Q_2'P_1$.

qr.qty signature(qr = "sparseQR", y = .): returns as a dgeMatrix or vector the result of multiplying y on the left by $Q'P_1$.

qr.qy signature(qr = "sparseQR", y = .): returns as a dgeMatrix or vector the result of multiplying y on the left by $P_1'Q_2$.

solve signature(a = "sparseQR", b = .): see solve-methods.

References


See Also

Class dgCMatrix.

Generic function qr from base, whose default method qr.default "defines" the S3 class qr of dense QR factorizations.

qr-methods for methods defined in Matrix.

Generic functions expand1 and expand2.


Examples

showClass("sparseQR")
set.seed(2)

m <- 300L
n <- 60L
A <- rsparsematrix(m, n, 0.05)

## With dimnames, to see that they are propagated :
dimnames(A) <- dn <- list(paste0("r", seq_len(m)), paste0("c", seq_len(n)))

(qr.A <- qr(A))
str(e.qr.A <- expand2(qr.A, complete = FALSE), max.level = 2L)
str(E.qr.A <- expand2(qr.A, complete = TRUE), max.level = 2L)

t(sapply(e.qr.A, dim))
t(sapply(E.qr.A, dim))

## Horribly inefficient, but instructive :
slowQ <- function(V, beta) {
  d <- dim(V)
Q <- diag(d[1L])
if(d[2L] > 0L) {
  for(j in d[2L]:1L) {
    cat(j, "\n", sep = "")
    Q <- Q - (beta[j] * tcrossprod(V[, j])) %*% Q
  }
}
Q

ae1 <- function(a, b, ...) all.equal(as(a, "matrix"), as(b, "matrix"), ...)
ae2 <- function(a, b, ...) ae1(unname(a), unname(b), ...)

## A ~ P1' Q R P2' ~ P1' Q1 R1 P2' in floating point
stopifnot(exprs = {
  identical(names(e.qr.A), c("P1.", "Q1", "R1", "P2."))
  identical(names(E.qr.A), c("P1.", "Q", "R", "P2."))
  identical(e.qr.A["P1."],
            new("pMatrix", Dim = c(m, m), Dimnames = c(dn[1L], list(NULL)),
                margin = 1L, perm = invertPerm(qr.A@p, 0L, 1L)))
  identical(e.qr.A["P2."],
            new("pMatrix", Dim = c(n, n), Dimnames = c(list(NULL), dn[2L]),
                margin = 2L, perm = invertPerm(qr.A@q, 0L, 1L)))
  identical(e.qr.A["R1"], triu(E.qr.A["R"][seq_len(n), ])
            )
  identical(e.qr.A["Q1"], E.qr.A["Q"][, seq_len(n)])
  identical(E.qr.A["R"], qr.A@R)
  ## ae1(E.qr.A["Q"], slowQ(qr.A@V, qr.A@beta))
  ae1(crossprod(E.qr.A["Q"]), diag(m))
  ae1(A, with(e.qr.A, P1. %*% Q1 %*% R1 %*% P2.))
  ae1(A, with(E.qr.A, P1. %*% Q %*% R %*% P2.))
  ae2(A.perm <- A[qr.A@p + 1L, qr.A@q + 1L], with(e.qr.A, Q1 %*% R1))
  ae2(A.perm , with(E.qr.A, Q %*% R ))
})

## More identities
b <- rnorm(m)
stopifnot(exprs = {
  ae1(qrX <- qr.X (qr.A ), A)
  ae2(qrQ <- qr.Q (qr.A ), with(e.qr.A, P1. %*% Q1))
  ae2( qr.R (qr.A ), with(e.qr.A, R1))
  ae2(qrc <- qr.coef (qr.A, b), with(e.qr.A, solve(R1 %*% P2., t(qrQ)) %*% b))
  ae2(qrf <- qr.fitted(qr.A, b), with(e.qr.A, tcrossprod(qrQ) %*% b))
  ae2(qrr <- qr.resid (qr.A, b), b - qrf)
  ae2(qrq <- qr.qy (qr.A, b), with(E.qr.A, P1. %*% Q %*% b))
  ae2(qrq <- qr.qty(qr.A, qrq), b)
})

## Sparse and dense computations should agree here
qr.Am <- qr(as(A, "matrix")) # <=> qr.default(A)
stopifnot(exprs = {
  ae2(qrX, qr.X (qr.Am ))
  ae2(qrc, qr.coef (qr.Am, b))
  ae2(qrf, qr.fitted(qr.Am, b))
  ae2(qrr, qr.resid (qr.Am, b))
})
sparseVector

Sparse Vector Construction from Nonzero Entries

Description

User friendly construction of sparse vectors, i.e., objects inheriting from class sparseVector, from indices and values of its non-zero entries.

Usage

sparseVector(x, i, length)

Arguments

x vector of the non zero entries; may be missing in which case a "nsparseVector" will be returned.

i integer vector (of the same length as x) specifying the indices of the non-zero (or non-TRUE) entries of the sparse vector.

length length of the sparse vector.

Details

zero entries in x are dropped automatically, analogously as drop0() acts on sparse matrices.

Value

a sparse vector, i.e., inheriting from class sparseVector.

Author(s)

Martin Maechler

See Also

sparseMatrix() constructor for sparse matrices; the class sparseVector.

Examples

str(sv <- sparseVector(x = 1:10, i = sample(999, 10), length=1000))
sx <- c(0,0,3, 3.2, 0,0,0,-3:1,0,0,2,0,0,5,0,0)
ss <- as(sx, "sparseVector")
stopifnot(identical(ss,
 sparseVector(x = c(2, -1, -2, 3, 1, -3, 5, 3.2),
 i = c(15L, 10:9, 3L,12L,8L,18L, 4L), length = 20L)))

(ns <- sparseVector(i= c(7, 3, 2), length = 10))
stopifnot(identical(ns,
 new("nsparseVector", length = 10, i = c(2, 3, 7))))
Sparse Vector Classes

Description

Sparse Vector Classes: The virtual mother class "sparseVector" has the five actual daughter classes "dsparseVector", "isparseVector", "lsparseVector", "nsparseVector", and "zsparseVector", where we’ve mainly implemented methods for the d*, l* and n* ones.

Slots

length: class "numeric" - the length of the sparse vector. Note that "numeric" can be considerably larger than the maximal "integer", .Machine$integer.max, on purpose.

i: class "numeric" - the (1-based) indices of the non-zero entries. Must not be NA and strictly sorted increasingly.
   Note that "integer" is "part of" "numeric", and can (and often will) be used for non-huge sparseVectors.

x: (for all but "nsparseVector"): the non-zero entries. This is of class "numeric" for class "dsparseVector", "logical" for class "lsparseVector", etc.

Methods

length signature(x = "sparseVector"): simply extracts the length slot.

show signature(object = "sparseVector"): The show method for sparse vectors prints "structural" zeroes as "." using the non-exported prSpVector function which allows further customization such as replacing "." by " " (blank).
   Note that options(max.print) will influence how many entries of large sparse vectors are printed at all.

as.vector signature(x = "sparseVector", mode = "character"): coerces sparse vectors to "regular", i.e., atomic vectors. This is the same as as(x, "vector").

as ..: see coerce below

coerce signature(from = "sparseVector", to = "sparseMatrix"), and

coerce signature(from = "sparseMatrix", to = "sparseVector"), etc: coercions to and from sparse matrices (sparseMatrix) are provided and work analogously as in standard R, i.e., a vector is coerced to a 1-column matrix.

dim<- signature(x = "sparseVector", value = "integer"): coerces a sparse vector to a sparse Matrix, i.e., an object inheriting from sparseMatrix, of the appropriate dimension.

head signature(x = "sparseVector"): as with R’s (package util) head, head(x, n) (for n >= 1) is equivalent to x[1:n], but here can be much more efficient, see the example.

tail signature(x = "sparseVector"): analogous to head, see above.

toeplitz signature(x = "sparseVector"): as toeplitz(x), produce the n × n Toeplitz matrix from x, where n = length(x).

rep signature(x = "sparseVector") repeat x, with the same argument list (x, times, length.out, each,...) as the default method for rep().

which signature(x = "nsparseVector") and

which signature(x = "lsparseVector") return the indices of the non-zero entries (which is trivial for sparse vectors).
**Ops** signature(e1 = "sparseVector", e2 = ".*") define arithmetic, compare and logic operations. (see **Ops**).

**Summary** signature(x = "sparseVector"): define all the **Summary** methods.

[ signature(x = "atomicVector", i = \ldots): not only can you subset (aka "index into") sparseVectors x[i] using sparseVectors i, but we also support efficient subsetting of traditional vectors x by logical sparse vectors (i.e., i of class "nsparseVector" or "lsparseVector").

**is.na, is.finite, is.infinite** (x = "sparseVector"), and **is.na, is.finite, is.infinite** (x = "nsparseVector") return **logical** or "nsparseVector" of the same length as x, indicating if/where x is NA (or NaN), finite or infinite, entirely analogously to the corresponding base **R** functions.

**c.sparseVector()** is a S3 method for all "sparseVector"s, but automatic dispatch only happens for the first argument, so it is useful also as regular **R** function, see the examples.

### See Also

**sparseVector()** for friendly construction of sparse vectors (apart from as(*, "sparseVector")).

### Examples

getClass("sparseVector")
getClass("dsparseVector")

sx <- c(0,0,3, 3.2, 0,0,0,-3:1,0,0,0,5,0,0,0)
( ss <- as(sx, "sparseVector") )

ix <- as.integer(round(sx))
(is <- as(ix, "sparseVector")) # an "isparseVector" (!)
(ns <- sparseVector(i= c(7, 3, 2), length = 10)) # "nsparseVector" # rep() works too:
(ri <- rep(is, length.out= 25))

## Using "dim<-" as in base **R**:

r <- ss
dim(r) <- c(4,5) # becomes a sparse Matrix:
r
## or coercion (as as.matrix() in base **R**): as(ss, "Matrix")
stopifnot(all(ss == print(as(ss, "CsparseMatrix"))))

## currently has "non-structural" FALSE -- printing as ":" 
( lis <- is & FALSE)
( nn <- is[is == 0]) # all "structural" FALSE

## NA-case

sN <- sx; sN[4] <- NA
(svN <- as(sN, "sparseVector") )

v <- as(c(0,0,3, 3.2, rep(0,9),-3,0,-1, rep(0,20),5,0), 
"sparseVector")

v <- rep(rep(v, 50), 5000)
set.seed(1); v[sample(v@i, 1e6)] <- 0
str(v)
### spMatrix

**Sparse Matrix Constructor From Triplet**

**Description**

User friendly construction of a sparse matrix (inheriting from class `TsparseMatrix`) from the triplet representation.

This is much less flexible than `sparseMatrix()` and hence somewhat *deprecated*.

**Usage**

```r
spMatrix(nrow, ncol, i = integer(0L), j = integer(0L), x = double(0L))
```
Arguments

nrow, ncol  integers specifying the desired number of rows and columns.
i, j  integer vectors of the same length specifying the locations of the non-zero (or non-TRUE) entries of the matrix.
x  atomic vector of the same length as i and j, specifying the values of the non-zero entries.

Value

A sparse matrix in triplet form, as an R object inheriting from both TsparseMatrix and generalMatrix.

The matrix $M$ will have $M[i[k], j[k]] == x[k]$, for $k = 1, 2, ..., n$, where $n = \text{length}(i)$ and $M[ i', j' ] == 0$ for all other pairs $(i', j')$.

See Also

Matrix(*, sparse=TRUE) for the more usual constructor of such matrices. Then, sparseMatrix is more general and flexible than spMatrix() and by default returns a CsparseMatrix which is often slightly more desirable. Further, bdiag and Diagonal for (block-)diagonal matrix constructors.

Consider TsparseMatrix and similar class definition help files.

Examples

## simple example
A <- spMatrix(10, 20, i = c(1, 3:8),
               j = c(2, 9, 6:10),
               x = 7 * (1:7))
A # a "dgTMatrix"
summary(A)
str(A) # note that *internally* 0-based indices (i, j) are used

L <- spMatrix(9, 30, i = rep(1:9, 3), 1:27,
              (1:27) %% 4 != 1)
L # an "lgTMatrix"

## A simplified predecessor of Matrix' r sparsematrix() function :

rSpMatrix <- function(nrow, ncol, nnz,
                      rand.x = function(n) round(rnorm(nnz), 2))
{
  ## Purpose: random sparse matrix
  ## --------------------------------------------------------------
  ## Arguments: (nrow,ncol): dimension
  ## nnz : number of non-zero entries
  ## rand.x: random number generator for 'x' slot
  ## --------------------------------------------------------------
  ## Author: Martin Maechler, Date: 14.-16. May 2007
  stopifnot((nnz <- as.integer(nnz)) >= 0,
             nrow >= 0, ncol >= 0, nnz <= nrow * ncol)
  spMatrix(nrow, ncol,
           i = sample(nrow, nnz, replace = TRUE),
           j = sample(ncol, nnz, replace = TRUE),
           x = rand.x(nnz))
M1 <- rSpMatrix(100000, 20, nnz = 200)
summary(M1)

Description

Methods for "[<-", i.e., extraction or subsetting mostly of matrices, in package Matrix.

Note: Contrary to standard matrix assignment in base R, in x[..] <- val it is typically an error (see stop) when the type or class of val would require the class of x to be changed, e.g., when x is logical, say "lsparseMatrix", and val is numeric. In other cases, e.g., when x is a "nsparseMatrix" and val is not TRUE or FALSE, a warning is signalled, and val is “interpreted” as logical, and (logical) NA is interpreted as TRUE.

Methods

There are many many more than these:

x = "Matrix", i = "missing", j = "missing", value= "ANY" is currently a simple fallback method implementation which ensures “readable” error messages.
x = "Matrix", i = "ANY", j = "ANY", value= "ANY" currently gives an error
x = "denseMatrix", i = "index", j = "missing", value= "numeric" ...
x = "denseMatrix", i = "index", j = "index", value= "numeric" ...
x = "denseMatrix", i = "missing", j = "index", value= "numeric" ...

See Also

[-methods for subsetting "Matrix" objects; the index class; Extract about the standard subset assignment (and extraction).

Examples

set.seed(101)
(a <- m <- Matrix(round(rnorm(7*4),2), nrow = 7))
a[] <- 2.2 # <<- replaces **every** entry
a
## as do these:
a[,] <- 3 ; a[TRUE,] <- 4
m[2, 3] <- 3.14 # simple number
m[3, 3:4]<- 3:4 # simple numeric of length 2

## sub matrix assignment:
m[-(4:7), 3:4] <- cbind(1,2:4) #-> upper right corner of 'm'
m[3:5, 2:3] <- 0
m[6:7, 1:2] <- Diagonal(2)
m
## rows or columns only:
m[1,] <- 10
m[,2] <- 1:7
m[-(1:6), ] <- 3:0 # not the first 6 rows, i.e. only the 7th
as(m, "sparseMatrix")

---

### Description

Methods for `"["`, i.e., extraction or subsetting mostly of matrices, in package `Matrix`.

### Methods

There are more than these:

- `x = "Matrix", i = "missing", j = "missing", drop= "ANY" ...
- `x = "Matrix", i = "numeric", j = "missing", drop= "missing" ...
- `x = "Matrix", i = "missing", j = "numeric", drop= "missing" ...
- `x = "dsparseMatrix", i = "missing", j = "numeric", drop= "logical" ...
- `x = "dsparseMatrix", i = "numeric", j = "missing", drop= "logical" ...
- `x = "dsparseMatrix", i = "numeric", j = "numeric", drop= "logical" ...

### See Also

- `[<-methods` for subassignment to "Matrix" objects. `Extract` about the standard extraction.

### Examples

```r
str(m <- Matrix(round(rnorm(7*4),2), nrow = 7))
stopifnot(identical(m, m[]))
m[2, 3] # simple number
m[2, 3:4] # simple numeric of length 2
m[2, 3:4, drop=FALSE] # sub matrix of class 'dgeMatrix'
## rows or columns only:
m[1,] # first row, as simple numeric vector
m[,1:2] # sub matrix of first two columns
showMethods("[", inherited = FALSE)
```
**Description**

The virtual class of symmetric matrices, "symmetricMatrix", from the package Matrix contains numeric and logical, dense and sparse matrices, e.g., see the examples with the “actual” subclasses. The main use is in methods (and C functions) that can deal with all symmetric matrices, and in as(*, "symmetricMatrix").

**Slots**

- **uplo**: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- **Dim, Dimnames**: The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the Matrix, see there. See below, about storing only one of the two Dimnames components.
- **factors**: a list of matrix factorizations, also from the Matrix class.

**Extends**

Class "Matrix", directly.

**Methods**

- **dimnames** signature(object = "symmetricMatrix"): returns symmetric dimnames, even when the Dimnames slot only has row or column names. This allows to save storage for large (typically sparse) symmetric matrices.
- **isSymmetric** signature(object = "symmetricMatrix"): returns TRUE trivially.

There's a C function symmetricMatrix_validate() called by the internal validity checking functions, and also from getValidity(getClass("symmetricMatrix")).

**Validity and dimnames**

The validity checks do not require a symmetric Dimnames slot, so it can be list(NULL, <character>), e.g., for efficiency. However, dimnames() and other functions and methods should behave as if the dimnames were symmetric, i.e., with both list components identical.

**See Also**

isSymmetric which has efficient methods (isSymmetric-methods) for the Matrix classes. Classes triangularMatrix, and, e.g., dsyMatrix for numeric dense matrices, or lscMatrix for a logical sparse matrix class.
**Examples**

```r
## An example about the symmetric Dimnames:
sy <- sparseMatrix(i = c(2,4,3:5), j = c(4,7:5,5), x = 1:5, dims = c(7,7),
                    symmetric = TRUE, dimnames = list(NULL, letters[1:7]))
sy # shows symmetrical dimnames
sy@Dimnames # internally only one part is stored
dimnames(sy) # both parts -- as sy *is* symmetrical

showClass("symmetricMatrix")

## The names of direct subclasses:
scl <- getClass("symmetricMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]

## Methods -- applicable to all subclasses above:
showMethods(classes = "symmetricMatrix")
```

---

**symmpart-methods**

**Symmetric Part and Skew(symmetric) Part of a Matrix**

**Description**

`symmpart(x)` computes the symmetric part \((x + t(x))/2\) and `skewpart(x)` the skew symmetric part \((x - t(x))/2\) of a square matrix \(x\), more efficiently for specific Matrix classes.

Note that \(x == \text{symmpart}(x) + \text{skewpart}(x)\) for all square matrices -- apart from extraneous \(NA\) values in the RHS.

**Usage**

```r
symmpart(x)
skewpart(x)
```

**Arguments**

- **x**
  
  *a square* matrix; either “traditional” of class "matrix", or typically, inheriting from the `Matrix` class.

**Details**

These are generic functions with several methods for different matrix classes, use e.g., `showMethods(symmpart)` to see them.

If the row and column names differ, the result will use the column names unless they are (partly) NULL where the row names are non-NULL (see also the examples).

**Value**

`symmpart(x)` returns a symmetric matrix, inheriting from `symmetricMatrix` or `diagonalMatrix` if \(x\) inherits from `Matrix`.

`skewpart(x)` returns a skew-symmetric matrix, inheriting from `generalMatrix`, `symmetricMatrix` or `diagonalMatrix` if \(x\) inherits from `Matrix`. 
See Also

isSymmetric.

Examples

```r
m <- Matrix(1:4, 2,2)
symmpart(m)
skewpart(m)

stopifnot(all(m == symmpart(m) + skewpart(m)))

dn <- dimnames(m) <- list(row = c("r1", "r2"), col = c("var.1", "var.2"))
stopifnot(all(m == symmpart(m) + skewpart(m)))
colnames(m) <- NULL
stopifnot(all(m == symmpart(m) + skewpart(m)))
dimnames(m) <- unname(dn)
stopifnot(all(m == symmpart(m) + skewpart(m)))

## investigate the current methods:
showMethods(skewpart, include = TRUE)
```

description
TsparseMatrix-class

See Also

isTriangular() for testing any matrix for triangularity; classes symmetricMatrix, and, e.g.,
dtrMatrix for numeric dense matrices, or ltrMatrix for a logical sparse matrix subclass of
"triangularMatrix".

Examples

showClass("triangularMatrix")

# The names of direct subclasses:
scl <- getClass("triangularMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]

(m <- matrix(c(5,1,0,3), 2))
as(m, "triangularMatrix")

---

TsparseMatrix-class  Class "TsparseMatrix" of Sparse Matrices in Triplet Form

Description

The "TsparseMatrix" class is the virtual class of all sparse matrices coded in triplet form. Since
it is a virtual class, no objects may be created from it. See showClass("TsparseMatrix") for its
subclasses.

Slots

Dim, Dimnames: from the "Matrix" class,
i: Object of class "integer" - the row indices of non-zero entries in 0-base, i.e., must be in
0:(nrow(.)-1).

j: Object of class "integer" - the column indices of non-zero entries. Must be the same length
as slot i and 0-based as well, i.e., in 0:(ncol(.)-1). For numeric Tsparse matrices, (i,j)
pairs can occur more than once, see dgTMatrix.

Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

Methods

Extraction ("[") methods, see [-methods.

Note

Most operations with sparse matrices are performed using the compressed, column-oriented or
CsparseMatrix representation. The triplet representation is convenient for creating a sparse ma-
trix or for reading and writing such matrices. Once it is created, however, the matrix is generally
coerced to a CsparseMatrix for further operations.

Note that all new(.), spMatrix and sparseMatrix(*, repr="T") constructors for
"TsparseMatrix" classes implicitly add (i.e., "sum up") x_k's that belong to identical (i_k,j_k)
pairs, see, the example below, or also "dgTMatrix".
For convenience, methods for some operations such as %*% and crossprod are defined for TsparseMatrix objects. These methods simply coerce the TsparseMatrix object to a CsparseMatrix object then perform the operation.

See Also
its superclass, sparseMatrix, and the dgTMatrix class, for the links to other classes.

Examples

showClass("TsparseMatrix")
## or just the subclasses' names
names(getClass("TsparseMatrix")@subclasses)

T3 <- spMatrix(3,4, i=c(1,3:1), j=c(2,4:2), x=1:4)
T3 # only 3 non-zero entries, 5 = 1+4 !
Description

Computes a rank-$k$ update or downdate of a sparse Cholesky factorization

$$P_1AP_1^T = L_1DL_1^T = LL^T$$

which for some $k$-column matrix $C$ is the factorization

$$P_1(A + sCC^T)P_1^T = \tilde{L}_1D\tilde{L}_1^T = \tilde{L}\tilde{L}^T$$

Here, $s = 1$ for an update and $s = -1$ for a downdate.

Usage

```r
updown(update, C, L)
```

Arguments

- `update` a logical (TRUE or FALSE) or character ("+" or "-"), indicating if $L$ should be updated (or otherwise downdated).
- `C` a finite matrix or `Matrix` such that `tcrossprod(C)` has the dimensions of $L$.
- `L` an object of class `dCHMsimpl` or `dCHMsuper` specifying a sparse Cholesky factorization.

Value

A sparse Cholesky factorization with dimensions matching $L$, typically of class `dCHMsimpl`.

Author(s)

Initial implementation by Nicholas Nagle, University of Tennessee.

References

### USCounties

#### Contiguity Matrix of U.S. Counties

#### Description

This matrix gives the contiguities of 3111 U.S. counties, using the queen criterion of at least one shared vertex or edge.

#### Usage

```r
data(USCounties)
```

#### Format

A $3111 \times 3111$ sparse, symmetric matrix of class `dsCMatrix` with 9101 nonzero entries.

#### Source

GAL lattice file `usc_q.GAL` (retrieved in 2008 from `http://sal.uiuc.edu/weights/zips/usc.zip` with permission from Luc Anselin for use and distribution) was read into R using function `read.gal` from package `spdep`.

Neighbour lists were augmented with row-standardized (and then symmetrized) spatial weights, using functions `nb2listw` and `similar.listw` from packages `spdep` and `spatialreg`. The resulting `listw` object was coerced to class `dsTMatrix` using `as_dsTMatrix_listw` from `spatialreg`, and subsequently to class `dsCMatrix`.

#### References

Examples

```r
data(USCounties, package = "Matrix")
(n <- ncol(USCounties))
I <- .symDiagonal(n)

set.seed(1)
r <- 50L
rho <- 1 / runif(r, 0, 0.5)

system.time(MJ0 <- sapply(rho, function(mult)
    determinant(USCounties + mult * I, logarithm = TRUE)$modulus))

## Can be done faster by updating the Cholesky factor:

C1 <- Cholesky(USCounties, Imult = 2)

system.time(MJ1 <- sapply(rho, function(mult)
    determinant(update(C1, USCounties, mult), sqrt = FALSE)$modulus))

stopifnot(all.equal(MJ0, MJ1))

C2 <- Cholesky(USCounties, super = TRUE, Imult = 2)

system.time(MJ2 <- sapply(rho, function(mult)
    determinant(update(C2, USCounties, mult), sqrt = FALSE)$modulus))

stopifnot(all.equal(MJ0, MJ2))
```

---

**wrld_1deg**

*Contiguity Matrix of World One-Degree Grid Cells*

**Description**

This matrix gives the contiguities of 15260 one-degree grid cells of world land areas, using a criterion based on the great-circle distance between centers.

**Usage**

data(wrld_1deg)

**Format**

A $15260 \times 15260$ sparse, symmetric matrix of class `dsCMatrix`, with 55973 nonzero entries.

**Source**

Shoreline data were read into R from the GSHHS database using function `RGSHHS` from package `maptools`. Antarctica was excluded. An approximately one-degree grid was generated using function `Sobj_SpatialGrid`, also from `maptools`. Grid cells with centers on land were identified using the over method for classes `SpatialPolygons` and `SpatialGrid`, defined in package `sp`. Neighbours of these were identified by passing the resulting `SpatialPixels` object to function `dnearneigh` from package `spdep`, using as a cut-off a great-circle distance of $\sqrt{2}$ kilometers between centers.

Neighbour lists were augmented with row-standardized (and then symmetrized) spatial weights, using functions `nb2listw` and `similar.listw` from packages `spdep` and `spatialreg`. The resulting listw object was coerced to class `dsTMatrix` using as_dsTMatrix_listw from `spatialreg`, and subsequently to class `dsCMatrix`.
References


Examples

data(wrld_1deg, package = "Matrix")
(n <- ncol(wrld_1deg))
I <- .symDiagonal(n)

doExtras <- interactive() || nzchar(Sys.getenv("R_MATRIX_CHECK_EXTRA"))
set.seed(1)
r <- if(doExtras) 20L else 3L
rho <- 1 / runif(r, 0, 0.5)

system.time(MJ0 <- sapply(rho, function(mult)
  determinant(wrld_1deg + mult * I, logarithm = TRUE)$modulus))

## Can be done faster by updating the Cholesky factor:

C1 <- Cholesky(wrld_1deg, Imult = 2)

system.time(MJ1 <- sapply(rho, function(mult)
  determinant(update(C1, wrld_1deg, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ1))

C2 <- Cholesky(wrld_1deg, super = TRUE, Imult = 2)

system.time(MJ2 <- sapply(rho, function(mult)
  determinant(update(C2, wrld_1deg, mult), sqrt = FALSE)$modulus))
stopifnot(all.equal(MJ0, MJ2))
Chapter 18

The boot package

abc.ci  Nonparametric ABC Confidence Intervals

Description

Calculate equi-tailed two-sided nonparametric approximate bootstrap confidence intervals for a parameter, given a set of data and an estimator of the parameter, using numerical differentiation.

Usage

abc.ci(data, statistic, index=1, strata=rep(1, n), conf=0.95, eps=0.001/n, ...)

Arguments

data  A data set expressed as a vector, matrix or data frame.
statistic  A function which returns the statistic of interest. The function must take at least 2 arguments; the first argument should be the data and the second a vector of weights. The weights passed to statistic will be normalized to sum to 1 within each stratum. Any other arguments should be passed to abc.ci as part of the ...() argument.
index  If statistic returns a vector of length greater than 1, then this indicates the position of the variable of interest within that vector.
strata  A factor or numerical vector indicating to which sample each observation belongs in multiple sample problems. The default is the one-sample case.
conf  A scalar or vector containing the confidence level(s) of the required interval(s).
eps  The value of epsilon to be used for the numerical differentiation.
...  Any other arguments for statistic. These will be passed unchanged to statistic each time it is called within abc.ci.
Details

This function is based on the function abcnon written by R. Tibshirani. A listing of the original function is available in DiCiccio and Efron (1996). The function uses numerical differentiation for the first and second derivatives of the statistic and then uses these values to approximate the bootstrap BCa intervals. The total number of evaluations of the statistic is $2*n+2+2*\text{length}(\text{conf})$ where $n$ is the number of data points (plus calculation of the original value of the statistic). The function works for the multiple sample case without the need to rewrite the statistic in an artificial form since the stratified normalization is done internally by the function.

Value

A $\text{length}(\text{conf})$ by 3 matrix where each row contains the confidence level followed by the lower and upper end-points of the ABC interval at that level.

References


See Also

*boot.ci*

Examples

```
# 90% and 95% confidence intervals for the correlation
# coefficient between the columns of the bigcity data
abc.ci(bigcity, corr, conf=c(0.90, 0.95))

# A 95% confidence interval for the difference between the means of
# the last two samples in gravity
mean.diff <- function(y, w)
{   gp1 <- 1:table(as.numeric(y$series))[1]
    sum(y[gp1, 1] * w[gp1]) - sum(y[-gp1, 1] * w[-gp1])
}
grav1 <- gravity[as.numeric(gravity[, 2]) >= 7, ]
## IGNORE_RDIFF_BEGIN
abc.ci(grav1, mean.diff, strata = grav1$series)
## IGNORE_RDIFF_END
```
Description

The `acme` data frame has 60 rows and 3 columns.
The excess return for the Acme Cleveland Corporation are recorded along with those for all stocks listed on the New York and American Stock Exchanges were recorded over a five year period. These excess returns are relative to the return on a risk-less investment such a U.S. Treasury bills.

Usage

`acme`

Format

This data frame contains the following columns:

- `month` A character string representing the month of the observation.
- `market` The excess return of the market as a whole.
- `acme` The excess return for the Acme Cleveland Corporation.

Source

The data were obtained from

References


Description

The `aids` data frame has 570 rows and 6 columns.
Although all cases of AIDS in England and Wales must be reported to the Communicable Disease Surveillance Centre, there is often a considerable delay between the time of diagnosis and the time that it is reported. In estimating the prevalence of AIDS, account must be taken of the unknown number of cases which have been diagnosed but not reported. The data set here records the reported cases of AIDS diagnosed from July 1983 and until the end of 1992. The data are cross-classified by the date of diagnosis and the time delay in the reporting of the cases.

Usage

`aids`
This data frame contains the following columns:

- **year**: The year of the diagnosis.
- **quarter**: The quarter of the year in which diagnosis was made.
- **delay**: The time delay (in months) between diagnosis and reporting. 0 means that the case was reported within one month. Longer delays are grouped in 3 month intervals and the value of delay is the midpoint of the interval (therefore a value of 2 indicates that reporting was delayed for between 1 and 3 months).
- **dud**: An indicator of censoring. These are categories for which full information is not yet available and the number recorded is a lower bound only.
- **time**: The time interval of the diagnosis. That is the number of quarters from July 1983 until the end of the quarter in which these cases were diagnosed.
- **y**: The number of AIDS cases reported.

**Source**


**References**


---

### Description

Proschan (1963) reported on the times between failures of the air-conditioning equipment in 10 Boeing 720 aircraft. The `aircondit` data frame contains the intervals for the ninth aircraft while `aircondit7` contains those for the seventh aircraft.

Both data frames have just one column. Note that the data have been sorted into increasing order.

### Usage

```r
aircondit
```

### Format

The data frames contain the following column:

- **hours**: The time interval in hours between successive failures of the air-conditioning equipment

### Source

amis

References


Car Speeding and Warning Signs

Description

The amis data frame has 8437 rows and 4 columns.

In a study into the effect that warning signs have on speeding patterns, Cambridgeshire County Council considered 14 pairs of locations. The locations were paired to account for factors such as traffic volume and type of road. One site in each pair had a sign erected warning of the dangers of speeding and asking drivers to slow down. No action was taken at the second site. Three sets of measurements were taken at each site. Each set of measurements was nominally of the speeds of 100 cars but not all sites have exactly 100 measurements. These speed measurements were taken before the erection of the sign, shortly after the erection of the sign, and again after the sign had been in place for some time.

Usage

amis

Format

This data frame contains the following columns:

speed  Speeds of cars (in miles per hour).
period A numeric column indicating the time that the reading was taken. A value of 1 indicates a reading taken before the sign was erected, a 2 indicates a reading taken shortly after erection of the sign and a 3 indicates a reading taken after the sign had been in place for some time.
warning A numeric column indicating whether the location of the reading was chosen to have a warning sign erected. A value of 1 indicates presence of a sign and a value of 2 indicates that no sign was erected.
pair A numeric column giving the pair number at which the reading was taken. Pairs were numbered from 1 to 14.

Source

The data were kindly made available by Mr. Graham Amis, Cambridgeshire County Council, U.K.

References

Description

The `aml` data frame has 23 rows and 3 columns.

A clinical trial to evaluate the efficacy of maintenance chemotherapy for acute myelogenous leukaemia was conducted by Embury et al. (1977) at Stanford University. After reaching a stage of remission through treatment by chemotherapy, patients were randomized into two groups. The first group received maintenance chemotherapy and the second group did not. The aim of the study was to see if maintenance chemotherapy increased the length of the remission. The data here formed a preliminary analysis which was conducted in October 1974.

Usage

`aml`

Format

This data frame contains the following columns:

- `time`: The length of the complete remission (in weeks).
- `cens`: An indicator of right censoring. 1 indicates that the patient had a relapse and so `time` is the length of the remission. 0 indicates that the patient had left the study or was still in remission in October 1974, that is the length of remission is right-censored.
- `group`: The group into which the patient was randomized. Group 1 received maintenance chemotherapy, group 2 did not.

Note

Package `survival` also has a dataset `aml`. It is the same data with different names and with `group` replaced by a factor `x`.

Source

The data were obtained from


References


beaver

Beaver Body Temperature Data

Description

The beaver data frame has 100 rows and 4 columns. It is a multivariate time series of class "ts" and also inherits from class "data.frame".

This data set is part of a long study into body temperature regulation in beavers. Four adult female beavers were live-trapped and had a temperature-sensitive radio transmitter surgically implanted. Readings were taken every 10 minutes. The location of the beaver was also recorded and her activity level was dichotomized by whether she was in the retreat or outside of it since high-intensity activities only occur outside of the retreat.

The data in this data frame are those readings for one of the beavers on a day in autumn.

Usage

beaver

Format

This data frame contains the following columns:

day The day number. The data includes only data from day 307 and early 308.
time The time of day formatted as hour-minute.
temp The body temperature in degrees Celsius.
activ The dichotomized activity indicator. 1 indicates that the beaver is outside of the retreat and therefore engaged in high-intensity activity.

Source

The data were obtained from


References

**bigcity**  Population of U.S. Cities

**Description**

The bigcity data frame has 49 rows and 2 columns.

The city data frame has 10 rows and 2 columns.

The measurements are the population (in 1000's) of 49 U.S. cities in 1920 and 1930. The 49 cities are a random sample taken from the 196 largest cities in 1920. The city data frame consists of the first 10 observations in bigcity.

**Usage**

bigcity

**Format**

This data frame contains the following columns:

- u  The 1920 population.
- x  The 1930 population.

**Source**

The data were obtained from Cochran, W.G. (1977) *Sampling Techniques*. Third edition. John Wiley

**References**


---

**boot**  Bootstrap Resampling

**Description**

Generate R bootstrap replicates of a statistic applied to data. Both parametric and nonparametric resampling are possible. For the nonparametric bootstrap, possible resampling methods are the ordinary bootstrap, the balanced bootstrap, antithetic resampling, and permutation. For nonparametric multi-sample problems stratified resampling is used: this is specified by including a vector of strata in the call to boot. Importance resampling weights may be specified.

**Usage**

```
boot(data, statistic, R, sim = "ordinary", stype = c("i", "f", "w"),
    strata = rep(1,n), L = NULL, m = 0, weights = NULL,
    ran.gen = function(d, p) d, mle = NULL, simple = FALSE, ..., 
    parallel = c("no", "multicore", "snow"),
    ncpus = getOption("boot.ncpus", 1L), cl = NULL)
```
Arguments

**data**
The data as a vector, matrix or data frame. If it is a matrix or data frame then each row is considered as one multivariate observation.

**statistic**
A function which when applied to data returns a vector containing the statistic(s) of interest. When sim = "parametric", the first argument to statistic must be the data. For each replicate a simulated dataset returned by ran.gen will be passed. In all other cases statistic must take at least two arguments. The first argument passed will always be the original data. The second will be a vector of indices, frequencies or weights which define the bootstrap sample. Further, if predictions are required, then a third argument is required which would be a vector of the random indices used to generate the bootstrap predictions. Any further arguments can be passed to statistic through the ... argument.

**R**
The number of bootstrap replicates. Usually this will be a single positive integer. For importance resampling, some resamples may use one set of weights and others use a different set of weights. In this case R would be a vector of integers where each component gives the number of resamples from each of the rows of weights.

**sim**
A character string indicating the type of simulation required. Possible values are "ordinary" (the default), "parametric", "balanced", "permutation", or "antithetic". Importance resampling is specified by including importance weights; the type of importance resampling must still be specified but may only be "ordinary" or "balanced" in this case.

**stype**
A character string indicating what the second argument of statistic represents. Possible values of stype are "i" (indices - the default), "f" (frequencies), or "w" (weights). Not used for sim = "parametric".

**strata**
An integer vector or factor specifying the strata for multi-sample problems. This may be specified for any simulation, but is ignored when sim = "parametric". When strata is supplied for a nonparametric bootstrap, the simulations are done within the specified strata.

**L**
Vector of influence values evaluated at the observations. This is used only when sim is "antithetic". If not supplied, they are calculated through a call to empinf. This will use the infinitesimal jackknife provided that stype is "w", otherwise the usual jackknife is used.

**m**
The number of predictions which are to be made at each bootstrap replicate. This is most useful for (generalized) linear models. This can only be used when sim is "ordinary". m will usually be a single integer but, if there are strata, it may be a vector with length equal to the number of strata, specifying how many of the errors for prediction should come from each strata. The actual predictions should be returned as the final part of the output of statistic, which should also take an argument giving the vector of indices of the errors to be used for the predictions.

**weights**
Vector or matrix of importance weights. If a vector then it should have as many elements as there are observations in data. When simulation from more than one set of weights is required, weights should be a matrix where each row of the matrix is one set of importance weights. If weights is a matrix then R must be a vector of length nrow(weights). This parameter is ignored if sim is not "ordinary" or "balanced".

**ran.gen**
This function is used only when sim = "parametric" when it describes how random values are to be generated. It should be a function of two arguments.
The first argument should be the observed data and the second argument consists of any other information needed (e.g., parameter estimates). The second argument may be a list, allowing any number of items to be passed to ran.gen. The returned value should be a simulated data set of the same form as the observed data which will be passed to statistic to get a bootstrap replicate. It is important that the returned value be of the same shape and type as the original dataset. If ran.gen is not specified, the default is a function which returns the original data in which case all simulation should be included as part of statistic. Use of sim = "parametric" with a suitable ran.gen allows the user to implement any types of nonparametric resampling which are not supported directly.

mle
The second argument to be passed to ran.gen. Typically these will be maximum likelihood estimates of the parameters. For efficiency mle is often a list containing all of the objects needed by ran.gen which can be calculated using the original data set only.

simple
logical, only allowed to be TRUE for sim = "ordinary", stype = "i", n = 0 (otherwise ignored with a warning). By default a n by R index array is created: this can be large and if simple = TRUE this is avoided by sampling separately for each replication, which is slower but uses less memory.

... Other named arguments for statistic which are passed unchanged each time it is called. Any such arguments to statistic should follow the arguments which statistic is required to have for the simulation. Beware of partial matching to arguments of boot listed above, and that arguments named X and FUN cause conflicts in some versions of boot (but not this one).

parallel
The type of parallel operation to be used (if any). If missing, the default is taken from the option "boot.parallel" (and if that is not set, "no").

ncpus
integer: number of processes to be used in parallel operation: typically one would chose this to the number of available CPUs.

cl
An optional parallel or snow cluster for use if parallel = "snow". If not supplied, a cluster on the local machine is created for the duration of the boot call.

Details
The statistic to be bootstrapped can be as simple or complicated as desired as long as its arguments correspond to the dataset and (for a nonparametric bootstrap) a vector of indices, frequencies or weights. statistic is treated as a black box by the boot function and is not checked to ensure that these conditions are met.

The first order balanced bootstrap is described in Davison, Hinkley and Schechtman (1986). The antithetic bootstrap is described by Hall (1989) and is experimental, particularly when used with strata. The other non-parametric simulation types are the ordinary bootstrap (possibly with unequal probabilities), and permutation which returns random permutations of cases. All of these methods work independently within strata if that argument is supplied.

For the parametric bootstrap it is necessary for the user to specify how the resampling is to be conducted. The best way of accomplishing this is to specify the function ran.gen which will return a simulated data set from the observed data set and a set of parameter estimates specified in mle.

Value
The returned value is an object of class "boot", containing the following components:

t0
The observed value of statistic applied to data.
t  A matrix with \( \text{sum}(R) \) rows each of which is a bootstrap replicate of the result of calling \text{statistic}.

R  The value of \( R \) as passed to \text{boot}.

data  The data as passed to \text{boot}.

seed  The value of \texttt{.Random.seed} when \text{boot} started work.

\text{statistic}  The function \text{statistic} as passed to \text{boot}.

\text{sim}  Simulation type used.

\text{stype}  Statistic type as passed to \text{boot}.

call  The original call to \text{boot}.

\text{strata}  The strata used. This is the vector passed to \text{boot}, if it was supplied or a vector of ones if there were no strata. It is not returned if \text{sim} is "parametric".

\text{weights}  The importance sampling weights as passed to \text{boot} or the empirical distribution function weights if no importance sampling weights were specified. It is omitted if \text{sim} is not one of "ordinary" or "balanced".

\text{pred.i}  If predictions are required \((m > 0)\) this is the matrix of indices at which predictions were calculated as they were passed to \text{statistic}. Omitted if \(m \) is 0 or \text{sim} is not "ordinary".

\text{L}  The influence values used when \text{sim} is "antithetic". If no such values were specified and \text{stype} is not "w" then \text{L} is returned as consecutive integers corresponding to the assumption that data is ordered by influence values. This component is omitted when \text{sim} is not "antithetic".

\text{ran.gen}  The random generator function used if \text{sim} is "parametric". This component is omitted for any other value of \text{sim}.

\text{mle}  The parameter estimates passed to \text{boot} when \text{sim} is "parametric". It is omitted for all other values of \text{sim}.

There are \texttt{c}, \texttt{plot} and \texttt{print} methods for this class.

Parallel operation

When \text{parallel} = "multicore" is used (not available on Windows), each worker process inherits the environment of the current session, including the workspace and the loaded namespaces and attached packages (but not the random number seed: see below).

More work is needed when \text{parallel} = "snow" is used: the worker processes are newly created \texttt{R} processes, and \text{statistic} needs to arrange to set up the environment it needs: often a good way to do that is to make use of lexical scoping since when \text{statistic} is sent to the worker processes its enclosing environment is also sent. (E.g. see the example for \texttt{jack.after.boot} where ancillary functions are nested inside the \text{statistic} function.) \text{parallel} = "snow" is primarily intended to be used on multi-core Windows machines where \text{parallel} = "multicore" is not available.

For most of the \text{boot} methods the resampling is done in the master process, but not if \text{simple} = \texttt{TRUE} nor \text{sim} = "parametric". In those cases (or where \text{statistic} itself uses random numbers), more care is needed if the results need to be reproducible. Resampling is done in the worker processes by \texttt{censboot} (\text{sim} = "wierd") and by most of the schemes in \texttt{tsboot} (the exceptions being \text{sim} = "fixed" and \text{sim} = "geom" with the default \text{ran.gen}).

Where random-number generation is done in the worker processes, the default behaviour is that each worker chooses a separate seed, non-reproductibly. However, with \text{parallel} = "multicore" or \text{parallel} = "snow" using the default cluster, a second approach is used if
RNGkind("L'Ecuyer-CMRG") has been selected. In that approach each worker gets a different subsequence of the RNG stream based on the seed at the time the worker is spawned and so the results will be reproducible if ncpus is unchanged, and for parallel = "multicore" if parallel::mc.reset.stream() is called: see the examples for mclapply.

Note that loading the parallel namespace may change the random seed, so for maximum reproducibility this should be done before calling this function.

References

There are many references explaining the bootstrap and its variations. Among them are:

See Also

boot.array, boot.ci, censboot, empinf, jack.after.boot, tilt.boot, tsboot.

Examples

# Usual bootstrap of the ratio of means using the city data
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
boot(city, ratio, R = 999, stype = "w")

diff.means <- function(d, f)
{ n <- nrow(d)
gp1 <- 1:table(as.numeric(d$series))[1]
m1 <- sum(d[gp1,1] * f[gp1])/sum(f[gp1])
m2 <- sum(d[-gp1,1] * f[-gp1])/sum(f[-gp1])
ss1 <- sum(d[gp1,1]^2 * f[gp1]) - (m1 * m1 * sum(f[gp1]))
ss2 <- sum(d[-gp1,1]^2 * f[-gp1]) - (m2 * m2 * sum(f[-gp1]))
c(m1 - m2, (ss1 + ss2)/(sum(f) - 2))
}
In this example we show the use of boot in a prediction from regression based on the nuclear data. This example is taken from Example 6.8 of Davison and Hinkley (1997). Notice also that two extra arguments to 'statistic' are passed through boot.

```r
grav1 <- gravity[as.numeric(gravity[,2]) >= 7,]
boot(grav1, diff.means, R = 999, stype = "f", strata = grav1[,2])
```

We set up a new data frame with the data, the standardized residuals and the fitted values for use in the bootstrap.

```r
nuke.lm <- glm(log(cost) ~ date+log(cap)+ne+ct+log(cum.n)+pt, data = nuke)
nuke.diag <- glm.diag(nuke.lm)
nuke.res <- nuke.diag$res * nuke.diag$sd
nuke.res <- nuke.res - mean(nuke.res)
```

We now want a prediction of plant number 32 but at date 73.00

```r
new.data <- data.frame(cost = 1, date = 73.00, cap = 886, ne = 0, ct = 0, cum.n = 11, pt = 1)
new.fit <- predict(nuke.lm, new.data)
```

Finally a parametric bootstrap. For this example we shall look at the air-conditioning data. In this example our aim is to test the hypothesis that the true value of the index is 1 (i.e. that the data come from an exponential distribution) against the alternative that the data come from a gamma distribution with index not equal to 1.

```r
air.fun <- function(data) {
  ybar <- mean(data$hours)
  para <- c(log(ybar), mean(log(data$hours)))
  ll <- function(k) {
    if (k <= 0) 1e200 else lgamma(k)-k*(log(k)-1-para[1]+para[2])
  }
  khat <- nlm(ll, ybar^2/var(data$hours))$estimate
  c(ybar, khat)
}
air.rg <- function(data, mle) {
  # Function to generate random exponential variates.
  # mle will contain the mean of the original data
```
out <- data
out$hours <- rexp(nrow(out), 1/mle)
out
}

air.boot <- boot(aircondit, air.fun, R = 999, sim = "parametric",
ran.gen = air.rg, mle = mean(aircondit$hours))

# The bootstrap p-value can then be approximated by
sum(abs(air.boot$t[,2]-1) > abs(air.boot$t0[2]-1))/(1+air.boot$R)

---

boot.array  

### Description

This function takes a bootstrap object calculated by one of the functions boot, censboot, or tilt.boot and returns the frequency (or index) array for the bootstrap resamples.

### Usage

```r
boot.array(boot.out, indices)
```

### Arguments

- **boot.out**: An object of class "boot" returned by one of the generation functions for such an object.
- **indices**: A logical argument which specifies whether to return the frequency array or the raw index array. The default is `indices=FALSE` unless `boot.out` was created by `tsboot` in which case the default is `indices=TRUE`.

### Details

The process by which the original index array was generated is repeated with the same value of `.Random.seed`. If the frequency array is required then `freq.array` is called to convert the index array to a frequency array.

A resampling array can only be returned when such a concept makes sense. In particular it cannot be found for any parametric or model-based resampling schemes. Hence for objects generated by censboot the only resampling scheme for which such an array can be found is ordinary case resampling. Similarly if `boot.out$sim` is "parametric" in the case of `boot` or "model" in the case of `tsboot` the array cannot be found. Note also that for post-blackened bootstraps from `tsboot` the indices found will relate to those prior to any post-blackening and so will not be useful.

Frequency arrays are used in many post-bootstrap calculations such as the jackknife-after-bootstrap and finding importance sampling weights. They are also used to find empirical influence values through the regression method.

### Value

A matrix with `boot.out$R` rows and `n` columns where `n` is the number of observations in `boot.out$data`. If `indices` is `FALSE` then this will give the frequency of each of the original observations in each bootstrap resample. If `indices` is `TRUE` it will give the indices of the bootstrap resamples in the order in which they would have been passed to the statistic.
Side Effects

This function temporarily resets .Random.seed to the value in boot.out$seed and then returns it to its original value at the end of the function.

See Also

boot, censboot, freq.array, tilt.boot, tsboot

Examples

# A frequency array for a nonparametric bootstrap
城市.boot <- boot(city, corr, R = 40, stype = "w")
boot.array(city.boot)

perm.cor <- function(d, i) cor(d$x, d$y[i])
城市.perm <- boot(city, perm.cor, R = 40, sim = "permutation")
boot.array(city.perm, indices = TRUE)

Description

This function generates 5 different types of equi-tailed two-sided nonparametric confidence intervals. These are the first order normal approximation, the basic bootstrap interval, the studentized bootstrap interval, the bootstrap percentile interval, and the adjusted bootstrap percentile (BCa) interval. All or a subset of these intervals can be generated.

Usage

boot.ci(boot.out, conf = 0.95, type = "all",
        index = 1:min(2, length(boot.out$t0)),
        var.t0 = NULL, var.t = NULL, t0 = NULL, t = NULL, L = NULL,
        h = function(t) t, hdot = function(t) rep(1, length(t)),
        hinv = function(t) t, ...
)

Arguments

boot.out An object of class "boot" containing the output of a bootstrap calculation.
conf A scalar or vector containing the confidence level(s) of the required interval(s).
type A vector of character strings representing the type of intervals required. The value should be any subset of the values c("norm", "basic", "stud", "perc", "bca") or simply "all" which will compute all five types of intervals.
index This should be a vector of length 1 or 2. The first element of index indicates the position of the variable of interest in boot.out$t0 and the relevant column in boot.out$t. The second element indicates the position of the variance of the variable of interest. If both var.t0 and var.t are supplied then the second element of index (if present) is ignored. The default is that the variable of interest is in position 1 and its variance is in position 2 (as long as there are 2 positions in boot.out$t0).
If supplied, a value to be used as an estimate of the variance of the statistic for
the normal approximation and studentized intervals. If it is not supplied and
length(index) is 2 then var.t0 defaults to boot.out$t0[index[2]] otherwise var.t0 is undefined. For studentized intervals var.t0 must be defined.
For the normal approximation, if var.t0 is undefined it defaults to var(t). If a transformation is supplied through the argument h then var.t0 should be the variance of the untransformed statistic.

This is a vector (of length boot.out$R) of variances of the bootstrap replicates
of the variable of interest. It is used only for studentized intervals. If it is not sup-
plied and length(index) is 2 then var.t defaults to boot.out$t[,index[2]],
otherwise its value is undefined which will cause an error for studentized inter-
vals. If a transformation is supplied through the argument h then var.t should
be the variance of the untransformed bootstrap statistics.

The observed value of the statistic of interest. The default value is
boot.out$t0[index[1]]. Specification of t0 and t allows the user to get inter-
vals for a transformed statistic which may not be in the bootstrap output object.
See the second example below. An alternative way of achieving this would be
to supply the functions h, hdot, and hinv below.

The bootstrap replicates of the statistic of interest. It must be a vector of length
boot.out$R. It is an error to supply one of t0 or t but not the other. Also if
studentized intervals are required and t0 and t are supplied then so should be
var.t0 and var.t. The default value is boot.out$t[,index].

The empirical influence values of the statistic of interest for the observed data.
These are used only for BCa intervals. If a transformation is supplied through
the parameter h then L should be the influence values for t; the values for h(t)
are derived from these and hdot within the function. If L is not supplied then
the values are calculated using empinf if they are needed.

A function defining a transformation. The intervals are calculated on the scale of
h(t) and the inverse function hinv applied to the resulting intervals. It must be a
function of one variable only and for a vector argument, it must return a vector of
the same length, i.e. h(c(t1,t2,t3)) should return c(h(t1),h(t2),h(t3)).
The default is the identity function.

A function of one argument returning the derivative of h. It is a required argu-
ment if h is supplied and normal, studentized or BCa intervals are required. The
function is used for approximating the variances of h(t0) and h(t) using the
delta method, and also for finding the empirical influence values for BCa inter-
vals. Like h it should be able to take a vector argument and return a vector of
the same length. The default is the constant function 1.

A function, like h, which returns the inverse of h. It is used to transform the
intervals calculated on the scale of h(t) back to the original scale. The default is
the identity function. If h is supplied but hinv is not, then the intervals returned
will be on the transformed scale.

Any extra arguments that boot.out$statistic is expecting. These arguments
are needed only if BCa intervals are required and L is not supplied since in that
case L is calculated through a call to empinf which calls boot.out$statistic.

Details

The formulae on which the calculations are based can be found in Chapter 5 of Davison and Hinkley
(1997). Function boot must be run prior to running this function to create the object to be passed
as boot.out.
Variance estimates are required for studentized intervals. The variance of the observed statistic is optional for normal theory intervals. If it is not supplied then the bootstrap estimate of variance is used. The normal intervals also use the bootstrap bias correction.

Interpolation on the normal quantile scale is used when a non-integer order statistic is required. If the order statistic used is the smallest or largest of the R values in boot.out a warning is generated and such intervals should not be considered reliable.

Value

An object of type "bootci" which contains the intervals. It has components

- **R**: The number of bootstrap replicates on which the intervals were based.
- **t0**: The observed value of the statistic on the same scale as the intervals.
- **call**: The call to boot.ci which generated the object.
- **normal**: A matrix of intervals calculated using the normal approximation. It will have 3 columns, the first being the level and the other two being the upper and lower endpoints of the intervals.
- **basic**: The intervals calculated using the basic bootstrap method.
- **student**: The intervals calculated using the studentized bootstrap method.
- **percent**: The intervals calculated using the bootstrap percentile method.
- **bca**: The intervals calculated using the adjusted bootstrap percentile (BCa) method. These latter four components will be matrices with 5 columns, the first column containing the level, the next two containing the indices of the order statistics used in the calculations and the final two the calculated endpoints themselves.

References


See Also

abc.ci, boot.empinf, norm.ci

Examples

```r
# confidence intervals for the city data
to <- function(d, w) sum(d$x * w)/sum(d$u * w)
city.boot <- boot(city, ratio, R = 999, stype = "w", sim = "ordinary")
boot.ci(city.boot, conf = c(0.90, 0.95),
        type = c("norm", "basic", "perc", "bca"))

# studentized confidence interval for the two sample
difference of means problem using the final two series
d of the gravity data.
```
diff.means <- function(d, f)
{
  n <- nrow(d)
  gp1 <- 1:table(as.numeric(d$series))[1]
  m1 <- sum(d[gp1,1] * f[gp1])/sum(f[gp1])
  m2 <- sum(d[-gp1,1] * f[-gp1])/sum(f[-gp1])
  ss1 <- sum(d[gp1,1]^2 * f[gp1]) - (m1 * m1 * sum(f[gp1]))
  ss2 <- sum(d[-gp1,1]^2 * f[-gp1]) - (m2 * m2 * sum(f[-gp1]))
  c(m1 - m2, (ss1 + ss2)/(sum(f) - 2))
}

grav1 <- gravity[as.numeric(gravity[,2]) >= 7, ]
gravl.boot <- boot(grav1, diff.means, R = 999, strata = grav1[,2])
boot.ci(gravl.boot, type = c("stud", "norm"))

# Nonparametric confidence intervals for mean failure time # of the air-conditioning data as in Example 5.4 of Davison # and Hinkley (1997)
mean.fun <- function(d, i)
{
  m <- mean(d$hours[i])
  n <- length(i)
  v <- (n-1)*var(d$hours[i])/n^2
  c(m, v)
}

air.boot <- boot(aircondit, mean.fun, R = 999)
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"))

# Now using the log transformation # There are two ways of doing this and they both give the # same intervals.

# Method 1
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"),
       h = log, hdot = function(x) 1/x)

# Method 2
vt0 <- air.boot$t0[2]/air.boot$t0[1]^2
vt <- air.boot$t[, 2]/air.boot$t[, 1]^2
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"),
        t0 = log(air.boot$t0[1]), t = log(air.boot$t[,1]),
        var.t0 = vt0, var.t = vt)

brambles

brambles

Spatial Location of Bramble Canes

Description

The brambles data frame has 823 rows and 3 columns.
The location of living bramble canes in a 9m square plot was recorded. We take 9m to be the unit of
distance so that the plot can be thought of as a unit square. The bramble canes were also classified
by their age.

Usage

brambles
Format

This data frame contains the following columns:

- **x**: The x coordinate of the position of the cane in the plot.
- **y**: The y coordinate of the position of the cane in the plot.
- **age**: The age classification of the canes; 0 indicates a newly emerged cane, 1 indicates a one year old cane and 2 indicates a two year old cane.

Source

The data were obtained from


References


---

### breslow

**Smoking Deaths Among Doctors**

Description

The *breslow* data frame has 10 rows and 5 columns.

In 1961 Doll and Hill sent out a questionnaire to all men on the British Medical Register enquiring about their smoking habits. Almost 70% of such men replied. Death certificates were obtained for medical practitioners and causes of death were assigned on the basis of these certificates. The *breslow* data set contains the person-years of observations and deaths from coronary artery disease accumulated during the first ten years of the study.

Usage

*breslow*

Format

This data frame contains the following columns:

- **age**: The mid-point of the 10 year age-group for the doctors.
- **smoke**: An indicator of whether the doctors smoked (1) or not (0).
- **n**: The number of person-years in the category.
- **y**: The number of deaths attributed to coronary artery disease.
- **ns**: The number of smoker years in the category (smoke*n).

Source

The data were obtained from

References


---

**calcium**

*Calcium Uptake Data*

**Description**

The calcium data frame has 27 rows and 2 columns.

Howard Grimes from the Botany Department, North Carolina State University, conducted an experiment for biochemical analysis of intracellular storage and transport of calcium across plasma membrane. Cells were suspended in a solution of radioactive calcium for a certain length of time and then the amount of radioactive calcium that was absorbed by the cells was measured. The experiment was repeated independently with 9 different times of suspension each replicated 3 times.

**Usage**

calcium

**Format**

This data frame contains the following columns:

- **time** The time (in minutes) that the cells were suspended in the solution.
- **cal** The amount of calcium uptake (nmoles/mg).

**Source**

The data were obtained from


**References**

Description

The cane data frame has 180 rows and 5 columns. The data frame represents a randomized block design with 45 varieties of sugar-cane and 4 blocks.

Usage

cane

Format

This data frame contains the following columns:

n  The total number of shoots in each plot.
r  The number of diseased shoots.
x  The number of pieces of the stems, out of 50, planted in each plot.
var  A factor indicating the variety of sugar-cane in each plot.
block  A factor for the blocks.

Details

The aim of the experiment was to classify the varieties into resistant, intermediate and susceptible to a disease called "coal of sugar-cane" (carvao da cana-de-acucar). This is a disease that is common in sugar-cane plantations in certain areas of Brazil.

For each plot, fifty pieces of sugar-cane stem were put in a solution containing the disease agent and then some were planted in the plot. After a fixed period of time, the total number of shoots and the number of diseased shoots were recorded.

Source

The data were kindly supplied by Dr. C.G.B. Demetrio of Escola Superior de Agricultura, Universidade de Sao Paolo, Brazil.

References

capability

*Simulated Manufacturing Process Data*

**Description**

The capability data frame has 75 rows and 1 columns.

The data are simulated successive observations from a process in equilibrium. The process is assumed to have specification limits (5.49, 5.79).

**Usage**

`capability`

**Format**

This data frame contains the following column:

`y` The simulated measurements.

**Source**

The data were obtained from


**References**


catsM

*Weight Data for Domestic Cats*

**Description**

The catsM data frame has 97 rows and 3 columns.

144 adult (over 2kg in weight) cats used for experiments with the drug digitalis had their heart and body weight recorded. 47 of the cats were female and 97 were male. The catsM data frame consists of the data for the male cats. The full data are in dataset `cats` in package MASS.

**Usage**

`catsM`
The `cav` data frame has 138 rows and 2 columns.

The data gives the positions of the individual caveolae in a square region with sides of length 500 units. This grid was originally on a 2.65mm square of muscle fibre. The data are those points falling in the lower left hand quarter of the region used for the dataset `caveolae.dat` in the `spatial` package by B.D. Ripley (1994).

**Usage**

cav

**Format**

This data frame contains the following columns:

- x  The x coordinate of the caveola’s position in the region.
- y  The y coordinate of the caveola’s position in the region.

**References**


### Description

The `cd4` data frame has 20 rows and 2 columns.

CD4 cells are carried in the blood as part of the human immune system. One of the effects of the HIV virus is that these cells die. The count of CD4 cells is used in determining the onset of full-blown AIDS in a patient. In this study of the effectiveness of a new anti-viral drug on HIV, 20 HIV-positive patients had their CD4 counts recorded and then were put on a course of treatment with this drug. After using the drug for one year, their CD4 counts were again recorded. The aim of the experiment was to show that patients taking the drug had increased CD4 counts which is not generally seen in HIV-positive patients.

### Usage

`cd4`

### Format

This data frame contains the following columns:

- **baseline**: The CD4 counts (in 100’s) on admission to the trial.
- **oneyear**: The CD4 counts (in 100’s) after one year of treatment with the new drug.

### Source

The data were obtained from DiCiccio, T.J. and Efron B. (1996) Bootstrap confidence intervals (with Discussion). *Statistical Science, 11*, 189–228.

### References


### Description

This is an example of a nested bootstrap for the correlation coefficient of the `cd4` data frame. It is used in a practical in Chapter 5 of Davison and Hinkley (1997).

### References


### See Also

`cd4`
Description

This function applies types of bootstrap resampling which have been suggested to deal with right-censored data. It can also do model-based resampling using a Cox regression model.

Usage

censboot(data, statistic, R, F.surv, G.surv, strata = matrix(1,n,2),
         sim = "ordinary", cox = NULL, index = c(1, 2), ....,
         parallel = c("no", "multicore", "snow"),
         ncpus = getOption("boot.ncpus", 1L), cl = NULL)

Arguments

data
The data frame or matrix containing the data. It must have at least two columns, one of which contains the times and the other the censoring indicators. It is allowed to have as many other columns as desired (although efficiency is reduced for large numbers of columns) except for sim = "weird" when it should only have two columns - the times and censoring indicators. The columns of data referenced by the components of index are taken to be the times and censoring indicators.

statistic
A function which operates on the data frame and returns the required statistic. Its first argument must be the data. Any other arguments that it requires can be passed using the ... argument. In the case of sim = "weird", the data passed to statistic only contains the times and censoring indicator regardless of the actual number of columns in data. In all other cases the data passed to statistic will be of the same form as the original data. When sim = "weird", the actual number of observations in the resampled data sets may not be the same as the number in data. For this reason, if sim = "weird" and strata is supplied, statistic should also take a numeric vector indicating the strata. This allows the statistic to depend on the strata if required.

R
The number of bootstrap replicates.

F.surv
An object returned from a call to survfit giving the survivor function for the data. This is a required argument unless sim = "ordinary" or sim = "model" and cox is missing.

G.surv
Another object returned from a call to survfit but with the censoring indicators reversed to give the product-limit estimate of the censoring distribution. Note that for consistency the uncensored times should be reduced by a small amount in the call to survfit. This is a required argument whenever sim = "cond" or when sim = "model" and cox is supplied.

strata
The strata used in the calls to survfit. It can be a vector or a matrix with 2 columns. If it is a vector then it is assumed to be the strata for the survival distribution, and the censoring distribution is assumed to be the same for all observations. If it is a matrix then the first column is the strata for the survival distribution and the second is the strata for the censoring distribution. When sim = "weird" only the strata for the survival distribution are used since the
censoring times are considered fixed. When \( \text{sim} = \text{"ordinary"} \), only one set of strata is used to stratify the observations, this is taken to be the first column of \texttt{strata} when it is a matrix.

\begin{itemize}
\item \texttt{sim} - The simulation type. Possible types are \text{"ordinary"} (case resampling), \text{"model"} (equivalent to \text{"ordinary"} if \texttt{cox} is missing, otherwise it is model-based resampling), \text{"weird"} (the weird bootstrap - this cannot be used if \texttt{cox} is supplied), and \text{"cond"} (the conditional bootstrap, in which censoring times are resampled from the conditional censoring distribution).
\item \texttt{cox} - An object returned from \texttt{coxph}. If it is supplied, then \texttt{F.surv} should have been generated by a call of the form \texttt{survfit(cox)}.
\item \texttt{index} - A vector of length two giving the positions of the columns in \texttt{data} which correspond to the times and censoring indicators respectively.
\item \texttt{...} - Other named arguments which are passed unchanged to \texttt{statistic} each time it is called. Any such arguments to \texttt{statistic} must follow the arguments which \texttt{statistic} is required to have for the simulation. Beware of partial matching to arguments of \texttt{censboot} listed above, and that arguments named \texttt{X} and \texttt{FUN} cause conflicts in some versions of \texttt{boot} (but not this one).
\end{itemize}

\texttt{parallel, ncpus, cl} - See the help for \texttt{boot}.

### Details

The various types of resampling are described in Davison and Hinkley (1997) in sections 3.5 and 7.3. The simplest is case resampling which simply resamples with replacement from the observations.

The conditional bootstrap simulates failure times from the estimate of the survival distribution. Then, for each observation its simulated censoring time is equal to the observed censoring time if the observation was censored and generated from the estimated censoring distribution conditional on being greater than the observed failure time if the observation was uncensored. If the largest value is censored then it is given a nominal failure time of \texttt{Inf} and conversely if it is uncensored it is given a nominal censoring time of \texttt{Inf}. This is necessary to allow the largest observation to be in the resamples.

If a Cox regression model is fitted to the data and supplied, then the failure times are generated from the survival distribution using that model. In this case the censoring times can either be simulated from the estimated censoring distribution (\texttt{sim} = \text{"model"}) or from the conditional censoring distribution as in the previous paragraph (\texttt{sim} = \text{"cond"}).

The weird bootstrap holds the censored observations as fixed and also the observed failure times. It then generates the number of events at each failure time using a binomial distribution with mean 1 and denominator the number of failures that could have occurred at that time in the original data set. In our implementation we insist that there is a least one simulated event in each stratum for every bootstrap dataset.

When there are strata involved and \texttt{sim} is either \text{"model"} or \text{"cond"} the situation becomes more difficult. Since the strata for the survival and censoring distributions are not the same it is possible that for some observations both the simulated failure time and the simulated censoring time are infinite. To see this consider an observation in stratum 1F for the survival distribution and stratum 1G for the censoring distribution. Now if the largest value in stratum 1F is censored it is given a nominal failure time of \texttt{Inf}, also if the largest value in stratum 1G is uncensored it is given a nominal censoring time of \texttt{Inf} and so both the simulated failure and censoring times could be infinite. When this happens the simulated value is considered to be a failure at the time of the largest observed failure time in the stratum for the survival distribution.
When parallel = "snow" and cl is not supplied, library(survival) is run in each of the worker processes.

Value

An object of class "boot" containing the following components:

- **t0**: The value of statistic when applied to the original data.
- **t**: A matrix of bootstrap replicates of the values of statistic.
- **R**: The number of bootstrap replicates performed.
- **sim**: The simulation type used. This will usually be the input value of sim unless that was "model" but cox was not supplied, in which case it will be "ordinary".
- **data**: The data used for the bootstrap. This will generally be the input value of data unless sim = "weird", in which case it will just be the columns containing the times and the censoring indicators.
- **seed**: The value of .Random.seed when censboot started work.
- **statistic**: The input value of statistic.
- **strata**: The strata used in the resampling. When sim = "ordinary" this will be a vector which stratifies the observations, when sim = "weird" it is the strata for the survival distribution and in all other cases it is a matrix containing the strata for the survival distribution and the censoring distribution.
- **call**: The original call to censboot.

Author(s)

Angelo J. Canty. Parallel extensions by Brian Ripley

References


See Also

boot, coxph, survfit

Examples

```r
library(survival)
# Example 3.9 of Davison and Hinkley (1997) does a bootstrap on some
# remission times for patients with a type of leukaemia. The patients
# were divided into those who received maintenance chemotherapy and
# those who did not. Here we are interested in the median remission
```
# time for the two groups.
data(aml, package = "boot") # not the version in survival.
aml.fun <- function(data) {
  surv <- survfit(Surv(time, cens) ~ group, data = data)
  out <- NULL
  st <- 1
  for (s in 1:length(surv$strata)) {
    inds <- st:(st + surv$strata[s]-1)
    md <- min(surv$time[inds[1:surv$surv[inds] >= 0.5]])
    st <- st + surv$strata[s]
    out <- c(out, md)
  }
  out
}
aml.case <- censboot(aml, aml.fun, R = 499, strata = aml$group)

# Now we will look at the same statistic using the conditional
# bootstrap and the weird bootstrap. For the conditional bootstrap
# the survival distribution is stratified but the censoring
# distribution is not.

aml.s1 <- survfit(Surv(time, cens) ~ group, data = aml)
aml.s2 <- survfit(Surv(time-0.001*cens, 1-cens) ~ 1, data = aml)
aml.cond <- censboot(aml, aml.fun, R = 499, strata = aml$group,
                      F.surv = aml.s1, G.surv = aml.s2, sim = "cond")

# For the weird bootstrap we must redefine our function slightly since
# the data will not contain the group number.

aml.fun1 <- function(data, str) {
  surv <- survfit(Surv(data[, 1], data[, 2]) ~ str)
  out <- NULL
  st <- 1
  for (s in 1:length(surv$strata)) {
    inds <- st:(st + surv$strata[s]-1)
    md <- min(surv$time[inds[1:surv$surv[inds] >= 0.5]])
    st <- st + surv$strata[s]
    out <- c(out, md)
  }
  out
}
aml.wei <- censboot(cbind(aml$time, aml$cens), aml.fun1, R = 499,
                    strata = aml$group, F.surv = aml.s1, sim = "weird")

# Now for an example where a cox regression model has been fitted
# the data we will look at the melanoma data of Example 7.6 from
# Davison and Hinkley (1997). The fitted model assumes that there
# is a different survival distribution for the ulcerated and
# non-ulcerated groups but that the thickness of the tumour has a
# common effect. We will also assume that the censoring distribution
# is different in different age groups. The statistic of interest
# is the linear predictor. This is returned as the values at a
# number of equally spaced points in the range of interest.
data(melanoma, package = "boot")
library(splines)# for ns
mel.cox <- coxph(Surv(time, status == 1) ~ ns(thickness, df=4) + strata(ulcer),
                 data = melanoma)
mel.surv <- survfit(mel.cox)
agec <- cut(melanoma$age, c(0, 39, 49, 59, 69, 100))
mel.cens <- survfit(Surv(time - 0.001*(status == 1), status != 1) ~
                     strata(agen), data = melanoma)
mel.fun <- function(d) {
  t1 <- ns(d$thickness, df=4)
  cox <- coxph(Surv(d$time, d$status == 1) ~ t1+strata(d$ulcer))
  ind <- !duplicated(d$thickness)
  u <- d$thickness[!ind]
  eta <- cox$linear.predictors[!ind]
  sp <- smooth.spline(u, eta, df=20)
  th <- seq(from = 0.25, to = 10, by = 0.25)
  predict(sp, th)$y
}
mel.str <- cbind(melanoma$ulcer, agec)

# this is slow!
mel.mod <- censboot(melanoma, mel.fun, R = 499, F.surv = mel.surv,
                    G.surv = mel.cens, cox = mel.cox, strata = mel.str, sim = "model")
# To plot the original predictor and a 95% pointwise envelope for it
mel.env <- envelope(mel.mod)$point
th <- seq(0.25, 10, by = 0.25)
plot(th, mel.env[, 1], ylim = c(-2, 2),
     xlab = "thickness (mm)", ylab = "linear predictor", type = "n")
lines(th, mel.mod$t0, lty = 1)
matlines(th, t(mel.env), lty = 2)

---

**channing**

**Channing House Data**

**Description**

The *channing* data frame has 462 rows and 5 columns.

Channing House is a retirement centre in Palo Alto, California. These data were collected between the opening of the house in 1964 until July 1, 1975. In that time 97 men and 365 women passed through the centre. For each of these, their age on entry and also on leaving or death was recorded. A large number of the observations were censored mainly due to the resident being alive on July 1, 1975 when the data was collected. Over the time of the study 130 women and 46 men died at Channing House. Differences between the survival of the sexes, taking age into account, was one of the primary concerns of this study.

**Usage**

channing

**Format**

This data frame contains the following columns:

- **sex** A factor for the sex of each resident ("Male" or "Female").
- **entry** The residents age (in months) on entry to the centre
- **exit** The age (in months) of the resident on death, leaving the centre or July 1, 1975 whichever event occurred first.
**time**  The length of time (in months) that the resident spent at Channing House. 
(time=exit-entry)

**cens**  The indicator of right censoring. 1 indicates that the resident died at Channing House, 0 indicates that they left the house prior to July 1, 1975 or that they were still alive and living in the centre at that date.

**Source**

The data were obtained from


**References**


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**claridge**

*Genetic Links to Left-handedness*

**Description**

The `claridge` data frame has 37 rows and 2 columns.

The data are from an experiment which was designed to look for a relationship between a certain genetic characteristic and handedness. The 37 subjects were women who had a son with mental retardation due to inheriting a defective X-chromosome. For each such mother a genetic measurement of their DNA was made. Larger values of this measurement are known to be linked to the defective gene and it was hypothesized that larger values might also be linked to a progressive shift away from right-handedness. Each woman also filled in a questionnaire regarding which hand they used for various tasks. From these questionnaires a measure of hand preference was found for each mother. The scale of this measure goes from 1, indicating someone who always favours their right hand, to 8, indicating someone who always favours their left hand. Between these two extremes are people who favour one hand for some tasks and the other for other tasks.

**Usage**

`claridge`

**Format**

This data frame contains the following columns:

- **dnan**  The genetic measurement on each woman’s DNA.
- **hand**  The measure of left-handedness on an integer scale from 1 to 8.

**Source**

The data were kindly made available by Dr. Gordon S. Claridge from the Department of Experimental Psychology, University of Oxford.
### References


---

#### cloth

**Number of Flaws in Cloth**

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
<th>Usage</th>
<th>Format</th>
<th>Source</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>The cloth data frame has 32 rows and 2 columns.</td>
<td></td>
<td>This data frame contains the following columns:</td>
<td>The data were obtained from</td>
<td>Davison, A.C. and Hinkley, D.V. (1997) <em>Bootstrap Methods and Their Application</em>. Cambridge University Press.</td>
</tr>
</tbody>
</table>

#### co.transfer

**Carbon Monoxide Transfer**

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
<th>Usage</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>The co.transfer data frame has 7 rows and 2 columns. Seven smokers with chickenpox had their levels of carbon monoxide transfer measured on entry to hospital and then again after 1 week. The main question being whether one week of hospitalization has changed the carbon monoxide transfer factor.</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>co.transfer</td>
</tr>
</tbody>
</table>

---
Format

This data frame contains the following columns:

- **entry**  Carbon monoxide transfer factor on entry to hospital.
- **week**  Carbon monoxide transfer one week after admittance to hospital.

Source

The data were obtained from


References


---

### coal

*Dates of Coal Mining Disasters*

Description

The coal data frame has 191 rows and 1 columns. This data frame gives the dates of 191 explosions in coal mines which resulted in 10 or more fatalities. The time span of the data is from March 15, 1851 until March 22, 1962.

Usage

`coal`

Format

This data frame contains the following column:

- **date**  The date of the disaster. The integer part of `date` gives the year. The day is represented as the fraction of the year that had elapsed on that day.

Source

The data were obtained from


References


Description

This function will find control variate estimates from a bootstrap output object. It can either find the adjusted bias estimate using post-simulation balancing or it can estimate the bias, variance, third cumulant and quantiles, using the linear approximation as a control variate.

Usage

\[
\text{control}(\text{boot.out, L = NULL, distn = NULL, index = 1, t0 = NULL, t = NULL, bias.adj = FALSE, alpha = NULL, ...})
\]

Arguments

- **boot.out**: A bootstrap output object returned from `boot`. The bootstrap replicates must have been generated using the usual nonparametric bootstrap.
- **L**: The empirical influence values for the statistic of interest. If L is not supplied then `empinf` is called to calculate them from `boot.out`.
- **distn**: If present this must be the output from `smooth.spline` giving the distribution function of the linear approximation. This is used only if `bias.adj` is FALSE. Normally this would be found using a saddlepoint approximation. If it is not supplied in that case then it is calculated by `saddle.distn`.
- **index**: The index of the variable of interest in the output of `boot.out$statistic`.
- **t0**: The observed value of the statistic of interest on the original data set `boot.out$data`. This argument is used only if `bias.adj` is FALSE. The input value is ignored if t is not also supplied. The default value is `boot.out$t0[index]`.
- **t**: The bootstrap replicate values of the statistic of interest. This argument is used only if `bias.adj` is FALSE. The input is ignored if `t0` is not supplied also. The default value is `boot.out$t[,index]`.
- **bias.adj**: A logical variable which if TRUE specifies that the adjusted bias estimate using post-simulation balance is all that is required. If `bias.adj` is FALSE (default) then the linear approximation to the statistic is calculated and used as a control variate in estimates of the bias, variance and third cumulant as well as quantiles.
- **alpha**: The alpha levels for the required quantiles if `bias.adj` is FALSE.
- **...**: Any additional arguments that `boot.out$statistic` requires. These are passed unchanged every time `boot.out$statistic` is called. `boot.out$statistic` is called once if `bias.adj` is TRUE, otherwise it may be called by `empinf` for empirical influence calculations if `L` is not supplied.

Details

If `bias.adj` is FALSE then the linear approximation to the statistic is found and evaluated at each bootstrap replicate. Then using the equation \( T* = Tl* + (T*-Tl*) \), moment estimates can be found. For quantile estimation the distribution of the linear approximation to \( t \) is approximated very accurately by saddlepoint methods, this is then combined with the bootstrap replicates to approximate the bootstrap distribution of \( t \) and hence to estimate the bootstrap quantiles of \( t \).
Value

If `bias.adj` is `TRUE` then the returned value is the adjusted bias estimate.

If `bias.adj` is `FALSE` then the returned value is a list with the following components:

- **L** The empirical influence values used. These are the input values if supplied, and otherwise they are the values calculated by `empinf`.
- **tL** The linear approximations to the bootstrap replicates `t` of the statistic of interest.
- **bias** The control estimate of bias using the linear approximation to `t` as a control variate.
- **var** The control estimate of variance using the linear approximation to `t` as a control variate.
- **k3** The control estimate of the third cumulant using the linear approximation to `t` as a control variate.
- **quantiles** A matrix with two columns; the first column are the alpha levels used for the quantiles and the second column gives the corresponding control estimates of the quantiles using the linear approximation to `t` as a control variate.
- **distn** An output object from `smooth.spline` describing the saddlepoint approximation to the bootstrap distribution of the linear approximation to `t`. If `distn` was supplied on input then this is the same as the input otherwise it is calculated by a call to `saddle.distn`.

References


See Also

`boot`, `empinf`, `k3.linear`, `linear.approx`, `saddle.distn`, `smooth.spline`, `var.linear`

Examples

```R
# Use of control variates for the variance of the air-conditioning data
mean.fun <- function(d, i)
{ m <- mean(d$hours[i])
  n <- nrow(d)
  v <- (n-1)*var(d$hours[i])/n^2
  c(m, v)
}
air.boot <- boot(aircondit, mean.fun, R = 999)
control(air.boot, index = 2, bias.adj = TRUE)
air.cont <- control(air.boot, index = 2)
# Now let us try the variance on the log scale.
air.cont1 <- control(air.boot, t0 = log(air.boot$t0[2]),
  t = log(air.boot$t[, 2]))
```
**corr**

**Correlation Coefficient**

**Description**

Calculates the weighted correlation given a data set and a set of weights.

**Usage**

```r
corr(d, w = rep(1, nrow(d))/nrow(d))
```

**Arguments**

- `d`: A matrix with two columns corresponding to the two variables whose correlation we wish to calculate.
- `w`: A vector of weights to be applied to each pair of observations. The default is equal weights for each pair. Normalization takes place within the function so `sum(w)` need not equal 1.

**Details**

This function finds the correlation coefficient in weighted form. This is often useful in bootstrap methods since it allows for numerical differentiation to get the empirical influence values. It is also necessary to have the statistic in this form to find ABC intervals.

**Value**

The correlation coefficient between `d[,1]` and `d[,2]`.

**See Also**

`cor`

---

**cum3**

**Calculate Third Order Cumulants**

**Description**

Calculates an estimate of the third cumulant, or skewness, of a vector. Also, if more than one vector is specified, a product-moment of order 3 is estimated.

**Usage**

```r
cum3(a, b = a, c = a, unbiased = TRUE)
```
Arguments

- **a**: A vector of observations.
- **b**: Another vector of observations, if not supplied it is set to the value of \(a\). If supplied then it must be the same length as \(a\).
- **c**: Another vector of observations, if not supplied it is set to the value of \(a\). If supplied then it must be the same length as \(a\).
- **unbiased**: A logical value indicating whether the unbiased estimator should be used.

Details

The unbiased estimator uses a multiplier of \(\frac{n}{(n-1)(n-2)}\) where \(n\) is the sample size, if unbiased is FALSE then a multiplier of \(\frac{1}{n}\) is used. This is multiplied by \(\text{sum}(a-\text{mean}(a))*(b-\text{mean}(b))*(c-\text{mean}(c))\) to give the required estimate.

Value

The required estimate.

cv.glm

Cross-validation for Generalized Linear Models

Description

This function calculates the estimated K-fold cross-validation prediction error for generalized linear models.

Usage

cv.glm(data, glmfit, cost, K)

Arguments

- **data**: A matrix or data frame containing the data. The rows should be cases and the columns correspond to variables, one of which is the response.
- **glmfit**: An object of class "glm" containing the results of a generalized linear model fitted to data.
- **cost**: A function of two vector arguments specifying the cost function for the cross-validation. The first argument to \(\text{cost}\) should correspond to the observed responses and the second argument should correspond to the predicted or fitted responses from the generalized linear model. \(\text{cost}\) must return a non-negative scalar value. The default is the average squared error function.
- **K**: The number of groups into which the data should be split to estimate the cross-validation prediction error. The value of \(K\) must be such that all groups are of approximately equal size. If the supplied value of \(K\) does not satisfy this criterion then it will be set to the closest integer which does and a warning is generated specifying the value of \(K\) used. The default is to set \(K\) equal to the number of observations in \(\text{data}\) which gives the usual leave-one-out cross-validation.
Details
The data is divided randomly into $K$ groups. For each group the generalized linear model is fit to data omitting that group, then the function `cost` is applied to the observed responses in the group that was omitted from the fit and the prediction made by the fitted models for those observations.
When $K$ is the number of observations leave-one-out cross-validation is used and all the possible splits of the data are used. When $K$ is less than the number of observations the $K$ splits to be used are found by randomly partitioning the data into $K$ groups of approximately equal size. In this latter case a certain amount of bias is introduced. This can be reduced by using a simple adjustment (see equation 6.48 in Davison and Hinkley, 1997). The second value returned in `delta` is the estimate adjusted by this method.

Value
The returned value is a list with the following components.

- **call**: The original call to `cv.glm`.
- **$K$**: The value of $K$ used for the K-fold cross validation.
- **$delta$**: A vector of length two. The first component is the raw cross-validation estimate of prediction error. The second component is the adjusted cross-validation estimate. The adjustment is designed to compensate for the bias introduced by not using leave-one-out cross-validation.
- **seed**: The value of `.Random.seed` when `cv.glm` was called.

Side Effects
The value of `.Random.seed` is updated.

References

See Also
`glm`, `glm.diag`, `predict`

Examples
```r
# leave-one-out and 6-fold cross-validation prediction error for
# the mammals data set.
data(mammals, package="MASS")
mammals.glm <- glm(log(brain) ~ log(body), data = mammals)
(cv.err <- cv.glm(mammals, mammals.glm)$delta)
```
(cv.err.6 <- cv.glm(mammals, mammals.glm, K = 6)$delta)

# As this is a linear model we could calculate the leave-one-out
# cross-validation estimate without any extra model-fitting.
muhat <- fitted(mammals.glm)
mammals.diag <- glm.diag(mammals.glm)
(cv.err <- mean((mammals.glm$y - muhat)^2/(1 - mammals.diag$h)^2))

# leave-one-out and 11-fold cross-validation prediction error for
# the nodal data set. Since the response is a binary variable an
# appropriate cost function is

cost <- function(r, pi = 0) mean(abs(r - pi) > 0.5)
nodal glm <- glm(r ~ stage+xray+acid, binomial, data = nodal)
(cv.err <- cv.glm(nodal, nodal glm, cost, K = nrow(nodal))$delta)
(cv.11.err <- cv.glm(nodal, nodal glm, cost, K = 11)$delta)

darwin

**Darwin’s Plant Height Differences**

**Description**

The darwin data frame has 15 rows and 1 columns.

Charles Darwin conducted an experiment to examine the superiority of cross-fertilized plants over
self-fertilized plants. 15 pairs of plants were used. Each pair consisted of one cross-fertilized plant
and one self-fertilized plant which germinated at the same time and grew in the same pot. The
plants were measured at a fixed time after planting and the difference in heights between the cross-
and self-fertilized plants are recorded in eighths of an inch.

**Usage**

darwin

**Format**

This data frame contains the following column:

y  The difference in heights for the pairs of plants (in units of 0.125 inches).

**Source**

The data were obtained from


**References**

Murray.

University Press.
**dogs**

**Cardiac Data for Domestic Dogs**

**Description**

The `dogs` data frame has 7 rows and 2 columns.

Data on the cardiac oxygen consumption and left ventricular pressure were gathered on 7 domestic dogs.

**Usage**

dogs

**Format**

This data frame contains the following columns:

- **mvo** Cardiac Oxygen Consumption
- **lvp** Left Ventricular Pressure

**References**


---

**downs.bc**

**Incidence of Down's Syndrome in British Columbia**

**Description**

The `downs.bc` data frame has 30 rows and 3 columns.

Down’s syndrome is a genetic disorder caused by an extra chromosome 21 or a part of chromosome 21 being translocated to another chromosome. The incidence of Down’s syndrome is highly dependent on the mother’s age and rises sharply after age 30. In the 1960’s a large scale study of the effect of maternal age on the incidence of Down’s syndrome was conducted at the British Columbia Health Surveillance Registry. These are the data which was collected in that study.

Mothers were classified by age. Most groups correspond to the age in years but the first group comprises all mothers with ages in the range 15-17 and the last is those with ages 46-49. No data for mothers over 50 or below 15 were collected.

**Usage**

downs.bc

**Format**

This data frame contains the following columns:

- **age** The average age of all mothers in the age category.
- **m** The total number of live births to mothers in the age category.
- **r** The number of cases of Down’s syndrome.
Source

The data were obtained from

References


---

**ducks**

*Behavioral and Plumage Characteristics of Hybrid Ducks*

Description

The ducks data frame has 11 rows and 2 columns.

Each row of the data frame represents a male duck who is a second generation cross of mallard and pintail ducks. For 11 such ducks a behavioural and plumage index were calculated. These were measured on scales devised for this experiment which was to examine whether there was any link between which species the ducks resembled physically and which they resembled in behaviour. The scale for the physical appearance ranged from 0 (identical in appearance to a mallard) to 20 (identical to a pintail). The behavioural traits of the ducks were on a scale from 0 to 15 with lower numbers indicating closer to mallard-like in behaviour.

Usage

ducks

Format

This data frame contains the following columns:

- **plumage** The index of physical appearance based on the plumage of individual ducks.
- **behaviour** The index of behavioural characteristics of the ducks.

Source

The data were obtained from

References


**Description**

Construct the empirical log likelihood or empirical exponential family log likelihood for a mean.

**Usage**

```r
EEF.profile(y, tmin = min(y) + 0.1, tmax = max(y) - 0.1, n.t = 25,
             u = function(y, t) y - t)
EL.profile(y, tmin = min(y) + 0.1, tmax = max(y) - 0.1, n.t = 25,
           u = function(y, t) y - t)
```

**Arguments**

- `y`: A vector or matrix of data.
- `tmin`: The minimum value of the range over which the likelihood should be computed. This must be larger than `min(y)`.
- `tmax`: The maximum value of the range over which the likelihood should be computed. This must be smaller than `max(y)`.
- `n.t`: The number of points between `tmin` and `tmax` at which the value of the log-likelihood should be computed.
- `u`: A function of the data and the parameter.

**Details**

These functions calculate the log likelihood for a mean using either an empirical likelihood or an empirical exponential family likelihood. They are supplied as part of the package `boot` for demonstration purposes with the practicals in chapter 10 of Davison and Hinkley (1997). The functions are not intended for general use and are not supported as part of the `boot` package. For more general and more robust code to calculate empirical likelihoods see Professor A. B. Owen’s empirical likelihood home page at the URL [https://artowen.su.domains/empirical/](https://artowen.su.domains/empirical/)

**Value**

A matrix with `n.t` rows. The first column contains the values of the parameter used. The second column of the output of `EL.profile` contains the values of the empirical log likelihood. The second and third columns of the output of `EEF.profile` contain two versions of the empirical exponential family log-likelihood. The final column of the output matrix contains the values of the Lagrange multiplier used in the optimization procedure.

**Author(s)**

Angelo J. Canty

**References**

empinf

**Empirical Influence Values**

### Description

This function calculates the empirical influence values for a statistic applied to a data set. It allows four types of calculation, namely the infinitesimal jackknife (using numerical differentiation), the usual jackknife estimates, the ‘positive’ jackknife estimates and a method which estimates the empirical influence values using regression of bootstrap replicates of the statistic. All methods can be used with one or more samples.

### Usage

```r
empinf(boot.out = NULL, data = NULL, statistic = NULL, type = NULL, stype = NULL, index = 1, t = NULL, strata = rep(1, n), eps = 0.001, ...)
```

### Arguments

- **boot.out**: A bootstrap object created by the function `boot`. If type is “reg” then this argument is required. For any of the other types it is an optional argument. If it is included when optional then the values of data, statistic, stype, and strata are taken from the components of boot.out and any values passed to `empinf` directly are ignored.

- **data**: A vector, matrix or data frame containing the data for which empirical influence values are required. It is a required argument if boot.out is not supplied. If boot.out is supplied then data is set to boot.out$data and any value supplied here is ignored.

- **statistic**: The statistic for which empirical influence values are required. It must be a function of at least two arguments, the data set and a vector of weights, frequencies or indices. The nature of the second argument is given by the value of stype. Any other arguments that it takes must be supplied to `empinf` and will be passed to statistic unchanged. This is a required argument if boot.out is not supplied, otherwise its value is taken from boot.out and any value supplied here will be ignored.

- **type**: The calculation type to be used for the empirical influence values. Possible values of type are “inf” (infinitesimal jackknife), “jack” (usual jackknife), “pos” (positive jackknife), and “reg” (regression estimation). The default value depends on the other arguments. If t is supplied then the default value of type is “reg” and boot.out should be present so that its frequency array can be found. If t is not supplied then if stype is “w”, the default value of type is “inf”; otherwise, if boot.out is present the default is “reg”. If none of these conditions apply then the default is “jack”. Note that it is an error for type to be “reg” if boot.out is missing or to be “inf” if stype is not “w”.

- **stype**: A character variable giving the nature of the second argument to statistic. It can take on three values: “w” (weights), “f” (frequencies), or “i” (indices). If boot.out is supplied the value of stype is set to boot.out$stype and any value supplied here is ignored. Otherwise it is an optional argument which defaults to “w”. If type is “inf” then stype MUST be “w”.


index  An integer giving the position of the variable of interest in the output of statistic.

`t`  A vector of length `boot.out$R` which gives the bootstrap replicates of the statistic of interest. `t` is used only when `type` is `reg` and it defaults to `boot.out$t[,index].`

`strata`  An integer vector or a factor specifying the strata for multi-sample problems. If `boot.out` is supplied the value of `strata` is set to `boot.out$strata`. Otherwise it is an optional argument which has default corresponding to the single sample situation.

`eps`  This argument is used only if `type` is “inf”. In that case the value of epsilon to be used for numerical differentiation will be `eps` divided by the number of observations in `data`.

...  Any other arguments that `statistic` takes. They will be passed unchanged to `statistic` every time that it is called.

**Details**

If `type` is “inf” then numerical differentiation is used to approximate the empirical influence values. This makes sense only for statistics which are written in weighted form (i.e. `stype` is “w”). If `type` is “jack” then the usual leave-one-out jackknife estimates of the empirical influence are returned. If `type` is “pos” then the positive (include-one-twice) jackknife values are used. If `type` is “reg” then a bootstrap object must be supplied. The regression method then works by regressing the bootstrap replicates of statistic on the frequency array from which they were derived. The bootstrap frequency array is obtained through a call to `boot.array`. Further details of the methods are given in Section 2.7 of Davison and Hinkley (1997).

Empirical influence values are often used frequently in nonparametric bootstrap applications. For this reason many other functions call `empinf` when they are required. Some examples of their use are for nonparametric delta estimates of variance, BCa intervals and finding linear approximations to statistics for use as control variates. They are also used for antithetic bootstrap resampling.

**Value**

A vector of the empirical influence values of statistic applied to `data`. The values will be in the same order as the observations in `data`.

**Warning**

All arguments to `empinf` must be passed using the `name = value` convention. If this is not followed then unpredictable errors can occur.

**References**


**See Also**

`boot`, `boot.array`, `boot.ci`, `control`, `jack.after.boot`, `linear.approx`, `var.linear`
Examples

# The empirical influence values for the ratio of means in
# the city data.
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
empinf(data = city, statistic = ratio)
city.boot <- boot(city, ratio, 499, stype = "w")
empinf(boot.out = city.boot, type = "reg")

# A statistic that may be of interest in the difference of means
# problem is the t-statistic for testing equality of means. In
# the bootstrap we get replicates of the difference of means and
# the variance of that statistic and then want to use this output
# to get the empirical influence values of the t-statistic.
grav1 <- gravity[as.numeric(gravity[, 2]) >= 7,]
grav.fun <- function(dat, w) {
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- as.vector(tapply(d * w, strata, sum)) # drop names
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2] - mns[1], s2hat)
}
grav.boot <- boot(grav1, grav.fun, R = 499, stype = "w",
  strata = grav1[, 2])

# Since the statistic of interest is a function of the bootstrap
# statistics, we must calculate the bootstrap replicates and pass
# them to empinf using the t argument.
grav.z <- (grav.boot$t[, 1] - grav.boot$t0[1])/sqrt(grav.boot$t[, 2])
empinf(boot.out = grav.boot, t = grav.z)

envelope

Confidence Envelopes for Curves

Description

This function calculates overall and pointwise confidence envelopes for a curve based on bootstrap
replicates of the curve evaluated at a number of fixed points.

Usage

envelope(boot.out = NULL, mat = NULL, level = 0.95, index = 1:ncol(mat))

Arguments

boot.out  An object of class "boot" for which boot.out$t contains the replicates of the
curve at a number of fixed points.

mat       A matrix of bootstrap replicates of the values of the curve at a number of fixed
points. This is a required argument if boot.out is not supplied and is set to
boot.out$t otherwise.
envelope 2549

level
The confidence level of the envelopes required. The default is to find 95% confidence envelopes. It can be a scalar or a vector of length 2. If it is scalar then both the pointwise and the overall envelopes are found at that level. If is a vector then the first element gives the level for the pointwise envelope and the second gives the level for the overall envelope.

index
The numbers of the columns of mat which contain the bootstrap replicates. This can be used to ensure that other statistics which may have been calculated in the bootstrap are not considered as values of the function.

Details
The pointwise envelope is found by simply looking at the quantiles of the replicates at each point. The overall error for that envelope is then calculated using equation (4.17) of Davison and Hinkley (1997). A sequence of pointwise envelopes is then found until one of them has overall error approximately equal to the level required. If no such envelope can be found then the envelope returned will just contain the extreme values of each column of mat.

Value
A list with the following components:

point
A matrix with two rows corresponding to the values of the upper and lower pointwise confidence envelope at the same points as the bootstrap replicates were calculated.

overall
A matrix similar to point but containing the envelope which controls the overall error.

k.pt
The quantiles used for the pointwise envelope.

err.pt
A vector with two components, the first gives the pointwise error rate for the pointwise envelope, and the second the overall error rate for that envelope.

k.ov
The quantiles used for the overall envelope.

err.ov
A vector with two components, the first gives the pointwise error rate for the overall envelope, and the second the overall error rate for that envelope.

err.nom
A vector of length 2 giving the nominal error rates for the pointwise and the overall envelopes.

References

See Also
boot, boot.ci

Examples
# Testing whether the final series of measurements of the gravity data may come from a normal distribution. This is done in Examples 4.7 and 4.8 of Davison and Hinkley (1997).
grav1 <- gravity$g[gravity$series == 8]
grav.z <- (grav1 - mean(grav1))/sqrt(var(grav1))
grav.gen <- function(dat, mle) rnorm(length(dat))
exp.tilt

Exponential Tilting

Description

This function calculates exponentially tilted multinomial distributions such that the resampling distributions of the linear approximation to a statistic have the required means.

Usage

exp.tilt(L, theta = NULL, t0 = 0, lambda = NULL, strata = rep(1, length(L)))

Arguments

- **L**: The empirical influence values for the statistic of interest based on the observed data. The length of L should be the same as the size of the original data set. Typically L will be calculated by a call to empinf.
- **theta**: The value at which the tilted distribution is to be centred. This is not required if lambda is supplied but is needed otherwise.
- **t0**: The current value of the statistic. The default is that the statistic equals 0.
- **lambda**: The Lagrange multiplier(s). For each value of lambda a multinomial distribution is found with probabilities proportional to \( \exp(\lambda L) \). In general lambda is not known and so theta would be supplied, and the corresponding value of lambda found. If both lambda and theta are supplied then lambda is ignored and the multipliers for tilting to theta are found.
- **strata**: A vector or factor of the same length as L giving the strata for the observed data and the empirical influence values L.

Details

Exponential tilting involves finding a set of weights for a data set to ensure that the bootstrap distribution of the linear approximation to a statistic of interest has mean theta. The weights chosen to achieve this are given by \( p[j] \) proportional to \( \exp(\lambda L[j]/n) \), where \( n \) is the number of data points. lambda is then chosen to make the mean of the bootstrap distribution, of the linear approximation to the statistic of interest, equal to the required value theta. Thus lambda is defined as the solution of a nonlinear equation. The equation is solved by minimizing the Euclidean distance between the left and right hand sides of the equation using the function nlm. If this minimum is not equal to zero then the method fails.
Typically exponential tilting is used to find suitable weights for importance resampling. If a small tail probability or quantile of the distribution of the statistic of interest is required then a more efficient simulation is to centre the resampling distribution close to the point of interest and then use the functions imp.prob or imp.quantile to estimate the required quantity.

Another method of achieving a similar shifting of the distribution is through the use of smooth.f. The function tilt.boot uses exp.tilt or smooth.f to find the weights for a tilted bootstrap.

Value
A list with the following components:

- **p** The tilted probabilities. There will be \( m \) distributions where \( m \) is the length of \( \theta \) (or \( \lambda \) if supplied). If \( m \) is 1 then \( p \) is a vector of \( \text{length}(L) \) probabilities. If \( m \) is greater than 1 then \( p \) is a matrix with \( m \) rows, each of which contain \( \text{length}(L) \) probabilities. In this case the vector \( p[i,] \) is the distribution tilted to \( \theta[i] \). \( p \) is in the form required by the argument weights of the function boot for importance resampling.

- **lambda** The Lagrange multiplier used in the equation to determine the tilted probabilities. \( \lambda \) is a vector of the same length as \( \theta \).

- **theta** The values of \( \theta \) to which the distributions have been tilted. In general this will be the input value of \( \theta \) but if \( \lambda \) was supplied then this is the vector of the corresponding \( \theta \) values.

References


See Also
empinf, imp.prob, imp.quantile, optim, smooth.f, tilt.boot

Examples
# Example 9.8 of Davison and Hinkley (1997) requires tilting the resampling # distribution of the studentized statistic to be centred at the observed # value of the test statistic 1.84. This can be achieved as follows.
grav1 <- gravity[as.numeric(gravity[,2]) >=7 , ]
grav.fun <- function(dat, w, orig) {
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- as.vector(tapply(d * w, strata, sum)) # drop names
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2]-mns[1], s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
grav.L <- empinf(data = grav1, statistic = grav.fun, stype = "w",
                 strata = grav1[,2], index = 3, orig = grav.z0[1])
grav.tilt <- exp.tilt(grav.L, grav.z0[3], strata = grav1[,2])
`boot(grav1, grav.fun, R = 499, stype = "w", weights = grav.tilt$p, strata = grav1[,2], orig = grav.z0[1])`

### Description

The `fir` data frame has 50 rows and 3 columns. The number of balsam-fir seedlings in each quadrant of a grid of 50 five foot square quadrants were counted. The grid consisted of 5 rows of 10 quadrants in each row.

### Usage

```r
fir
```

### Format

This data frame contains the following columns:

- **count**: The number of seedlings in the quadrant.
- **row**: The row number of the quadrant.
- **col**: The quadrant number within the row.

### Source


---

### Description

Take a matrix of indices for nonparametric bootstrap resamples and return the frequencies of the original observations in each resample.

### Usage

```r
freq.array(i.array)
```

### Arguments

- **i.array**: This will be a matrix of integers between 1 and n, where n is the number of observations in a data set. The matrix will have n columns and R rows where R is the number of bootstrap resamples. Such matrices are found by `boot` when doing nonparametric bootstraps. They can also be found after a bootstrap has been run through the function `boot.array`. 
Value

A matrix of the same dimensions as the input matrix. Each row of the matrix corresponds to a single bootstrap resample. Each column of the matrix corresponds to one of the original observations and specifies its frequency in each bootstrap resample. Thus the first column tells us how often the first observation appeared in each bootstrap resample. Such frequency arrays are often useful for diagnostic purposes such as the jackknife-after-bootstrap plot. They are also necessary for the regression estimates of empirical influence values and for finding importance sampling weights.

See Also

boot.array

---

### frets

*Head Dimensions in Brothers*

**Description**

The `frets` data frame has 25 rows and 4 columns.

The data consist of measurements of the length and breadth of the heads of pairs of adult brothers in 25 randomly sampled families. All measurements are expressed in millimetres.

**Usage**

frets

**Format**

This data frame contains the following columns:

- l1: The head length of the eldest son.
- b1: The head breadth of the eldest son.
- l2: The head length of the second son.
- b2: The head breadth of the second son.

**Source**

The data were obtained from


**References**


glm.diag

Generalized Linear Model Diagnostics

Description

Calculates jackknife deviance residuals, standardized deviance residuals, standardized Pearson residuals, approximate Cook statistic, leverage and estimated dispersion.

Usage

glm.diag(glmfit)

Arguments

glmfit

is a glm.object - the result of a call to glm()

Value

Returns a list with the following components:

res

The vector of jackknife deviance residuals.

rd

The vector of standardized deviance residuals.

rp

The vector of standardized Pearson residuals.

cook

The vector of approximate Cook statistics.

h

The vector of leverages of the observations.

sd

The value used to standardize the residuals. This is the estimate of residual standard deviation in the Gaussian family and is the square root of the estimated shape parameter in the Gamma family. In all other cases it is 1.

Note

See the help for glm.diag.plots for an example of the use of glm.diag.

References


See Also

glm, glm.diag.plots, summary.glm
glm.diag.plots

Diagnostics plots for generalized linear models

Description

Makes plot of jackknife deviance residuals against linear predictor, normal scores plots of standardized deviance residuals, plot of approximate Cook statistics against leverage/(1-leverage), and case plot of Cook statistic.

Usage

```r
glm.diag.plots(glmfit, glmdiag = glm.diag(glmfit), subset = NULL,
  iden = FALSE, labels = NULL, ret = FALSE)
```

Arguments

- `glmfit` - `glm.object`: the result of a call to `glm()`
- `glmdiag` - Diagnostics of `glmfit` obtained from a call to `glm.diag`. If it is not supplied then it is calculated.
- `subset` - Subset of data for which glm fitting performed: should be the same as the subset option used in the call to `glm()` which generated `glmfit`. Needed only if the subset= option was used in the call to `glm`.
- `iden` - A logical argument. If TRUE then, after the plots are drawn, the user will be prompted for an integer between 0 and 4. A positive integer will select a plot and invoke `identify()` on that plot. After exiting `identify()`, the user is again prompted, this loop continuing until the user responds to the prompt with 0. If `iden` is FALSE (default) the user cannot interact with the plots.
- `labels` - A vector of labels for use with `identify()` if `iden` is TRUE. If it is not supplied then the labels are derived from `glmfit`.
- `ret` - A logical argument indicating if `glmdiag` should be returned. The default is FALSE.

Details

The diagnostics required for the plots are calculated by `glm.diag`. These are then used to produce the four plots on the current graphics device.

The plot on the top left is a plot of the jackknife deviance residuals against the fitted values.

The plot on the top right is a normal QQ plot of the standardized deviance residuals. The dotted line is the expected line if the standardized residuals are normally distributed, i.e. it is the line with intercept 0 and slope 1.

The bottom two panels are plots of the Cook statistics. On the left is a plot of the Cook statistics against the standardized leverages. In general there will be two dotted lines on this plot. The horizontal line is at \( 8/(n-2p) \) where \( n \) is the number of observations and \( p \) is the number of parameters estimated. Points above this line may be points with high influence on the model. The vertical line is at \( 2p/(n-2p) \) and points to the right of this line have high leverage compared to the variance of the raw residual at that point. If all points are below the horizontal line or to the left of the vertical line then the line is not shown.

The final plot again shows the Cook statistic this time plotted against case number enabling us to find which observations are influential.
Use of `iden=T` is encouraged for proper exploration of these four plots as a guide to how well the model fits the data and whether certain observations have an unduly large effect on parameter estimates.

**Value**

If `ret` is `TRUE` then the value of `glm.diag` is returned otherwise there is no returned value.

**Side Effects**

The current device is cleared and four plots are plotted by use of `split.screen(c(2,2))`. If `iden` is `TRUE`, interactive identification of points is enabled. All screens are closed, but not cleared, on termination of the function.

**References**


**See Also**

`glm`, `glm.diag`, `identify`

**Examples**

# In this example we look at the leukaemia data which was looked at in
# Example 7.1 of Davison and Hinkley (1997)
data(leuk, package = "MASS")
leuk.mod <- glm(time ~ ag-1+log10(wbc), family = Gamma(log), data = leuk)
leuk.diag <- glm.diag(leuk.mod)
glm.diag.plots(leuk.mod, leuk.diag)

---

**Description**

The `gravity` data frame has 81 rows and 2 columns.

The `grav` data set has 26 rows and 2 columns.

Between May 1934 and July 1935, the National Bureau of Standards in Washington D.C. conducted a series of experiments to estimate the acceleration due to gravity, \( g \), at Washington. Each experiment produced a number of replicate estimates of \( g \) using the same methodology. Although the basic method remained the same for all experiments, that of the reversible pendulum, there were changes in configuration.

The `gravity` data frame contains the data from all eight experiments. The `grav` data frame contains the data from the experiments 7 and 8. The data are expressed as deviations from 980.000 in centimetres per second squared.
hirose

Usage

gravity

Format

This data frame contains the following columns:

- **g**: The deviation of the estimate from 980.000 centimetres per second squared.
- **series**: A factor describing from which experiment the estimate was derived.

Source


References


hirose

*Failure Time of PET Film*

Description

The hirose data frame has 44 rows and 3 columns.

PET film is used in electrical insulation. In this accelerated life test the failure times for 44 samples in gas insulated transformers. 4 different voltage levels were used.

Usage

hirose

Format

This data frame contains the following columns:

- **volt**: The voltage (in kV).
- **time**: The failure or censoring time in hours.
- **cens**: The censoring indicator; 1 means right-censored data.

Source


References

Description

Central moment, tail probability, and quantile estimates for a statistic under importance resampling.

Usage

```r
imp.moments(boot.out = NULL, index = 1, t = boot.out$t[, index],
            w = NULL, def = TRUE, q = NULL)
imp.prob(boot.out = NULL, index = 1, t0 = boot.out$t0[index],
         t = boot.out$t[, index], w = NULL, def = TRUE, q = NULL)
imp.quantile(boot.out = NULL, alpha = NULL, index = 1,
             t = boot.out$t[, index], w = NULL, def = TRUE, q = NULL)
```

Arguments

- **boot.out**: A object of class "boot" generated by a call to boot or tilt.boot. Use of these functions makes sense only when the bootstrap resampling used unequal weights for the observations. If the importance weights w are not supplied then boot.out is a required argument. It is also required if t is not supplied.
- **alpha**: The alpha levels for the required quantiles. The default is to calculate the 1%, 2.5%, 5%, 10%, 90%, 95%, 97.5% and 99% quantiles.
- **index**: The index of the variable of interest in the output of boot.out$statistic. This is not used if the argument t is supplied.
- **t0**: The values at which tail probability estimates are required. For each value t0[i] the function will estimate the bootstrap cdf evaluated at t0[i]. If imp.prob is called without the argument t0 then the bootstrap cdf evaluated at the observed value of the statistic is found.
- **t**: The bootstrap replicates of a statistic. By default these are taken from the bootstrap output object boot.out but they can be supplied separately if required (e.g. when the statistic of interest is a function of the calculated values in boot.out). Either boot.out or t must be supplied.
- **w**: The importance resampling weights for the bootstrap replicates. If they are not supplied then boot.out must be supplied, in which case the importance weights are calculated by a call to imp.weights.
- **def**: A logical value indicating whether a defensive mixture is to be used for weight calculation. This is used only if w is missing and it is passed unchanged to imp.weights to calculate w.
- **q**: A vector of probabilities specifying the resampling distribution from which any estimates should be found. In general this would correspond to the usual bootstrap resampling distribution which gives equal weight to each of the original observations. The estimates depend on this distribution only through the importance weights w so this argument is ignored if w is supplied. If w is missing then q is passed as an argument to imp.weights and used to find w.
Value

A list with the following components:

- **alpha**
  The alpha levels used for the quantiles, if `imp.quantile` is used.

- **t0**
  The values at which the tail probabilities are estimated, if `imp.prob` is used.

- **raw**
  The raw importance resampling estimates. For `imp.moments` this has length 2, the first component being the estimate of the mean and the second being the variance estimate. For `imp.prob`, `raw` is of the same length as `t0`, and for `imp.quantile` it is of the same length as `alpha`.

- **rat**
  The ratio importance resampling estimates. In this method the weights $w$ are rescaled to have average value one before they are used. The format of this vector is the same as `raw`.

- **reg**
  The regression importance resampling estimates. In this method the weights which are used are derived from a regression of $t_w$ on $w$. This choice of weights can be shown to minimize the variance of the weights and also the Euclidean distance of the weights from the uniform weights. The format of this vector is the same as `raw`.

References


See Also

- `boot.exp.tilt`, `imp.weights`, `smooth.f`, `tilt.boot`

Examples

```r
# Example 9.8 of Davison and Hinkley (1997) requires tilting the
# resampling distribution of the studentized statistic to be centred
# at the observed value of the test statistic, 1.84. In this example
# we show how certain estimates can be found using resamples taken from
# the tilted distribution.
grav1 <- gravity[as.numeric(gravity[,2]) >= 7, ]
grav.fun <- function(dat, w, orig) {
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mms <- as.vector(tapply(d * w, strata, sum)) # drop names
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mms^2)/ns)
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
grav.L <- empinf(data = grav1, statistic = grav.fun, stype = "w",
                 strata = grav1[, 2], index = 3, orig = grav.z0[1])
grav.tilt <- exp.tilt(grav.L, grav.z0[3], strata = grav1[, 2])
```
imp.weights <- boot(grav1, grav.fun, R = 199, stype = "w", strata = grav1[, 2], weights = grav.tilt$p, orig = grav.z0[1])

# Since the weights are needed for all calculations, we shall calculate
# them once only.
grav.w <- imp.weights(grav.tilt.boot)
grav.mom <- imp.moments(grav.tilt.boot, w = grav.w, index = 3)
grav.p <- imp.prob(grav.tilt.boot, w = grav.w, index = 3, t0 = grav.z0[3])
unlist(grav.p)
grav.q <- imp.quantile(grav.tilt.boot, w = grav.w, index = 3, alpha = c(0.9, 0.95, 0.975, 0.99))
as.data.frame(grav.q)

---

**imp.weights**

**Importance Sampling Weights**

**Description**

This function calculates the importance sampling weight required to correct for simulation from a distribution with probabilities \( p \) when estimates are required assuming that simulation was from an alternative distribution with probabilities \( q \).

**Usage**

```r
imp.weights(boot.out, def = TRUE, q = NULL)
```

**Arguments**

- `boot.out`: A object of class "boot" generated by boot or tilt.boot. Typically the bootstrap simulations would have been done using importance resampling and we wish to do our calculations under the assumption of sampling with equal probabilities.
- `def`: A logical variable indicating whether the defensive mixture distribution weights should be calculated. This makes sense only in the case where the replicates in `boot.out` were simulated under a number of different distributions. If this is the case then the defensive mixture weights use a mixture of the distributions used in the bootstrap. The alternative is to calculate the weights for each replicate using knowledge of the distribution from which the bootstrap resample was generated.
- `q`: A vector of probabilities specifying the resampling distribution from which we require inferences to be made. In general this would correspond to the usual bootstrap resampling distribution which gives equal weight to each of the original observations and this is the default. \( q \) must have length equal to the number of observations in the `boot.out$data` and all elements of \( q \) must be positive.

**Details**

The importance sampling weight for a bootstrap replicate with frequency vector \( f \) is given by \( \prod((q/p)^f) \). This reweights the replicates so that estimates can be found as if the bootstrap resamples were generated according to the probabilities \( q \) even though, in fact, they came from the distribution \( p \).
Value

A vector of importance weights of the same length as `boot.out$t`. These weights can then be used to reweight `boot.out$t` so that estimates can be found as if the simulations were from a distribution with probabilities q.

Note

See the example in the help for `imp.moments` for an example of using `imp.weights`.

References


See Also

`boot.exp.tilt, imp.moments, smooth.f, tilt.boot`

---

**inv.logit**

*Inverse Logit Function*

Description

Given a numeric object return the inverse logit of the values.

Usage

`inv.logit(x)`

Arguments

`x` A numeric object. Missing values (NAs) are allowed.

Details

The inverse logit is defined by \( \exp(x)/(1+\exp(x)) \). Values in `x` of \(-\infty\) or \(\infty\) return logits of 0 or 1 respectively. Any NAs in the input will also be NAs in the output.

Value

An object of the same type as `x` containing the inverse logits of the input values.

See Also

`logit, plogis` for which this is a wrapper.
**islay**

*Jura Quartzite Azimuths on Islay*

**Description**

The islay data frame has 18 rows and 1 columns.

Measurements were taken of paleocurrent azimuths from the Jura Quartzite on the Scottish island of Islay.

**Usage**

```r
islay
```

**Format**

This data frame contains the following column:

- **theta**  The angle of the azimuth in degrees East of North.

**Source**

The data were obtained from


**References**


---

**jack.after.boot**

*Jackknife-after-Bootstrap Plots*

**Description**

This function calculates the jackknife influence values from a bootstrap output object and plots the corresponding jackknife-after-bootstrap plot.

**Usage**

```r
jack.after.boot(boot.out, index = 1, t = NULL, L = NULL, useJ = TRUE, stinf = TRUE, alpha = NULL, main = '', ylab = NULL, ...)
```
Arguments

boot.out  An object of class "boot" which would normally be created by a call to boot. It should represent a nonparametric bootstrap. For reliable results boot.out$R should be reasonably large.

index  The index of the statistic of interest in the output of boot.out$statistic.

t  A vector of length boot.out$R giving the bootstrap replicates of the statistic of interest. This is useful if the statistic of interest is a function of the calculated bootstrap output. If it is not supplied then the default is boot.out$t[, index].

L  The empirical influence values for the statistic of interest. These are used only if useJ is FALSE. If they are not supplied and are needed, they are calculated by a call to empinf. If L is supplied then it is assumed that they are the infinitesimal jackknife values.

useJ  A logical variable indicating if the jackknife influence values calculated from the bootstrap replicates should be used. If FALSE the empirical influence values are used. The default is TRUE.

stinf  A logical variable indicating whether to standardize the jackknife values before plotting them. If TRUE then the jackknife values used are divided by their standard error.

alpha  The quantiles at which the plots are required. The default is c(0.05, 0.1, 0.16, 0.5, 0.84, 0.9, 0.95).

main  A character string giving the main title for the plot.

ylab  The label for the Y axis. If the default values of alpha are used and ylab is not supplied then a label indicating which percentiles are plotted is used. If alpha is supplied then the default label will not say which percentiles were used.

...  Any extra arguments required by boot.out$statistic. These are required only if useJ is FALSE and L is not supplied, in which case they are passed to empinf for use in calculation of the empirical influence values.

Details

The centred jackknife quantiles for each observation are estimated from those bootstrap samples in which the particular observation did not appear. These are then plotted against the influence values. If useJ is TRUE then the influence values are found in the same way as the difference between the mean of the statistic in the samples excluding the observations and the mean in all samples. If useJ is FALSE then empirical influence values are calculated by calling empinf.

The resulting plots are useful diagnostic tools for looking at the way individual observations affect the bootstrap output.

The plot will consist of a number of horizontal dotted lines which correspond to the quantiles of the centred bootstrap distribution. For each data point the quantiles of the bootstrap distribution calculated by omitting that point are plotted against the (possibly standardized) jackknife values. The observation number is printed below the plots. To make it easier to see the effect of omitting points on quantiles, the plotted quantiles are joined by line segments. These plots provide a useful diagnostic tool in establishing the effect of individual observations on the bootstrap distribution. See the references below for some guidelines on the interpretation of the plots.

Value

There is no returned value but a plot is generated on the current graphics display.
Side Effects

A plot is created on the current graphics device.

References


See Also

boot.empinf

Examples

```r
# To draw the jackknife-after-bootstrap plot for the head size data as in
# Example 3.24 of Davison and Hinkley (1997)
frets.fun <- function(data, i) {
  pcorr <- function(x) {
    # Function to find the correlations and partial correlations between
    # the four measurements.
    v <- cor(x)
    v.d <- diag(var(x))
    iv <- solve(v)
    iv.d <- sqrt(diag(iv))
    iv <- diag(1/iv.d) %*% iv %*% diag(1/iv.d)
    q <- NULL
    n <- nrow(v)
    for (i in 1:(n-1))
      q <- rbind( q, c(v[i, 1:i], iv[i,(i+1):n]) )
    q <- rbind( q, v[n, ] )
    diag(q) <- round(diag(q))
    q
  }
  d <- data[i, ]
  v <- pcorr(d)
  c(v[1,], v[2,], v[3,], v[4,])
}
frets.boot <- boot(log(as.matrix(frets)), frets.fun, R = 999)
# we will concentrate on the partial correlation between head breadth
# for the first son and head length for the second. This is the 7th
# element in the output of frets.fun so we set index = 7
jack.after.boot(frets.boot, useJ = FALSE, stinf = FALSE, index = 7)
```

k3.linear

Linear Skewness Estimate

Description

Estimates the skewness of a statistic from its empirical influence values.
Usage

k3.linear(L, strata = NULL)

Arguments

L  Vector of the empirical influence values of a statistic. These will usually be calculated by a call to empinf.

strata  A numeric vector or factor specifying which observations (and hence which components of L) come from which strata.

Value

The skewness estimate calculated from L.

References


See Also

tempf, linear.approx, var.linear

Examples

# To estimate the skewness of the ratio of means for the city data.
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
k3.linear(empinf(data = city, statistic = ratio))

deprecated

linear.approx  Linear Approximation of Bootstrap Replicates

Description

This function takes a bootstrap object and for each bootstrap replicate it calculates the linear approximation to the statistic of interest for that bootstrap sample.

Usage

linear.approx(boot.out, L = NULL, index = 1, type = NULL,
t0 = NULL, t = NULL, ...)

Arguments

boot.out  An object of class "boot" representing a nonparametric bootstrap. It will usually be created by the function boot.

L  A vector containing the empirical influence values for the statistic of interest. If it is not supplied then L is calculated through a call to empinf.

index  The index of the variable of interest within the output of boot.out$statistic.
linear.approx

This gives the type of empirical influence values to be calculated. It is not used if \( L \) is supplied. The possible types of empirical influence values are described in the help for \texttt{empinf}.

\texttt{t0}

The observed value of the statistic of interest. The input value is used only if one of \( t \) or \( L \) is also supplied. The default value is \texttt{boot.out$t0[index]}\. If \( t0 \) is supplied but neither \( t \) nor \( L \) are supplied then \( t0 \) is set to \texttt{boot.out$t0[index]} and a warning is generated.

\texttt{t}

A vector of bootstrap replicates of the statistic of interest. If \( t0 \) is missing then \( t \) is not used, otherwise it is used to calculate the empirical influence values (if they are not supplied in \( L \)).

... Any extra arguments required by \texttt{boot.out$statistic}. These are needed if \( L \) is not supplied as they are used by \texttt{empinf} to calculate empirical influence values.

Details

The linear approximation to a bootstrap replicate with frequency vector \( f \) is given by \( t0 + \sum(L \times f)/n \) in the one sample with an easy extension to the stratified case. The frequencies are found by calling \texttt{boot.array}.

Value

A vector of length \texttt{boot.out$R} with the linear approximations to the statistic of interest for each of the bootstrap samples.

References


See Also

\texttt{boot.empinf.control}

Examples

# Using the city data let us look at the linear approximation to the # ratio statistic and its logarithm. We compare these with the # corresponding plots for the bigcity data

\begin{verbatim}
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
city.boot <- boot(city, ratio, R = 499, stype = "w")
bigcity.boot <- boot(bigcity, ratio, R = 499, stype = "w")
op <- par(pty = "s", mfrow = c(2, 2))

# The first plot is for the city data ratio statistic.
city.lin1 <- linear.approx(city.boot)
lim <- range(c(city.boot$t, city.lin1))
plot(city.boot$t, city.lin1, xlim = lim, ylim = lim,
main = "Ratio; n=10", xlab = "t*", ylab = "tL*")
abline(0, 1)

# Now for the log of the ratio statistic for the city data.
city.lin2 <- linear.approx(city.boot, t0 = log(city.boot$t0),
\end{verbatim}
\[
t = \log(\text{city.boot}$t))
\]
\[
\text{lim} \leftarrow \text{range(c(log(city.boot}$t),city.lin2))
\]
\[
\text{plot(log(city.boot}$t), city.lin2, x\text{lim = lim, y\text{lim = lim,}
\]
\[
\text{main = "Log(Ratio); n=10", x\text{lab = "t*", y\text{lab = "tL*"})}
\]
\[
\text{abline}(0, 1)
\]

# The ratio statistic for the bigcity data.
bigcity.lin1 \leftarrow \text{linear.approx(bigcity.boot)
\]
\[
\text{lim} \leftarrow \text{range(c(bigcity.boot}$t,bigcity.lin1))
\]
\[
\text{plot(bigcity.lin1, bigcity.boot}$t, x\text{lim = lim, y\text{lim = lim,}
\]
\[
\text{main = "Ratio; n=49", x\text{lab = "t*", y\text{lab = "tL*"})}
\]
\[
\text{abline}(0, 1)
\]

# Finally the log of the ratio statistic for the bigcity data.
bigcity.lin2 \leftarrow \text{linear.approx(bigcity.boot, t0 = log(bigcity.boot}$t0),
\]
\[
t = \log(bigcity.boot}$t))
\]
\[
\text{lim} \leftarrow \text{range(c(log(bigcity.boot}$t),bigcity.lin2))
\]
\[
\text{plot(bigcity.lin2, log(bigcity.boot}$t), x\text{lim = lim, y\text{lim = lim,}
\]
\[
\text{main = "Log(Ratio); n=49", x\text{lab = "t*", y\text{lab = "tL*"})}
\]
\[
\text{abline}(0, 1)
\]
\[
\text{par(op)}
\]

---

**lines.saddle.distn**

**Add a Saddlepoint Approximation to a Plot**

**Description**

This function adds a line corresponding to a saddlepoint density or distribution function approximation to the current plot.

**Usage**

```r
## S3 method for class 'saddle.distn'
lines(x, dens = TRUE, h = function(u) u, J = function(u) 1,
      npts = 50, lty = 1, ...)
```

**Arguments**

- `x`: An object of class "saddle.distn" (see saddle.distn.object representing a saddlepoint approximation to a distribution.
- `dens`: A logical variable indicating whether the saddlepoint density (TRUE; the default) or the saddlepoint distribution function (FALSE) should be plotted.
- `h`: Any transformation of the variable that is required. Its first argument must be the value at which the approximation is being performed and the function must be vectorized.
- `J`: When `dens=TRUE` this function specifies the Jacobian for any transformation that may be necessary. The first argument of `J` must the value at which the approximation is being performed and the function must be vectorized. If `h` is supplied `J` must also be supplied and both must have the same argument list.
- `npts`: The number of points to be used for the plot. These points will be evenly spaced over the range of points used in finding the saddlepoint approximation.
The line type to be used.

Any additional arguments to h and J.

Details

The function uses smooth.spline to produce the saddlepoint curve. When dens=TRUE the spline is on the log scale and when dens=FALSE it is on the probit scale.

Value

sad.d is returned invisibly.

Side Effects

A line is added to the current plot.

References


See Also

saddle.distn

Examples

# In this example we show how a plot such as that in Figure 9.9 of
# Davison and Hinkley (1997) may be produced. Note the large number of
# bootstrap replicates required in this example.
expdata <- rexp(12)
vfun <- function(d, i) {
  n <- length(d)
  (n-1)/n*var(d[i])
}
exp.boot <- boot(expdata,vfun, R = 9999)
exp.L <- (expdata - mean(expdata))^2 - exp.boot$t0
exp.tL <- linear.approx(exp.boot, L = exp.L)
hist(exp.tL, nclass = 50, probability = TRUE)
exp.t0 <- c(0, sqrt(var(exp.boot$t)));
exp.sp <- saddle.distn(A = exp.L/12, wdist = "m", t0 = exp.t0)

# The saddlepoint approximation in this case is to the density of
# t-t0 and so t0 must be added for the plot.
lines(exp.sp, h = function(u, t0) u+t0, J = function(u, t0) 1,
     t0 = exp.boot$t0)
logit

Logit of Proportions

Description
This function calculates the logit of proportions.

Usage
logit(p)

Arguments
p A numeric Splus object, all of whose values are in the range [0,1]. Missing values (NAs) are allowed.

Details
If any elements of p are outside the unit interval then an error message is generated. Values of p equal to 0 or 1 (to within machine precision) will return -Inf or Inf respectively. Any NAs in the input will also be NAs in the output.

Value
A numeric object of the same type as p containing the logits of the input values.

See Also
inv.logit, qlogis for which this is a wrapper.

manaus
Average Heights of the Rio Negro river at Manaus

Description
The manaus time series is of class "ts" and has 1080 observations on one variable.

The data values are monthly averages of the daily stages (heights) of the Rio Negro at Manaus. Manaus is 18km upstream from the confluence of the Rio Negro with the Amazon but because of the tiny slope of the water surface and the lower courses of its flatland affluents, they may be regarded as a good approximation of the water level in the Amazon at the confluence. The data here cover 90 years from January 1903 until December 1992.

The Manaus gauge is tied in with an arbitrary bench mark of 100m set in the steps of the Municipal Prefecture; gauge readings are usually referred to sea level, on the basis of a mark on the steps leading to the Parish Church (Matriz), which is assumed to lie at an altitude of 35.874 m according to observations made many years ago under the direction of Samuel Pereira, an engineer in charge of the Manaus Sanitation Committee. Whereas such an altitude cannot, by any means, be considered to be a precise datum point, observations have been provisionally referred to it. The measurements are in metres.
The data were kindly made available by Professors H. O’Reilly Sternberg and D. R. Brillinger of the University of California at Berkeley.

References


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**melanoma**

**Survival from Malignant Melanoma**

**Description**

The melanoma data frame has 205 rows and 7 columns.

The data consist of measurements made on patients with malignant melanoma. Each patient had their tumour removed by surgery at the Department of Plastic Surgery, University Hospital of Odense, Denmark during the period 1962 to 1977. The surgery consisted of complete removal of the tumour together with about 2.5cm of the surrounding skin. Among the measurements taken were the thickness of the tumour and whether it was ulcerated or not. These are thought to be important prognostic variables in that patients with a thick and/or ulcerated tumour have an increased chance of death from melanoma. Patients were followed until the end of 1977.

**Usage**

melanoma

**Format**

This data frame contains the following columns:

- **time** Survival time in days since the operation, possibly censored.
- **status** The patients status at the end of the study. 1 indicates that they had died from melanoma, 2 indicates that they were still alive and 3 indicates that they had died from causes unrelated to their melanoma.
- **sex** The patients sex; 1=male, 0=female.
- **age** Age in years at the time of the operation.
- **year** Year of operation.
- **thickness** Tumour thickness in mm.
- **ulcer** Indicator of ulceration; 1=present, 0=absent.

**Note**

This dataset is not related to the dataset in the *lattice* package with the same name.
motor

Source
The data were obtained from

References

motor

Data from a Simulated Motorcycle Accident

Description
The motor data frame has 94 rows and 4 columns. The rows are obtained by removing replicate values of time from the dataset mcycle. Two extra columns are added to allow for strata with a different residual variance in each stratum.

Usage
motor

Format
This data frame contains the following columns:
times The time in milliseconds since impact.
accel The recorded head acceleration (in g).
strata A numeric column indicating to which of the three strata (numbered 1, 2 and 3) the observations belong.
v An estimate of the residual variance for the observation. v is constant within the strata but a different estimate is used for each of the three strata.

Source
The data were obtained from

References

See Also
mcycle
neuro

**Neurophysiological Point Process Data**

**Description**

neuro is a matrix containing times of observed firing of a neuron in windows of 250ms either side of the application of a stimulus to a human subject. Each row of the matrix is a replication of the experiment and there were a total of 469 replicates.

**Note**

There are a lot of missing values in the matrix as different numbers of firings were observed in different replicates. The number of firings observed varied from 2 to 6.

**Source**

The data were collected and kindly made available by Dr. S.J. Boniface of the Neurophysiology Unit at the Radcliffe Infirmary, Oxford.

**References**


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nitrofen

**Toxicity of Nitrofen in Aquatic Systems**

**Description**

The nitrofen data frame has 50 rows and 5 columns.

Nitrofen is a herbicide that was used extensively for the control of broad-leaved and grass weeds in cereals and rice. Although it is relatively non-toxic to adult mammals, nitrofen is a significant tetragen and mutagen. It is also acutely toxic and reproductively toxic to cladoceran zooplankton. Nitrofen is no longer in commercial use in the U.S., having been the first pesticide to be withdrawn due to tetragenic effects.

The data here come from an experiment to measure the reproductive toxicity of nitrofen on a species of zooplankton (*Ceriodaphnia dubia*). 50 animals were randomized into batches of 10 and each batch was put in a solution with a measured concentration of nitrofen. Then the number of live offspring in each of the three broods to each animal was recorded.

**Usage**

nitrofen
**nodal**

**Format**

This data frame contains the following columns:

- **conc**: The nitrofen concentration in the solution (mug/litre).
- **brood1**: The number of live offspring in the first brood.
- **brood2**: The number of live offspring in the second brood.
- **brood3**: The number of live offspring in the third brood.
- **total**: The total number of live offspring in the first three broods.

**Source**

The data were obtained from


**References**


---

**nodal**

**Nodal Involvement in Prostate Cancer**

**Description**

The nodal data frame has 53 rows and 7 columns.

The treatment strategy for a patient diagnosed with cancer of the prostate depend highly on whether the cancer has spread to the surrounding lymph nodes. It is common to operate on the patient to get samples from the nodes which can then be analysed under a microscope but clearly it would be preferable if an accurate assessment of nodal involvement could be made without surgery.

For a sample of 53 prostate cancer patients, a number of possible predictor variables were measured before surgery. The patients then had surgery to determine nodal involvement. It was required to see if nodal involvement could be accurately predicted from the predictor variables and which ones were most important.

**Usage**

nodal

**Format**

This data frame contains the following columns:

- **m**: A column of ones.
- **r**: An indicator of nodal involvement.
- **aged**: The patients age dichotomized into less than 60 (0) and 60 or over 1.
- **stage**: A measurement of the size and position of the tumour observed by palpitation with the fingers via the rectum. A value of 1 indicates a more serious case of the cancer.
grade  Another indicator of the seriousness of the cancer, this one is determined by a pathology
reading of a biopsy taken by needle before surgery. A value of 1 indicates a more serious case
of the cancer.
xray  A third measure of the seriousness of the cancer taken from an X-ray reading. A value of 1
indicates a more serious case of the cancer.
acid  The level of acid phosphatase in the blood serum.

Source

The data were obtained from

References

University Press.

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**norm.ci**

**Normal Approximation Confidence Intervals**

**Description**

Using the normal approximation to a statistic, calculate equi-tailed two-sided confidence intervals.

**Usage**

```r
norm.ci(boot.out = NULL, conf = 0.95, index = 1, var.t0 = NULL,
       t0 = NULL, t = NULL, L = NULL, h = function(t) t,
       hdot = function(t) 1, hinv = function(t) t)
```

**Arguments**

- `boot.out` A bootstrap output object returned from a call to `boot`. If `t0` is missing then
  `boot.out` is a required argument. It is also required if both `var.t0` and `t` are
  missing.
- `conf` A scalar or vector containing the confidence level(s) of the required interval(s).
- `index` The index of the statistic of interest within the output of a call to
  `boot.out$statistic`. It is not used if `boot.out` is missing, in which case
  `t0` must be supplied.
- `var.t0` The variance of the statistic of interest. If it is not supplied then `var(t)` is used.
- `t0` The observed value of the statistic of interest. If it is missing then it is taken
  from `boot.out` which is required in that case.
- `t` Bootstrap replicates of the variable of interest. These are used to estimate the
  variance of the statistic of interest if `var.t0` is not supplied. The default value
  is `boot.out$t[, index]`.
- `L` The empirical influence values for the statistic of interest. These are used to cal-
  culate `var.t0` if neither `var.t0` nor `boot.out` are supplied. If a transformation
  is supplied through `h` then the influence values must be for the untransformed
  statistic `t0`.
**norm.ci**

h  A function defining a monotonic transformation, the intervals are calculated on the scale of $h(t)$ and the inverse function $h^{-1}$ is applied to the resulting intervals. $h$ must be a function of one variable only and must be vectorized. The default is the identity function.

$hdot$  A function of one argument returning the derivative of $h$. It is a required argument if $h$ is supplied and is used for approximating the variance of $h(t_0)$. The default is the constant function 1.

$h^{-1}$  A function, like $h$, which returns the inverse of $h$. It is used to transform the intervals calculated on the scale of $h(t)$ back to the original scale. The default is the identity function. If $h$ is supplied but $h^{-1}$ is not, then the intervals returned will be on the transformed scale.

**Details**

It is assumed that the statistic of interest has an approximately normal distribution with variance $\text{var}.t_0$ and so a confidence interval of length $2\times qnorm((1+\text{conf})/2)\times \text{sqrt}(\text{var}.t_0)$ is found. If boot.out or $t$ are supplied then the interval is bias-corrected using the bootstrap bias estimate, and so the interval would be centred at $2\times t_0 - \text{mean}(t)$. Otherwise the interval is centred at $t_0$.

**Value**

If $\text{length}(\text{conf})$ is 1 then a vector containing the confidence level and the endpoints of the interval is returned. Otherwise, the returned value is a matrix where each row corresponds to a different confidence level.

**Note**

This function is primarily designed to be called by boot.ci to calculate the normal approximation after a bootstrap but it can also be used without doing any bootstrap calculations as long as $t_0$ and $\text{var}.t_0$ can be supplied. See the examples below.

**References**


**See Also**

boot.ci

**Examples**

# In Example 5.1 of Davison and Hinkley (1997), normal approximation
air.mean <- mean(aircondit$hours)
ar.next <- nrow(aircondit)
air.v <- air.mean^2/air.n
norm.ci(t0 = air.mean, var.t0 = air.v)
exp(norm.ci(t0 = log(air.mean), var.t0 = 1/air.n)[2:3])

# Now a more complicated example - the ratio estimate for the city data.
ratio <- function(d, w)
sum(d$x * w)/sum(d$s * w)
city.v <- var.linear(empinf(data = city, statistic = ratio))
norm.ci(t0 = ratio(city, rep(0.1,10)), var.t0 = city.v)
Nuclear Power Station Construction Data

Description

The nuclear data frame has 32 rows and 11 columns.

The data relate to the construction of 32 light water reactor (LWR) plants constructed in the U.S.A in the late 1960's and early 1970's. The data was collected with the aim of predicting the cost of construction of further LWR plants. 6 of the power plants had partial turnkey guarantees and it is possible that, for these plants, some manufacturers’ subsidies may be hidden in the quoted capital costs.

Usage

nuclear

Format

This data frame contains the following columns:

cost  The capital cost of construction in millions of dollars adjusted to 1976 base.
date  The date on which the construction permit was issued. The data are measured in years since January 1 1990 to the nearest month.
t1  The time between application for and issue of the construction permit.
t2  The time between issue of operating license and construction permit.
cap  The net capacity of the power plant (MWe).
pr  A binary variable where 1 indicates the prior existence of a LWR plant at the same site.
ne  A binary variable where 1 indicates that the plant was constructed in the north-east region of the U.S.A.
ct  A binary variable where 1 indicates the use of a cooling tower in the plant.
bw  A binary variable where 1 indicates that the nuclear steam supply system was manufactured by Babcock-Wilcox.
cum.n  The cumulative number of power plants constructed by each architect-engineer.
pt  A binary variable where 1 indicates those plants with partial turnkey guarantees.

Source

The data were obtained from


References

Description

The paulsen data frame has 346 rows and 1 columns.
Sections were prepared from the brain of adult guinea pigs. Spontaneous currents that flowed into individual brain cells were then recorded and the peak amplitude of each current measured. The aim of the experiment was to see if the current flow was quantal in nature (i.e. that it is not a single burst but instead is built up of many smaller bursts of current). If the current was indeed quantal then it would be expected that the distribution of the current amplitude would be multimodal with modes at regular intervals. The modes would be expected to decrease in magnitude for higher current amplitudes.

Usage

paulsen

Format

This data frame contains the following column:

y The current flowing into individual brain cells. The currents are measured in pico-amperes.

Source

The data were kindly made available by Dr. O. Paulsen from the Department of Pharmacology at the University of Oxford.

References


plot.boot

Plots of the Output of a Bootstrap Simulation

Description

This takes a bootstrap object and produces plots for the bootstrap replicates of the variable of interest.

Usage

```r
## S3 method for class 'boot'
plot(x, index = 1, t0 = NULL, t = NULL, jack = FALSE,
     qdist = "norm", nclass = NULL, df, ...)
```
Arguments

x
An object of class "boot" returned from one of the bootstrap generation functions.

index
The index of the variable of interest within the output of boot.out. This is ignored if t and t0 are supplied.

t0
The original value of the statistic. This defaults to boot.out$t0[index] unless t is supplied when it defaults to NULL. In that case no vertical line is drawn on the histogram.

t
The bootstrap replicates of the statistic. Usually this will take on its default value of boot.out$t[,index], however it may be useful sometimes to supply a different set of values which are a function of boot.out$t.

jack
A logical value indicating whether a jackknife-after-bootstrap plot is required. The default is not to produce such a plot.

qdist
The distribution against which the Q-Q plot should be drawn. At present "norm" (normal distribution - the default) and "chisq" (chi-squared distribution) are the only possible values.

nclass
An integer giving the number of classes to be used in the bootstrap histogram. The default is the integer between 10 and 100 closest to ceiling(length(t)/25).

df
If qdist is "chisq" then this is the degrees of freedom for the chi-squared distribution to be used. It is a required argument in that case.

...
When jack is TRUE additional parameters to jack.after.boot can be supplied. See the help file for jack.after.boot for details of the possible parameters.

Details

This function will generally produce two side-by-side plots. The left plot will be a histogram of the bootstrap replicates. Usually the breaks of the histogram will be chosen so that t0 is at a breakpoint and all intervals are of equal length. A vertical dotted line indicates the position of t0. This cannot be done if t is supplied but t0 is not and so, in that case, the breakpoints are computed by hist using the nclass argument and no vertical line is drawn.

The second plot is a Q-Q plot of the bootstrap replicates. The order statistics of the replicates can be plotted against normal or chi-squared quantiles. In either case the expected line is also plotted. For the normal, this will have intercept mean(t) and slope sqrt(var(t)) while for the chi-squared it has intercept 0 and slope 1.

If jack is TRUE a third plot is produced beneath these two. That plot is the jackknife-after-bootstrap plot. This plot may only be requested when nonparametric simulation has been used. See jack.after.boot for further details of this plot.

Value

boot.out is returned invisibly.

Side Effects

All screens are closed and cleared and a number of plots are produced on the current graphics device. Screens are closed but not cleared at termination of this function.

See Also

boot, jack.after.boot, print.boot
Examples

# We fit an exponential model to the air-conditioning data and use
# that for a parametric bootstrap. Then we look at plots of the
# resampled means.
air.rg <- function(data, mle) rexp(length(data), 1/mle)

air.boot <- boot(aircondit$hours, mean, R = 999, sim = "parametric",
                 ran.gen = air.rg, mle = mean(aircondit$hours))
plot(air.boot)

# In the difference of means example for the last two series of the
# gravity data
grav1 <- gravity[as.numeric(gravity[, 2]) >= 7, ]
grav.fun <- function(dat, w) {
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- as.vector(tapply(d * w, strata, sum)) # drop names
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2] - mns[1], s2hat)
}

grav.boot <- boot(grav1, grav.fun, R = 499, stype = "w", strata = grav1[, 2])
plot(grav.boot)

# now suppose we want to look at the studentized differences.
grav.z <- (grav.boot$t[, 1]-grav.boot$t0[1])/sqrt(grav.boot$t[, 2])
plot(grav.boot, t = grav.z, t0 = 0)

# In this example we look at the one of the partial correlations for the
# head dimensions in the dataset frets.
frets.fun <- function(data, i) {
  pcorr <- function(x) {
    # Function to find the correlations and partial correlations between
    # the four measurements.
    v <- cor(x)
    v.d <- diag(var(x))
    iv <- solve(v)
    iv.d <- sqrt(diag(iv))
    iv <- - diag(1/iv.d) %*% iv %*% diag(1/iv.d)
    q <- NULL
    n <- nrow(v)
    for (i in 1:(n-1))
      q <- rbind( q, c(v[i, 1:i], iv[i,(i+1):n]) )
    q <- rbind( q, v[n, ]
                     diag(q) <- round(diag(q))
    q
  }
  d <- data[i, ]
  v <- pcorr(d)
  c(v[1,], v[2,], v[3,], v[4,])
}

frets.boot <- boot(log(as.matrix(frets)), frets.fun, R = 999)
plot(frets.boot, index = 7, jack = TRUE, stinf = FALSE, useJ = FALSE)
poisons

*Animal Survival Times*

**Description**

The poisons data frame has 48 rows and 3 columns.

The data form a 3x4 factorial experiment, the factors being three poisons and four treatments. Each combination of the two factors was used for four animals, the allocation to animals having been completely randomized.

**Usage**

poisons

**Format**

This data frame contains the following columns:

- **time**  The survival time of the animal in units of 10 hours.
- **poison** A factor with levels 1, 2 and 3 giving the type of poison used.
- **treat**  A factor with levels A, B, C and D giving the treatment.

**Source**

The data were obtained from


**References**


---

polar

*Pole Positions of New Caledonian Laterites*

**Description**

The polar data frame has 50 rows and 2 columns.

The data are the pole positions from a paleomagnetic study of New Caledonian laterites.

**Usage**

polar
Format

This data frame contains the following columns:

lat  The latitude (in degrees) of the pole position. Note that all latitudes are negative as the axis is taken to be in the lower hemisphere.
long The longitude (in degrees) of the pole position.

Source

The data were obtained from


References


---

**print.boot**  
*Print a Summary of a Bootstrap Object*

**Description**

This is a method for the function `print()` for objects of the class "boot" created by a call to `boot`, `censboot`, `tilt.boot` or `tsboot`.

**Usage**

```r
## S3 method for class 'boot'
print(x, digits =getOption("digits"),
index = 1:ncol(boot.out$t), ...) 
```

**Arguments**

- **x**  
  A bootstrap output object of class "boot" generated by one of the bootstrap functions.

- **digits**  
  The number of digits to be printed in the summary statistics.

- **index**  
  Indices indicating for which elements of the bootstrap output summary statistics are required.

- **...**  
  Further arguments passed to or from other methods.

**Details**

For each statistic calculated in the bootstrap the original value and the bootstrap estimates of its bias and standard error are printed. If `boot.out$t0` is missing (such as when it was created by a call to `tsboot` with `orig.t = FALSE`) the bootstrap mean and standard error are printed. If resampling was done using importance resampling weights, then the bootstrap estimates are reweighted as if uniform resampling had been done. The ratio importance sampling estimates are used and if there were a number of distributions then defensive mixture distributions are used. In this case an extra column with the mean of the observed bootstrap statistics is also printed.
print.bootci

Value

The bootstrap object is returned invisibly.

See Also

boot, censboot, imp.moments, plot.boot, tilt.boot, tsboot

print.bootci  Print Bootstrap Confidence Intervals

Description

This is a method for the function print() to print objects of the class "bootci".

Usage

## S3 method for class 'bootci'
print(x, hinv = NULL, ...)

Arguments

x  The output from a call to boot.ci.
hinv  A transformation to be made to the interval end-points before they are printed.
...  further arguments passed to or from other methods.

Details

This function prints out the results from boot.ci in a "nice" format. It also notes whether the scale of the intervals is the original scale of the input to boot.ci or a different scale and whether the calculations were done on a transformed scale. It also looks at the order statistics that were used in calculating the intervals. If the smallest or largest values were used then it prints a message

Warning : Intervals used Extreme Quantiles

Such intervals should be considered very unstable and not relied upon for inferences. Even if the extreme values are not used, it is possible that the intervals are unstable if they used quantiles close to the extreme values. The function alerts the user to intervals which use the upper or lower 10 order statistics with the message

Some intervals may be unstable

Value

The object ci.out is returned invisibly.

See Also

boot.ci
**print.saddle.distn**

Print Quantiles of Saddlepoint Approximations

**Description**

This is a method for the function print() to print objects of class "saddle.distn".

**Usage**

```r
## S3 method for class 'saddle.distn'
print(x, ...)
```

**Arguments**

- `x` An object of class "saddle.distn" created by a call to saddle.distn.
- `...` further arguments passed to or from other methods.

**Details**

The quantiles of the saddlepoint approximation to the distribution are printed along with the original call and some other useful information.

**Value**

The input is returned invisibly.

**See Also**

lines.saddle.distn, saddle.distn

---

**print.simplex**

Print Solution to Linear Programming Problem

**Description**

This is a method for the function print() to print objects of class "simplex".

**Usage**

```r
## S3 method for class 'simplex'
print(x, ...)
```

**Arguments**

- `x` An object of class "simplex" created by calling the function simplex to solve a linear programming problem.
- `...` further arguments passed to or from other methods.
Details

The coefficients of the objective function are printed. If a solution to the linear programming problem was found then the solution and the optimal value of the objective function are printed. If a feasible solution was found but the maximum number of iterations was exceeded then the last feasible solution and the objective function value at that point are printed. If no feasible solution could be found then a message stating that is printed.

Value

x is returned silently.

See Also

simplex

---

### remission

**Cancer Remission and Cell Activity**

Description

The remission data frame has 27 rows and 3 columns.

Usage

remission

Format

This data frame contains the following columns:

- LI  A measure of cell activity.
- m   The number of patients in each group (all values are actually 1 here).
- r   The number of patients (out of m) who went into remission.

Source

The data were obtained from


References

Description

This function calculates a saddlepoint approximation to the distribution of a linear combination of \( W \) at a particular point \( u \), where \( W \) is a vector of random variables. The distribution of \( W \) may be multinomial (default), Poisson or binary. Other distributions are possible also if the adjusted cumulant generating function and its second derivative are given. Conditional saddlepoint approximations to the distribution of one linear combination given the values of other linear combinations of \( W \) can be calculated for \( W \) having binary or Poisson distributions.

Usage

\[
saddle(A = \text{NULL}, u = \text{NULL}, wdist = "m", type = "simp", d = \text{NULL},
    d1 = 1, \text{init} = \text{rep}(0.1, d), \text{mu} = \text{rep}(0.5, n), \text{LR} = \text{FALSE},
    \text{strata} = \text{NULL}, \text{K.adj} = \text{NULL}, \text{K2} = \text{NULL})
\]

Arguments

- **A**: A vector or matrix of known coefficients of the linear combinations of \( W \). It is a required argument unless \( K\text{.adj} \) and \( K2 \) are supplied, in which case it is ignored.
- **u**: The value at which it is desired to calculate the saddlepoint approximation to the distribution of the linear combination of \( W \). It is a required argument unless \( K\text{.adj} \) and \( K2 \) are supplied, in which case it is ignored.
- **wdist**: The distribution of \( W \). This can be one of "m" (multinomial), "p" (Poisson), "b" (binary) or "o" (other). If \( K\text{.adj} \) and \( K2 \) are given \( wdist \) is set to "o".
- **type**: The type of saddlepoint approximation. Possible types are "simp" for simple saddlepoint and "cond" for the conditional saddlepoint. When \( wdist \) is "o" or "m", type is automatically set to "simp", which is the only type of saddlepoint currently implemented for those distributions.
- **d**: This specifies the dimension of the whole statistic. This argument is required only when \( wdist = "o" \) and defaults to 1 if not supplied in that case. For other distributions it is set to \( \text{ncol}(A) \).
- **d1**: When type is "cond" this is the dimension of the statistic of interest which must be less than \( \text{length}(u) \). Then the saddlepoint approximation to the conditional distribution of the first \( d1 \) linear combinations given the values of the remaining combinations is found. Conditional distribution function approximations can only be found if the value of \( d1 \) is 1.
- **init**: Used if \( wdist \) is either "m" or "o", this gives initial values to \( \text{nls} \) which is used to solve the saddlepoint equation.
- **mu**: The values of the parameters of the distribution of \( W \) when \( wdist \) is "m", "p" or "b". \( \mu \) must be of the same length as \( W \) (i.e. \( \text{nrow}(A) \)). The default is that all values of \( \mu \) are equal and so the elements of \( W \) are identically distributed.
- **LR**: If TRUE then the Lugananni-Rice approximation to the cdf is used, otherwise the approximation used is based on Barndorff-Nielsen’s \( r^* \).
- **strata**: The strata for stratified data.
K.adj

The adjusted cumulant generating function used when wdist is "o". This is a function of a single parameter, zeta, which calculates K(zeta)-u%*%zeta, where K(zeta) is the cumulant generating function of W.

K2

This is a function of a single parameter zeta which returns the matrix of second derivatives of K(zeta) for use when wdist is "o". If K.adj is given then this must be given also. It is called only once with the calculated solution to the saddlepoint equation being passed as the argument. This argument is ignored if K.adj is not supplied.

Details

If wdist is "o" or "m", the saddlepoint equations are solved using nlmin to minimize K.adj with respect to its parameter zeta. For the Poisson and binary cases, a generalized linear model is fitted such that the parameter estimates solve the saddlepoint equations. The response variable 'y' for the glm must satisfy the equation t(A)%*%y = u (t() being the transpose function). Such a vector can be found as a feasible solution to a linear programming problem. This is done by a call to simplex. The covariate matrix for the glm is given by A.

Value

A list consisting of the following components

spa The saddlepoint approximations. The first value is the density approximation and the second value is the distribution function approximation.

zeta.hat The solution to the saddlepoint equation. For the conditional saddlepoint this is the solution to the saddlepoint equation for the numerator.

zeta2.hat If type is "cond" this is the solution to the saddlepoint equation for the denominator. This component is not returned for any other value of type.

References


See Also

`saddle.distn`, `simplex`

Examples

# To evaluate the bootstrap distribution of the mean failure time of
# air-conditioning equipment at 80 hours
saddle(A = aircondit$hours/12, u = 80)

# Alternatively this can be done using a conditional poisson
saddle(A = cbind(aircondit$hours/12,1), u = c(80, 12),
saddle.distn

Saddlepoint Distribution Approximations for Bootstrap Statistics

Description
Approximate an entire distribution using saddlepoint methods. This function can calculate simple and conditional saddlepoint distribution approximations for a univariate quantity of interest. For the simple saddlepoint the quantity of interest is a linear combination of \( W \) where \( W \) is a vector of random variables. For the conditional saddlepoint we require the distribution of one linear combination given the values of any number of other linear combinations. The distribution of \( W \) must be one of multinomial, Poisson or binary. The primary use of this function is to calculate quantiles of bootstrap distributions using saddlepoint approximations. Such quantiles are required by the function control to approximate the distribution of the linear approximation to a statistic.

Usage
```r
saddle.distn(A, u = NULL, alpha = NULL, wdist = "m", type = "simp", npts = 20, t = NULL, t0 = NULL, init = rep(0.1, d), mu = rep(0.5, n), LR = FALSE, strata = NULL, ...)
```

Arguments

A
This is a matrix of known coefficients or a function which returns such a matrix. If a function then its first argument must be the point \( t \) at which a saddlepoint is required. The most common reason for \( A \) being a function would be if the statistic is not itself a linear combination of the \( W \) but is the solution to a linear estimating equation.
If A is a function then u must also be a function returning a vector with length equal to the number of columns of the matrix returned by A. Usually all components other than the first will be constants as the other components are the values of the conditioning variables. If A is a matrix with more than one column (such as when \( \text{wdist} = "\text{cond}" \)) then u should be a vector with length one less than \( ncol(A) \). In this case u specifies the values of the conditioning variables. If A is a matrix with one column or a vector then u is not used.

**alpha**

The alpha levels for the quantiles of the distribution which should be returned. By default the 0.1, 0.5, 1, 2.5, 5, 10, 20, 50, 90, 95, 97.5, 99, 99.5 and 99.9 percentiles are calculated.

**wdist**

The distribution of W. Possible values are "m" (multinomial), "p" (Poisson), or "b" (binary).

**type**

The type of saddlepoint to be used. Possible values are "simp" (simple saddlepoint) and "cond" (conditional). If \( \text{wdist} = "m" \), type is set to "simp".

**npts**

The number of points at which the saddlepoint approximation should be calculated and then used to fit the spline.

**t**

A vector of points at which the saddlepoint approximations are calculated. These points should extend beyond the extreme quantiles required but still be in the possible range of the bootstrap distribution. The observed value of the statistic should not be included in t as the distribution function approximation breaks down at that point. The points should, however cover the entire effective range of the distribution including close to the centre. If t is supplied then npts is set to \( \text{length}(t) \). When t is not supplied, the function attempts to find the effective range of the distribution and then selects points to cover this range.

**t0**

If t is not supplied then a vector of length 2 should be passed as t0. The first component of t0 should be the centre of the distribution and the second should be an estimate of spread (such as a standard error). These two are then used to find the effective range of the distribution. The range finding mechanism does rely on an accurate estimate of location in t0[1].

**init**

When \( \text{wdist} = "m" \), this vector should contain the initial values to be passed to \nlinm when it is called to solve the saddlepoint equations.

**mu**

The vector of parameter values for the distribution. The default is that the components of W are identically distributed.

**LR**

A logical flag. When LR is TRUE the Lugananni-Rice cdf approximations are calculated and used to fit the spline. Otherwise the cdf approximations used are based on Barndorff-Nielsen's \( r^* \).

**strata**

A vector giving the strata when the rows of A relate to stratified data. This is used only when \( \text{wdist} = "m" \).

**...**

When A and u are functions any additional arguments are passed unchanged each time one of them is called.

**Details**

The range at which the saddlepoint is used is such that the cdf approximation at the endpoints is more extreme than required by the extreme values of alpha. The lower endpoint is found by evaluating the saddlepoint at the points \( t0[1]-2*t0[2], t0[1]-4*t0[2], t0[1]-8*t0[2] \) etc. until a point is found with a cdf approximation less than \( \text{min}(\alpha)/10 \). Then a bisection method is used to find the endpoint which has cdf approximation in the range \( \text{min}(\alpha)/1000, \text{min}(\alpha)/10 \). Then a number of, equally spaced, points are chosen between the lower endpoint and t0[1] until
a total of npts/2 approximations have been made. The remaining npts/2 points are chosen to the
right of t₀[1] in a similar manner. Any points which are very close to the centre of the distribution
are then omitted as the cdf approximations are not reliable at the centre. A smoothing spline is then
fitted to the probit of the saddlepoint distribution function approximations at the remaining points
and the required quantiles are predicted from the spline.

Sometimes the function will terminate with the message "Unable to find range". There are two
main reasons why this may occur. One is that the distribution is too discrete and/or the required
quantiles too extreme, this can cause the function to be unable to find a point within the allowable
range which is beyond the extreme quantiles. Another possibility is that the value of t₀[2] is too
small and so too many steps are required to find the range. The first problem cannot be solved except
by asking for less extreme quantiles, although for very discrete distributions the approximations may
not be very good. In the second case using a larger value of t₀[2] will usually solve the problem.

Value

The returned value is an object of class "saddle.distn". See the help file for
saddle.distn.object for a description of such an object.

References


distributions. Computing Science and Statistics: Proceedings of the 28th Symposium on the Inter-
face 248–253.

University Press.


See Also

lines.saddle.distn, saddle, saddle.distn.object, smooth.spline

Examples

# The bootstrap distribution of the mean of the air-conditioning
# failure data: fails to find value on R (and probably on S too)
air.t0 <- c(mean(aircondit$hours), sqrt(var(aircondit$hours)/12))
## Not run: saddle.distn(A = aircondit$hours/12, t0 = air.t0)

# alternatively using the conditional poisson
saddle.distn(A = cbind(aircondit$hours/12, 1), u = 12, wdist = "p",
          type = "cond", t0 = air.t0)

# Distribution of the ratio of a sample of size 10 from the bigcity
# data, taken from Example 9.16 of Davison and Hinkley (1997).
ratio <- function(d, w) sum(d$x *w)/sum(d$u * w)
city.v <- var.linear(empinf(data = city, statistic = ratio))
bigcity.t0 <- c(mean(bigcity$x)/mean(bigcity$u), sqrt(city.v))
Afn <- function(t, data) cbind(data$x - t*data$u, 1)
ufn <- function(t, data) c(0,10)
saddle.distn(A = Afn, u = ufn, wdist = "b", type = "cond",
          t0 = bigcity.t0, data = bigcity)
# From Example 9.16 of Davison and Hinkley (1997) again, we find the
# conditional distribution of the ratio given the sum of city$u.
Afn <- function(t, data) cbind(data$x-t*data$u, data$u, 1)
ufn <- function(t, data) c(0, sum(data$u), 10)
city.t0 <- c(mean(city$x)/mean(city$u), sqrt(city.v))
saddle.distn(A = Afn, u = ufn, wdist = "p", type = "cond", t0 = city.t0,
data = city)

saddle.distn.object  Saddlepoint Distribution Approximation Objects

Description

Class of objects that result from calculating saddlepoint distribution approximations by a call to saddle.distn.

Generation

This class of objects is returned from calls to the function saddle.distn.

Methods

The class "saddle.distn" has methods for the functions lines and print.

Structure

Objects of class "saddle.distn" are implemented as a list with the following components.

quantiles  A matrix with 2 columns. The first column contains the probabilities alpha and the second column contains the estimated quantiles of the distribution at those probabilities derived from the spline.

points  A matrix of evaluations of the saddlepoint approximation. The first column contains the values of t which were used, the second and third contain the density and cdf approximations at those points and the rest of the columns contain the solutions to the saddlepoint equations. When type is "simp", there is only one of those. When type is "cond" there are 2*d-1 where d is the number of columns in A or the output of A(t,. . .()). The first d of these correspond to the numerator and the remainder correspond to the denominator.

distn  An object of class smooth.spline. This corresponds to the spline fitted to the saddlepoint cdf approximations in points in order to approximate the entire distribution. For the structure of the object see smooth.spline.

call  The original call to saddle.distn which generated the object.

LR  A logical variable indicating whether the Lugananni-Rice approximations were used.

See Also

lines.saddle.distn, saddle.distn, print.saddle.distn
Description

The salinity data frame has 28 rows and 4 columns.

Biweekly averages of the water salinity and river discharge in Pamlico Sound, North Carolina were recorded between the years 1972 and 1977. The data in this set consists only of those measurements in March, April and May.

Usage

salinity

Format

This data frame contains the following columns:

- sal: The average salinity of the water over two weeks.
- lag: The average salinity of the water lagged two weeks. Since only spring is used, the value of lag is not always equal to the previous value of sal.
- trend: A factor indicating in which of the 6 biweekly periods between March and May, the observations were taken. The levels of the factor are from 0 to 5 with 0 being the first two weeks in March.
- dis: The amount of river discharge during the two weeks for which sal is the average salinity.

Source

The data were obtained from


References


Description

This function will optimize the linear function \( a^T x \) subject to the constraints \( A1^T x \leq b1 \), \( A2^T x \geq b2 \), \( A3^T x = b3 \) and \( x \geq 0 \). Either maximization or minimization is possible but the default is minimization.
simplex

Usage

`simplex(a, A1 = NULL, b1 = NULL, A2 = NULL, b2 = NULL, A3 = NULL,
        b3 = NULL, maxi = FALSE, n.iter = n + 2 * m, eps = 1e-10)`

Arguments

`a`  A vector of length `n` which gives the coefficients of the objective function.

`A1`  An `m1` by `n` matrix of coefficients for the ≤ type of constraints.

`b1`  A vector of length `m1` giving the right hand side of the ≤ constraints. This argument is required if `A1` is given and ignored otherwise. All values in `b1` must be non-negative.

`A2`  An `m2` by `n` matrix of coefficients for the ≥ type of constraints.

`b2`  A vector of length `m2` giving the right hand side of the ≥ constraints. This argument is required if `A2` is given and ignored otherwise. All values in `b2` must be non-negative. Note that the constraints x >= 0 are included automatically and so should not be repeated here.

`A3`  An `m3` by `n` matrix of coefficients for the equality constraints.

`b3`  A vector of length `m3` giving the right hand side of equality constraints. This argument is required if `A3` is given and ignored otherwise. All values in `b3` must be non-negative.

`maxi`  A logical flag which specifies minimization if `FALSE` (default) and maximization otherwise. If `maxi` is `TRUE` then the maximization problem is recast as a minimization problem by changing the objective function coefficients to their negatives.

`n.iter`  The maximum number of iterations to be conducted in each phase of the simplex method. The default is `n+2*(m1+m2+m3)`.

`eps`  The floating point tolerance to be used in tests of equality.

Details

The method employed by this function is the two phase tableau simplex method. If there are ≥ or equality constraints an initial feasible solution is not easy to find. To find a feasible solution an artificial variable is introduced into each ≥ or equality constraint and an auxiliary objective function is defined as the sum of these artificial variables. If a feasible solution to the set of constraints exists then the auxiliary objective will be minimized when all of the artificial variables are 0. These are then discarded and the original problem solved starting at the solution to the auxiliary problem. If the only constraints are of the ≤ form, the origin is a feasible solution and so the first stage can be omitted.

Value

An object of class "simplex": see `simplex.object`.

Note

The method employed here is suitable only for relatively small systems. Also if possible the number of constraints should be reduced to a minimum in order to speed up the execution time which is approximately proportional to the cube of the number of constraints. In particular if there are any constraints of the form x[i] >= b2[i] they should be omitted by setting x[i] = x[i]-b2[i], changing all the constraints and the objective function accordingly and then transforming back after the solution has been found.
simplex.object

References


Examples

# This example is taken from Exercise 7.5 of Gill, Murray and Wright (1991).
enj <- c(200, 6000, 3000, -200)
fat <- c(800, 6000, 1000, 400)
vitx <- c(50, 3, 150, 100)
vity <- c(10, 10, 75, 100)
vitz <- c(150, 35, 75, 5)
simplex(a = enj, A1 = fat, b1 = 13800, A2 = rbind(vitx, vity, vitz), b2 = c(600, 300, 550), maxi = TRUE)

---

simplex.object

*Linear Programming Solution Objects*

Description

Class of objects that result from solving a linear programming problem using `simplex`.

Generation

This class of objects is returned from calls to the function `simplex`.

Methods

The class "`saddle.distn`" has a method for the function `print`.

Structure

Objects of class "`simplex`" are implemented as a list with the following components.

- `soln` The values of x which optimize the objective function under the specified constraints provided those constraints are jointly feasible.
- `solved` This indicates whether the problem was solved. A value of -1 indicates that no feasible solution could be found. A value of 0 that the maximum number of iterations was reached without termination of the second stage. This may indicate an unbounded function or simply that more iterations are needed. A value of 1 indicates that an optimal solution has been found.
- `value` The value of the objective function at `soln`.
- `val.aux` This is NULL if a feasible solution is found. Otherwise it is a positive value giving the value of the auxiliary objective function when it was minimized.
- `obj` The original coefficients of the objective function.
- `a` The objective function coefficients re-expressed such that the basic variables have coefficient zero.
- `a.aux` This is NULL if a feasible solution is found. Otherwise it is the re-expressed auxiliary objective function at the termination of the first phase of the simplex method.
A The final constraint matrix which is expressed in terms of the non-basic variables. If a feasible solution is found then this will have dimensions \( m_1+m_2+m_3 \) by \( n+m_1+m_2 \), where the final \( m_1+m_2 \) columns correspond to slack and surplus variables. If no feasible solution is found there will be an additional \( m_1+m_2+m_3 \) columns for the artificial variables introduced to solve the first phase of the problem.

**basic** The indices of the basic (non-zero) variables in the solution. Indices between \( n+1 \) and \( n+m_1 \) correspond to slack variables, those between \( n+m_1+1 \) and \( n+m_2 \) correspond to surplus variables and those greater than \( n+m_2 \) are artificial variables. Indices greater than \( n+m_2 \) should occur only if solved is \(-1\) as the artificial variables are discarded in the second stage of the simplex method.

**slack** The final values of the \( m_1 \) slack variables which arise when the "\( \leq \)" constraints are re-expressed as the equalities \( A_1 x + \text{slack} = b_1 \).

**surplus** The final values of the \( m_2 \) surplus variables which arise when the "\( \leq \)" constraints are re-expressed as the equalities \( A_2 x - \text{surplus} = b_2 \).

**artificial** This is NULL if a feasible solution can be found. If no solution can be found then this contains the values of the \( m_1+m_2+m_3 \) artificial variables which minimize their sum subject to the original constraints. A feasible solution exists only if all of the artificial variables can be made 0 simultaneously.

**See Also**

`print.simplex`, `simplex`

---

### smooth.f

**Smooth Distributions on Data Points**

#### Description

This function uses the method of frequency smoothing to find a distribution on a data set which has a required value, \( \theta \), of the statistic of interest. The method results in distributions which vary smoothly with \( \theta \).

#### Usage

```r
smooth.f(theta, boot.out, index = 1, t = boot.out$t[, index], width = 0.5)
```

#### Arguments

- **theta**
  - The required value for the statistic of interest. If \( \theta \) is a vector, a separate distribution will be found for each element of \( \theta \).

- **boot.out**
  - A bootstrap output object returned by a call to `boot`.

- **index**
  - The index of the variable of interest in the output of `boot.out$statistic`. This argument is ignored if \( t \) is supplied. \( \text{index} \) must be a scalar.

- **t**
  - The bootstrap values of the statistic of interest. This must be a vector of length \( \text{boot.out}$$R \) and the values must be in the same order as the bootstrap replicates in `boot.out`.

- **width**
  - The standardized width for the kernel smoothing. The smoothing uses a value of \( \text{width} \times s \) for epsilon, where \( s \) is the bootstrap estimate of the standard error of the statistic of interest. \( \text{width} \) should take a value in the range \((0.2, 1)\) to produce a reasonable smoothed distribution. If \( \text{width} \) is too large then the distribution becomes closer to uniform.
smooth.f

Details

The new distributional weights are found by applying a normal kernel smoother to the observed values of t weighted by the observed frequencies in the bootstrap simulation. The resulting distribution may not have parameter value exactly equal to the required value theta but it will typically have a value which is close to theta. The details of how this method works can be found in Davison, Hinkley and Worton (1995) and Section 3.9.2 of Davison and Hinkley (1997).

Value

If length(theta) is 1 then a vector with the same length as the data set boot.out$data is returned. The value in position 1 is the probability to be given to the data point in position 1 so that the distribution has parameter value approximately equal to theta. If length(theta) is bigger than 1 then the returned value is a matrix with length(theta) rows each of which corresponds to a distribution with the parameter value approximately equal to the corresponding value of theta.

References


See Also

boot, exp.tilt, tilt.boot

Examples

# Example 9.8 of Davison and Hinkley (1997) requires tilting the resampling # distribution of the studentized statistic to be centred at the observed # value of the test statistic 1.84. In the book exponential tilting was used # but it is also possible to use smooth.f.
grav1 <- gravity[as.numeric(gravity[, 2]) >= 7, ]
grav.fun <- function(dat, w, orig) {
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- as.vector(tapply(d * w, strata, sum)) # drop names
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2] - mns[1], s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
grav.boot <- boot(grav1, grav.fun, R = 499, stype = "w",
  strata = grav1[, 2], orig = grav.z0[1])
grav.sm <- smooth.f(grav.z0[3], grav.boot, index = 3)

# Now we can run another bootstrap using these weights
grav.boot2 <- boot(grav1, grav.fun, R = 499, stype = "w",
  strata = grav1[, 2], orig = grav.z0[1],
  weights = grav.sm)

# Estimated p-values can be found from these as follows
mean(grav.boot$t[, 3] >= grav.z0[3])
imp.prob(grav.boot2, t0 = -grav.z0[3], t = -grav.boot2$t[, 3])

# Note that for the importance sampling probability we must
# multiply everything by -1 to ensure that we find the correct
# probability. Raw resampling is not reliable for probabilities
# greater than 0.5. Thus
1 - imp.prob(grav.boot2, index = 3, t0 = grav.z0[3])$raw
# can give very strange results (negative probabilities).

sunspot

Annual Mean Sunspot Numbers

Description
sunspot is a time series and contains 289 observations.
The Zurich sunspot numbers have been analyzed in almost all books on time series analysis as well
as numerous papers. The data set, usually attributed to Rudolf Wolf, consists of means of daily
relative numbers of sunspot sightings. The relative number for a day is given by k(f+10g) where
g is the number of sunspot groups observed, f is the total number of spots within the groups and k
is a scaling factor relating the observer and telescope to a baseline. The relative numbers are then
averaged to give an annual figure. See Inzenman (1983) for a discussion of the relative numbers.
The figures are for the years 1700-1988.

Source
The data were obtained from

References
University Press.

survival

Survival of Rats after Radiation Doses

Description
The survival data frame has 14 rows and 2 columns.
The data measured the survival percentages of batches of rats who were given varying doses of
radiation. At each of 6 doses there were two or three replications of the experiment.

Usage
survival
**tau**

**Format**

This data frame contains the following columns:

- dose: The dose of radiation administered (rads).
- surv: The survival rate of the batches expressed as a percentage.

**Source**

The data were obtained from

**References**


---

**tau**

*Tau Particle Decay Modes*

**Description**

The tau data frame has 60 rows and 2 columns.

The tau particle is a heavy electron-like particle discovered in the 1970’s by Martin Perl at the Stanford Linear Accelerator Center. Soon after its production the tau particle decays into various collections of more stable particles. About 86% of the time the decay involves just one charged particle. This rate has been measured independently 13 times.

The one-charged-particle event is made up of four major modes of decay as well as a collection of other events. The four main types of decay are denoted rho, pi, e and mu. These rates have been measured independently 6, 7, 14 and 19 times respectively. Due to physical constraints each experiment can only estimate the composite one-charged-particle decay rate or the rate of one of the major modes of decay.

Each experiment consists of a major research project involving many years work. One of the goals of the experiments was to estimate the rate of decay due to events other than the four main modes of decay. These are uncertain events and so cannot themselves be observed directly.

**Usage**

tau

**Format**

This data frame contains the following columns:

- rate: The decay rate expressed as a percentage.
- decay: The type of decay measured in the experiment. It is a factor with levels 1, rho, pi, e and mu.

**Source**

The data were obtained from
References


**tilt.boot**

Non-parametric Tilted Bootstrap

**Description**

This function will run an initial bootstrap with equal resampling probabilities (if required) and will use the output of the initial run to find resampling probabilities which put the value of the statistic at required values. It then runs an importance resampling bootstrap using the calculated probabilities as the resampling distribution.

**Usage**

```
tilt.boot(data, statistic, R, sim = "ordinary", stype = "i",
          strata = rep(1, n), L = NULL, theta = NULL,
          alpha = c(0.025, 0.975), tilt = TRUE, width = 0.5,
          index = 1, ...)
```

**Arguments**

- **data**: The data as a vector, matrix or data frame. If it is a matrix or data frame then each row is considered as one (multivariate) observation.

- **statistic**: A function which when applied to data returns a vector containing the statistic(s) of interest. It must take at least two arguments. The first argument will always be `data` and the second should be a vector of indices, weights or frequencies describing the bootstrap sample. Any other arguments must be supplied to `tilt.boot` and will be passed unchanged to statistic each time it is called.

- **R**: The number of bootstrap replicates required. This will generally be a vector, the first value stating how many uniform bootstrap simulations are to be performed at the initial stage. The remaining values of `R` are the number of simulations to be performed resampling from each reweighted distribution. The first value of `R` must always be present, a value of 0 implying that no uniform resampling is to be carried out. Thus `length(R)` should always equal `1+length(theta)`.

- **sim**: This is a character string indicating the type of bootstrap simulation required. There are only two possible values that this can take: "ordinary" and "balanced". If other simulation types are required for the initial un-weighted bootstrap then it will be necessary to run boot, calculate the weights appropriately, and run boot again using the calculated weights.

- **stype**: A character string indicating the type of second argument expected by `statistic`. The possible values that `stype` can take are "i" (indices), "w" (weights) and "f" (frequencies).

- **strata**: An integer vector or factor representing the strata for multi-sample problems.
L  The empirical influence values for the statistic of interest. They are used only for exponential tilting when \( \text{tilt} \) is \( \text{TRUE} \). If \( \text{tilt} \) is \( \text{TRUE} \) and they are not supplied then \( \text{tilt.boot} \) uses \text{empinf} to calculate them.

\( \theta \)  The required parameter value(s) for the tilted distribution(s). There should be one value of \( \theta \) for each of the non-uniform distributions. If \( R[1] \) is 0 \( \theta \) is a required argument. Otherwise \( \theta \) values can be estimated from the initial uniform bootstrap and the values in \( \alpha \).

\( \alpha \)  The alpha level to which tilting is required. This parameter is ignored if \( R[1] \) is 0 or if \( \theta \) is supplied, otherwise it is used to find the values of \( \theta \) as quantiles of the initial uniform bootstrap. In this case \( R[1] \) should be large enough that \( \min(c(\alpha, 1-\alpha)) \times R[1] > 5 \), if this is not the case then a warning is generated to the effect that the \( \theta \) are extreme values and so the tilted output may be unreliable.

\( \text{tilt} \)  A logical variable which if \( \text{TRUE} \) (the default) indicates that exponential tilting should be used, otherwise local frequency smoothing (\text{smooth.f}) is used. If \( \text{tilt} \) is \( \text{FALSE} \) then \( R[1] \) must be positive. In fact in this case the value of \( R[1] \) should be fairly large (in the region of 500 or more).

\( \text{width} \)  This argument is used only if \( \text{tilt} \) is \( \text{FALSE} \), in which case it is passed unchanged to \text{smooth.f} as the standardized bandwidth for the smoothing operation. The value should generally be in the range \((0.2, 1)\). See \text{smooth.f} for more details.

\( \text{index} \)  The index of the statistic of interest in the output from \text{statistic}. By default the first element of the output of \text{statistic} is used.

... Any additional arguments required by \text{statistic}. These are passed unchanged to \text{statistic} each time it is called.

**Value**

An object of class "boot" with the following components

- \( t_0 \)  The observed value of the statistic on the original data.
- \( t \)  The values of the bootstrap replicates of the statistic. There will be \( \text{sum}(R) \) of these, the first \( R[1] \) corresponding to the uniform bootstrap and the remainder to the tilted bootstrap(s).
- \( R \)  The input vector of the number of bootstrap replicates.
- \( \text{data} \)  The original data as supplied.
- \( \text{statistic} \)  The statistic function as supplied.
- \( \text{sim} \)  The simulation type used in the bootstrap(s), it can either be "ordinary" or "balanced".
- \( \text{stype} \)  The type of statistic supplied, it is the same as the input value \( \text{stype} \).
- \( \text{call} \)  A copy of the original call to \text{tilt.boot}.
- \( \text{strata} \)  The strata as supplied.
- \( \text{weights} \)  The matrix of weights used. If \( R[1] \) is greater than 0 then the first row will be the uniform weights and each subsequent row the tilted weights. If \( R[1] \) equals 0 then the uniform weights are omitted and only the tilted weights are output.
- \( \theta \)  The values of \( \theta \) used for the tilted distributions. These are either the input values or the values derived from the uniform bootstrap and \( \alpha \).
References


See Also

*boot.exp.tilt*, *Imp.Estimates*, *imp.weights*, *smooth.f*

Examples

# Note that these examples can take a while to run.

# Example 9.9 of Davison and Hinkley (1997).
grav1 <- gravity[as.numeric(gravity[,2]) >= 7,1]
grav.fun <- function(dat, w, orig) {
  strata <- tapply(dat[,2], as.numeric(dat[,2]))
  d <- dat[,1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- as.vector(tapply(d*w, strata, sum)) # drop names
  mn2 <- tapply(d*d*w, strata, sum)
  s2hat <- sum((mn2-mns^2)/ns)
  c(mns[2]-mns[1], s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1, 26), 0)
tilt.boot(grav1, grav.fun, R = c(249, 375, 375), stype = "w", strata = grav1[,2], tilt = TRUE, index = 3, orig = grav.z0[1])

# Example 9.10 of Davison and Hinkley (1997) requires a balanced
# importance resampling bootstrap to be run. In this example we
# show how this might be run.
acme.fun <- function(data, i, bhat) {
  d <- data[i,]
  n <- nrow(d)
  d.lm <- glm(d$acme~d$market)
  beta.b <- coef(d.lm)[2]
  d.diag <- boot::glm.diag(d.lm)
  SSx <- (n-1)*var(d$market)
  tmp <- (d$market-mean(d$market))*d.diag$res*d.diag$sd
  sr <- sqrt(sum(tmp^2))/SSx
  c(beta.b, sr, (beta.b-bhat)/sr)
}
acme.b <- acme.fun(acme, 1:nrow(acme), 0)
acme.boot1 <- tilt.boot(acme, acme.fun, R = c(499, 250, 250),
    stype = "i", sim = "balanced", alpha = c(0.05, 0.95),
    tilt = TRUE, index = 3, bhat = acme.b[1])
**tsboot**  

*Bootstrapping of Time Series*

**Description**

Generate R bootstrap replicates of a statistic applied to a time series. The replicate time series can be generated using fixed or random block lengths or can be model based replicates.

**Usage**

```r
tsboot(tseries, statistic, R, l = NULL, sim = "model",  
       endcorr = TRUE, n.sim = NROW(tseries), orig.t = TRUE,  
       ran.gen, ran.args = NULL, norm = TRUE, ...,  
       parallel = c("no", "multicore", "snow"),  
       ncpus = getOption("boot.ncpus", 1L), cl = NULL)
```

**Arguments**

- `tseries` A univariate or multivariate time series.
- `statistic` A function which when applied to `tseries` returns a vector containing the statistic(s) of interest. Each time `statistic` is called it is passed a time series of length `n.sim` which is of the same class as the original `tseries`. Any other arguments which `statistic` takes must remain constant for each bootstrap replicate and should be supplied through the `...` argument to `tsboot`.
- `R` A positive integer giving the number of bootstrap replicates required.
- `sim` The type of simulation required to generate the replicate time series. The possible input values are "model" (model based resampling), "fixed" (block resampling with fixed block lengths of `l`), "geom" (block resampling with block lengths having a geometric distribution with mean `l`) or "scramble" (phase scrambling).
- `l` If `sim` is "fixed" then `l` is the fixed block length used in generating the replicate time series. If `sim` is "geom" then `l` is the mean of the geometric distribution used to generate the block lengths. `l` should be a positive integer less than the length of `tseries`. This argument is not required when `sim` is "model" but it is required for all other simulation types.
- `endcorr` A logical variable indicating whether end corrections are to be applied when `sim` is "fixed". When `sim` is "geom", `endcorr` is automatically set to TRUE; `endcorr` is not used when `sim` is "model" or "scramble".
- `n.sim` The length of the simulated time series. Typically this will be equal to the length of the original time series but there are situations when it will be larger. One obvious situation is if prediction is required. Another situation in which `n.sim` is larger than the original length is if `tseries` is a residual time series from fitting some model to the original time series. In this case, `n.sim` would usually be the length of the original time series.
- `orig.t` A logical variable which indicates whether `statistic` should be applied to `tseries` itself as well as the bootstrap replicate series. If `statistic` is expecting a longer time series than `tseries` or if applying `statistic` to `tseries` will not yield any useful information then `orig.t` should be set to FALSE.
This is a function of three arguments. The first argument is a time series. If sim is "model" then it will always be tsseries that is passed. For other simulation types it is the result of selecting n.sim observations from tseries by some scheme and converting the result back into a time series of the same form as tseries (although of length n.sim). The second argument to ran.gen is always the value n.sim, and the third argument is ran.args, which is used to supply any other objects needed by ran.gen. If sim is "model" then the generation of the replicate time series will be done in ran.gen (for example through use of arima.sim). For the other simulation types ran.gen is used for 'post-blackening'. The default is that the function simply returns the time series passed to it.

This will be supplied to ran.gen each time it is called. If ran.gen needs any extra arguments then they should be supplied as components of ran.args. Multiple arguments may be passed by making ran.args a list. If ran.args is NULL then it should not be used within ran.gen but note that ran.gen must still have its third argument.

A logical argument indicating whether normal margins should be used for phase scrambling. If norm is FALSE then margins corresponding to the exact empirical margins are used.

Extra named arguments to statistic may be supplied here. Beware of partial matching to the arguments of tsboot listed above.

See the help for boot.

Details

If sim is "fixed" then each replicate time series is found by taking blocks of length l, from the original time series and putting them end-to-end until a new series of length n.sim is created. When sim is "geom" a similar approach is taken except that now the block lengths are generated from a geometric distribution with mean l. Post-blackening can be carried out on these replicate time series by including the function ran.gen in the call to tsboot and having tseries as a time series of residuals.

Model based resampling is very similar to the parametric bootstrap and all simulation must be in one of the user specified functions. This avoids the complicated problem of choosing the block length but relies on an accurate model choice being made.

Phase scrambling is described in Section 8.2.4 of Davison and Hinkley (1997). The types of statistic for which this method produces reasonable results is very limited and the other methods seem to do better in most situations. Other types of resampling in the frequency domain can be accomplished using the function boot with the argument sim = "parametric".

Value

An object of class "boot" with the following components.

- **t0**: If orig.t is TRUE then t0 is the result of statistic(tseries,...{}) otherwise it is NULL.
- **t**: The results of applying statistic to the replicate time series.
- **R**: The value of R as supplied to tsboot.
- **tseries**: The original time series.
- **statistic**: The function statistic as supplied.
The simulation type used in generating the replicates.

endcorr

The value of endcorr used. The value is meaningful only when sim is "fixed"; it is ignored for model based simulation or phase scrambling and is always set to TRUE if sim is "geom".

n.sim

The value of n.sim used.

1

The value of 1 used for block based resampling. This will be NULL if block based resampling was not used.

ran.gen

The ran.gen function used for generating the series or for 'post-blackening'.

ran.args

The extra arguments passed to ran.gen.

call

The original call to tsboot.

References


See Also

boot, arima.sim

Examples

lynx.fun <- function(tsb) {
  ar.fit <- ar(tsb, order.max = 25)
  c(ar.fit$order, mean(tsb), tsb)
}

# the stationary bootstrap with mean block length 20
lynx.1 <- tsboot(log(lynx), lynx.fun, R = 99, l = 20, sim = "geom")

# the fixed block bootstrap with length 20
lynx.2 <- tsboot(log(lynx), lynx.fun, R = 99, l = 20, sim = "fixed")

# Now for model based resampling we need the original model
# Note that for all of the bootstraps which use the residuals as their
# data, we set orig.t to FALSE since the function applied to the residual
# time series will be meaningless.
lynx.ar <- ar(log(lynx))
lynx.model <- list(order = c(lynx.ar$order, 0, 0), ar = lynx.ar$ar)
lynx.res <- lynx.ar$resid[!is.na(lynx.ar$resid)]
lynx.res <- lynx.res - mean(lynx.res)
 lynx.sim <- function(res,n.sim, ran.args) {
  # random generation of replicate series using arima.sim
  rg1 <- function(n, res) sample(res, n, replace = TRUE)
  ts.orig <- ran.args$ts
  ts.mod <- ran.args$model
  mean(ts.orig)+ts(arima.sim(model = ts.mod, n = n.sim, 
    rand.gen = rg1, res = as.vector(res)))
}
tuna <- tsboot(lynx.res, lynx.fun, R = 99, sim = "model", n.sim = 114, orig.t = FALSE, ran.gen = lynx.sim, ran.args = list(ts = log(lynx), model = lynx.model))

# For "post-blackening" we need to define another function
lynx.black <- function(res, n.sim, ran.args) {
  ts.orig <- ran.args$ts
  ts.mod <- ran.args$model
  mean(ts.orig) + ts(arima.sim(model = ts.mod, n = n.sim, innov = res))
}

# Now we can run apply the two types of block resampling again but this # time applying post-blackening.
lynx.1b <- tsboot(lynx.res, lynx.fun, R = 99, l = 20, sim = "fixed", n.sim = 114, orig.t = FALSE, ran.gen = lynx.black, ran.args = list(ts = log(lynx), model = lynx.model))

lynx.2b <- tsboot(lynx.res, lynx.fun, R = 99, l = 20, sim = "geom", n.sim = 114, orig.t = FALSE, ran.gen = lynx.black, ran.args = list(ts = log(lynx), model = lynx.model))

# To compare the observed order of the bootstrap replicates we # proceed as follows.
table(lynx.1$t[, 1])
table(lynx.1b$t[, 1])
table(lynx.2$t[, 1])
table(lynx.2b$t[, 1])
table(lynx.3$t[, 1])

# Notice that the post-blackened and model-based bootstraps preserve # the true order of the model (11) in many more cases than the others.

---

**tuna**

**Tuna Sighting Data**

**Description**

The tuna data frame has 64 rows and 1 columns.

The data come from an aerial line transect survey of Southern Bluefin Tuna in the Great Australian Bight. An aircraft with two spotters on board flies randomly allocated line transects. Each school of tuna sighted is counted and its perpendicular distance from the transect measured. The survey was conducted in summer when tuna tend to stay on the surface.

**Usage**

`tuna`

**Format**

This data frame contains the following column:

`y` The perpendicular distance, in miles, from the transect for 64 independent sightings of tuna schools.
**Source**

The data were obtained from


**References**


---

**urine**  

*Urine Analysis Data*

---

**Description**

The urine data frame has 79 rows and 7 columns.  
79 urine specimens were analyzed in an effort to determine if certain physical characteristics of the urine might be related to the formation of calcium oxalate crystals.

**Usage**

urine

**Format**

This data frame contains the following columns:  

- r  Indicator of the presence of calcium oxalate crystals.  
- gravity The specific gravity of the urine.  
- ph The pH reading of the urine.  
- osmo The osmolarity of the urine. Osmolarity is proportional to the concentration of molecules in solution.  
- cond The conductivity of the urine. Conductivity is proportional to the concentration of charged ions in solution.  
- urea The urea concentration in millimoles per litre.  
- calc The calcium concentration in millimoles per litre.

**Source**

The data were obtained from


**References**

**var.linear**  
*Linear Variance Estimate*

**Description**
Estimates the variance of a statistic from its empirical influence values.

**Usage**

```r
var.linear(L, strata = NULL)
```

**Arguments**
- `L`: Vector of the empirical influence values of a statistic. These will usually be calculated by a call to `empinf`.
- `strata`: A numeric vector or factor specifying which observations (and hence empirical influence values) come from which strata.

**Value**
The variance estimate calculated from `L`.

**References**

**See Also**
`empinf`, `linear.approx`, `k3.linear`

**Examples**

```r
# To estimate the variance of the ratio of means for the city data.
ratio <- function(d,w) sum(d$x * w)/sum(d$u * w)
var.linear(empinf(data = city, statistic = ratio))
```

---

**wool**  
*Australian Relative Wool Prices*

**Description**
`wool` is a time series of class "ts" and contains 309 observations.

Each week that the market is open the Australian Wool Corporation set a floor price which determines their policy on intervention and is therefore a reflection of the overall price of wool for the week in question. Actual prices paid can vary considerably about the floor price. The series here is the log of the ratio between the price for fine grade wool and the floor price, each market week between July 1976 and Jun 1984.
Source

The data were obtained from


References

Chapter 19

The class package

\begin{verbatim}
batchSOM                   Self-Organizing Maps: Batch Algorithm

Description

Kohonen’s Self-Organizing Maps are a crude form of multidimensional scaling.

Usage

batchSOM(data, grid = somgrid(), radii, init)

Arguments

data  a matrix or data frame of observations, scaled so that Euclidean distance is appropriate.
grid  A grid for the representatives: see somgrid.
radii the radii of the neighbourhood to be used for each pass: one pass is run for each element of radii.
init  the initial representatives. If missing, chosen (without replacement) randomly from data.

Details

The batch SOM algorithm of Kohonen(1995, section 3.14) is used.

Value

An object of class "SOM" with components

grid  the grid, an object of class "somgrid".

codes  a matrix of representatives.

References

\end{verbatim}
See Also

somgrid, SOM

Examples

```r
require(graphics)
data(crabs, package = "MASS")

lcrabs <- log(crabs[, 4:8])
crabs.grp <- factor(c("B", "b", "O", "o")[, rep(1:4, rep(50, 4))])
gr <- somgrid(topo = "hexagonal")
crabs.som <- batchSOM(lcrabs, gr, c(4, 4, 2, 1, 1, 0, 0))
plot(crabs.som)

bins <- as.numeric(knn1(crabs.som$codes, lcrabs, 0:47))
plot(crabs.som$grid, type = "n")
symbols(crabs.som$grid$pts[, 1], crabs.som$grid$pts[, 2],
circles = rep(0.4, 48), inches = FALSE, add = TRUE)
text(crabs.som$grid$pts[bins, ] + rnorm(400, 0, 0.1),
as.character(crabs.grp))
```

---

**condense**  
Condense training set for k-NN classifier

**Description**
Condense training set for k-NN classifier

**Usage**

```r
condense(train, class, store, trace = TRUE)
```

**Arguments**

- `train`  
  matrix for training set
- `class`  
  vector of classifications for test set
- `store`  
  initial store set. Default one randomly chosen element of the set.
- `trace`  
  logical. Trace iterations?

**Details**

The store set is used to 1-NN classify the rest, and misclassified patterns are added to the store set. The whole set is checked until no additions occur.

**Value**

Index vector of cases to be retained (the final store set).
knn

k-Nearest Neighbour Classification

Description

k-nearest neighbour classification for test set from training set. For each row of the test set, the k nearest (in Euclidean distance) training set vectors are found, and the classification is decided by majority vote, with ties broken at random. If there are ties for the kth nearest vector, all candidates are included in the vote.

Usage

```r
knn(train, test, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
```

Arguments

- `train`: matrix or data frame of training set cases.
- `test`: matrix or data frame of test set cases. A vector will be interpreted as a row vector for a single case.
- `cl`: factor of true classifications of training set
- `k`: number of neighbours considered.
- `l`: minimum vote for definite decision, otherwise doubt. (More precisely, less than k-l dissenting votes are allowed, even if k is increased by ties.)
- `prob`: If this is true, the proportion of the votes for the winning class are returned as attribute `prob`.
- `use.all`: controls handling of ties. If true, all distances equal to the kth largest are included. If false, a random selection of distances equal to the kth is chosen to use exactly k neighbours.

Examples

```r
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
keep <- condense(train, cl)
knn(train[keep, , drop=FALSE], test, cl[keep])
keep2 <- reduce.nn(train, keep, cl)
knn(train[keep2, , drop=FALSE], test, cl[keep2])
```
Value

Factor of classifications of test set. doubt will be returned as NA.

References


See Also

knn1, knn.cv

Examples

```
train <- rbind(iris3[1:25,1], iris3[1:25,2], iris3[1:25,3])
test <- rbind(iris3[26:50,1], iris3[26:50,2], iris3[26:50,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
knn(train, test, cl, k = 3, prob=TRUE)
attributes(.Last.value)
```

---

### knn.cv

k-Nearest Neighbour Cross-Validatory Classification

---

Description

k-nearest neighbour cross-validatory classification from training set.

Usage

```
knn.cv(train, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
```

Arguments

- **train**: matrix or data frame of training set cases.
- **cl**: factor of true classifications of training set
- **k**: number of neighbours considered.
- **l**: minimum vote for definite decision, otherwise doubt. (More precisely, less than k-l dissenting votes are allowed, even if k is increased by ties.)
- **prob**: If this is true, the proportion of the votes for the winning class are returned as attribute prob.
- **use.all**: controls handling of ties. If true, all distances equal to the kth largest are included. If false, a random selection of distances equal to the kth is chosen to use exactly k neighbours.

Details

This uses leave-one-out cross validation. For each row of the training set *train*, the k nearest (in Euclidean distance) other training set vectors are found, and the classification is decided by majority vote, with ties broken at random. If there are ties for the kth nearest vector, all candidates are included in the vote.
value

Factor of classifications of training set. doubt will be returned as NA.

References


See Also

knn

Examples

```r
train <- rbind(iris3[,1], iris3[,2], iris3[,3])
cl <- factor(c(rep("s",50), rep("c",50), rep("v",50)))
knn.cv(train, cl, k = 3, prob = TRUE)
attributes(.Last.value)
```

Description

Nearest neighbour classification for test set from training set. For each row of the test set, the nearest (by Euclidean distance) training set vector is found, and its classification used. If there is more than one nearest, a majority vote is used with ties broken at random.

Usage

```r
knn1(train, test, cl)
```

Arguments

- **train** matrix or data frame of training set cases.
- **test** matrix or data frame of test set cases. A vector will be interpreted as a row vector for a single case.
- **cl** factor of true classification of training set.

Value

Factor of classifications of test set.

References


See Also

knn
Examples

```r
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
c1 <- factor(c(rep("s",25), rep("c",25), rep("v",25)))

c1nn1(train, test, c1)
```

---

**lvq1**

*Learning Vector Quantization 1*

**Description**

Moves examples in a codebook to better represent the training set.

**Usage**

```r
lvq1(x, cl, codebk, niter = 100 * nrow(codebk$x), alpha = 0.03)
```

**Arguments**

- `x` a matrix or data frame of examples
- `cl` a vector or factor of classifications for the examples
- `codebk` a codebook
- `niter` number of iterations
- `alpha` constant for training

**Details**

Selects `niter` examples at random with replacement, and adjusts the nearest example in the codebook for each.

**Value**

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

**References**


**See Also**

`lvqinit, olvq1, lvq2, lvq3, lvqtest`
Examples

```r
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
classification <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
codebook <- lvqinit(train, classification, 10)
lvqtest(codebook, train)
```

1vq2  

Learning Vector Quantization 2.1

Description

Moves examples in a codebook to better represent the training set.

Usage

```r
1vq2(x, cl, codebk, niter = 100 * nrow(codebk$x), alpha = 0.03, win = 0.3)
```

Arguments

- **x**: a matrix or data frame of examples
- **cl**: a vector or factor of classifications for the examples
- **codebk**: a codebook
- **niter**: number of iterations
- **alpha**: constant for training
- **win**: a tolerance for the closeness of the two nearest vectors.

Details

Selects **niter** examples at random with replacement, and adjusts the nearest two examples in the codebook if one is correct and the other incorrect.

Value

A codebook, represented as a list with components **x** and **cl** giving the examples and classes.

References

See Also

lvqinit, lvq1, olvq1, lvq3, lvqtest

Examples

```r
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])

test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])

cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))

cd <- lvqinit(train, cl, 10)

lvqtest(cd, train)

cd0 <- olvq1(train, cl, cd)

lvqtest(cd0, train)

cd2 <- lvq2(train, cl, cd0)

lvqtest(cd2, train)
```

---

**lvq3**  
*Learning Vector Quantization 3*

**Description**

Moves examples in a codebook to better represent the training set.

**Usage**

```r
lvq3(x, cl, codebk, niter = 100*nrow(codebk$x), alpha = 0.03, win = 0.3, epsilon = 0.1)
```

**Arguments**

- `x`: a matrix or data frame of examples
- `cl`: a vector or factor of classifications for the examples
- `codebk`: a codebook
- `niter`: number of iterations
- `alpha`: constant for training
- `win`: a tolerance for the closeness of the two nearest vectors.
- `epsilon`: proportion of move for correct vectors

**Details**

Selects `niter` examples at random with replacement, and adjusts the nearest two examples in the codebook for each.

**Value**

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.
References


See Also

lvqinit, lvq1, olvq1, lvq2, lvqtest

Examples

```r
train <- rbind(iris3[,1:25,1], iris3[,1:25,2], iris3[,1:25,3])
set <- rbind(iris3[,26:50,1], iris3[,26:50,2], iris3[,26:50,3])
c1 <- factor(c(rep("s", 25), rep("c", 25), rep("v", 25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd0 <- olvq1(train, cl, cd)
lvqtest(cd0, train)
cd3 <- lvq3(train, cl, cd)
lvqtest(cd3, train)
```

**Description**

Construct an initial codebook for LVQ methods.

**Usage**

`lvqinit(x, cl, size, prior, k = 5)`

**Arguments**

- `x`: a matrix or data frame of training examples, n by p.
- `cl`: the classifications for the training examples. A vector or factor of length n.
- `size`: the size of the codebook. Defaults to min(round(0.4*ng*(ng-1 + p/2),0), n) where ng is the number of classes.
- `prior`: Probabilities to represent classes in the codebook. Default proportions in the training set.
- `k`: k used for k-NN test of correct classification. Default is 5.

**Details**

Selects size examples from the training set without replacement with proportions proportional to the prior or the original proportions.

**Value**

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.
References


See Also

lvq1, lvq2, lvq3, olvq1, lvqtest

Examples

```r
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
c1 <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, c1, 10)
 lvqtest(cd, train)
cd1 <- olvq1(train, c1, cd)
lvqtest(cd1, train)
```

---

**lvqtest**

**Classify Test Set from LVQ Codebook**

Description

Classify a test set by 1-NN from a specified LVQ codebook.

Usage

```
lvqtest(codebk, test)
```

Arguments

- `codebk`: codebook object returned by other LVQ software
- `test`: matrix of test examples

Details

Uses 1-NN to classify each test example against the codebook.

Value

Factor of classification for each row of `x`

References

**multiedit**

**See Also**

lvqinit, olvq1

**Examples**

```r
# The function is currently defined as
function(codebk, test) knn(codebk$x, test, codebk$cl)
```

---

**multiedit**  
*Multiedit for k-NN Classifier*

**Description**

Multiedit for k-NN classifier

**Usage**

```r
multiedit(x, class, k = 1, V = 3, I = 5, trace = TRUE)
```

**Arguments**

- `x`: matrix of training set.
- `class`: vector of classification of training set.
- `k`: number of neighbours used in k-NN.
- `V`: divide training set into V parts.
- `I`: number of null passes before quitting.
- `trace`: logical for statistics at each pass.

**Value**

Index vector of cases to be retained.

**References**


**See Also**

condense, reduce.nn
Examples

```r
tr <- sample(1:50, 25)
train <- rbind(iris3[, tr, 1], iris3[, tr, 2], iris3[, tr, 3])
test <- rbind(iris3[-tr, , 1], iris3[-tr, , 2], iris3[-tr, , 3])
cl <- factor(c(rep(1, 25), rep(2, 25), rep(3, 25)), labels=c("s", "c", "v"))
table(cl, knn(train, test, cl, 3))
ind1 <- multiedit(train, cl, 3)
length(ind1)
table(cl, knn(train[ind1, , drop=FALSE], test, cl[ind1], 1))
ntrain <- train[ind1, ]; ncl <- cl[ind1]
ind2 <- condense(ntrain, ncl)
length(ind2)
table(cl, knn(ntrain[ind2, , drop=FALSE], test, ncl[ind2], 1))
```

olvq1

Optimized Learning Vector Quantization 1

Description

Moves examples in a codebook to better represent the training set.

Usage

```r
olvq1(x, cl, codebk, niter = 40 * nrow(codebk$x), alpha = 0.3)
```

Arguments

- `x`: a matrix or data frame of examples
- `cl`: a vector or factor of classifications for the examples
- `codebk`: a codebook
- `niter`: number of iterations
- `alpha`: constant for training

Details

Selects `niter` examples at random with replacement, and adjusts the nearest example in the codebook for each.

Value

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

References

reduce.nn

**Reduce Training Set for a k-NN Classifier**

**Description**
Reduce training set for a k-NN classifier. Used after condense.

**Usage**

\[
\text{reduce.nn}(\text{train, ind, class})
\]

**Arguments**

- `train`: matrix for training set
- `ind`: Initial list of members of the training set (from condense).
- `class`: vector of classifications for test set

**Details**

All the members of the training set are tried in random order. Any which when dropped do not cause any members of the training set to be wrongly classified are dropped.

**Value**

Index vector of cases to be retained.

**References**


**See Also**

- `condense`, `multiedit`
Examples

```r
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s", 25), rep("c", 25), rep("v", 25)))
keep <- condense(train, cl)
nkn(train[keep,], test, cl[keep])
keep2 <- reduce.nn(train, keep, cl)
nkn(train[keep2,], test, cl[keep2])
```

SOM

Self-Organizing Maps: Online Algorithm

Description

Kohonen's Self-Organizing Maps are a crude form of multidimensional scaling.

Usage

```r
SOM(data, grid = somgrid(), rlen = 10000, alpha, radii, init)
```

Arguments

- **data**: a matrix or data frame of observations, scaled so that Euclidean distance is appropriate.
- **grid**: A grid for the representatives: see `somgrid`.
- **rlen**: the number of updates: used only in the defaults for `alpha` and `radii`.
- **alpha**: the amount of change: one update is done for each element of alpha. Default is to decline linearly from 0.05 to 0 over `rlen` updates.
- **radii**: the radii of the neighbourhood to be used for each update: must be the same length as `alpha`. Default is to decline linearly from 4 to 1 over `rlen` updates.
- **init**: the initial representatives. If missing, chosen (without replacement) randomly from `data`.

Details

`alpha` and `radii` can also be lists, in which case each component is used in turn, allowing two- or more phase training.

Value

An object of class "SOM" with components

- **grid**: the grid, an object of class "somgrid".
- **codes**: a matrix of representatives.
References


See Also

somgrid, batchSOM

Examples

require(graphics)
data(crabs, package = "MASS")

lcrabs <- log(crabs[, 4:8])
crabs.grp <- factor(c("B", "b", "O", "o") [rep(1:4, rep(50,4))])
gr <- somgrid(topo = "hexagonal")
crabs.som <- SOM(lcrabs, gr)
plot(crabs.som)

## 2-phase training

crabs.som2 <- SOM(lcrabs, gr,
alpha = list(seq(0.05, 0, length.out = 1e4), seq(0.02, 0, length.out = 1e5)),
radii = list(seq(8, 1, length.out = 1e4), seq(4, 1, length.out = 1e5)))
plot(crabs.som2)

somgrid

Plot SOM Fits

Description

Plotting functions for SOM results.

Usage

somgrid(xdim = 8, ydim = 6, topo = c("rectangular", "hexagonal"))

## S3 method for class 'somgrid'
plot(x, type = "p", ...)

## S3 method for class 'SOM'
plot(x, ...)

Arguments

xdim, ydim dimensions of the grid
topo the topology of the grid.x an object inheriting from class "somgrid" or "SOM".
type, ... graphical parameters.
The class "somgrid" records the coordinates of the grid to be used for (batch or on-line) SOM: this has a plot method. The plot method for class "SOM" plots a stars plot of the representative at each grid point.

Value

For somgrid, an object of class "somgrid", a list with components

pts a two-column matrix giving locations for the grid points.
xdim, ydim, topo as in the arguments to somgrid.

References


See Also

batchSOM, SOM
Chapter 20

The cluster package

agnes

Agglomerative Nesting (Hierarchical Clustering)

Description

Computes agglomerative hierarchical clustering of the dataset.

Usage

agnes(x, diss = inherits(x, "dist"), metric = "euclidean",
        stand = FALSE, method = "average", par.method,
        keep.diss = n < 100, keep.data = !diss, trace.lev = 0)

Arguments

x  data matrix or data frame, or dissimilarity matrix, depending on the value of the
diss argument.
   In case of a matrix or data frame, each row corresponds to an observation, and
each column corresponds to a variable. All variables must be numeric. Missing
values (NAs) are allowed.
   In case of a dissimilarity matrix, x is typically the output of daisy or dist.
   Also a vector with length n*(n-1)/2 is allowed (where n is the number of ob-
servations), and will be interpreted in the same way as the output of the above-
mentioned functions. Missing values (NAs) are not allowed.

diss  logical flag: if TRUE (default for dist or dissimilarity objects), then x is
       assumed to be a dissimilarity matrix. If FALSE, then x is treated as a matrix of
       observations by variables.

metric  character string specifying the metric to be used for calculating dissimilarities
        between observations. The currently available options are "euclidean" and
        "manhattan". Euclidean distances are root sum-of-squares of differences, and
        manhattan distances are the sum of absolute differences. If x is already a dis-
        similarity matrix, then this argument will be ignored.

stand  logical flag: if TRUE, then the measurements in x are standardized before cal-
        culating the dissimilarities. Measurements are standardized for each variable
agnes (column), by subtracting the variable’s mean value and dividing by the variable’s mean absolute deviation. If \( x \) is already a dissimilarity matrix, then this argument will be ignored.

**method** character string defining the clustering method. The six methods implemented are "average" ([unweighted pair]-group [arithMetic] average method, aka 'UPGMA'), "single" (single linkage), "complete" (complete linkage), "ward" (Ward’s method), "weighted" (weighted average linkage, aka 'WPGMA'), its generalization "flexible" which uses (a constant version of) the Lance-Williams formula and the par.method argument, and "gaverage" a generalized "average" aka “flexible UPGMA” method also using the Lance-Williams formula and par.method.

The default is "average".

**par.method** If method is "flexible" or "gaverage", a numeric vector of length 1, 3, or 4, (with a default for "gaverage"), see in the details section.

**keep.diss, keep.data** logicals indicating if the dissimilarities and/or input data \( x \) should be kept in the result. Setting these to FALSE can give much smaller results and hence even save memory allocation time.

**trace.lev** integer specifying a trace level for printing diagnostics during the algorithm. Default 0 does not print anything; higher values print increasingly more.

### Details

**agnes** is fully described in chapter 5 of Kaufman and Rousseeuw (1990). Compared to other agglomerative clustering methods such as hclust, agnes has the following features: (a) it yields the agglomerative coefficient (see **agnes.object**) which measures the amount of clustering structure found; and (b) apart from the usual tree it also provides the banner, a novel graphical display (see **plot.agnes**).

The agnes-algorithm constructs a hierarchy of clusterings. At first, each observation is a small cluster by itself. Clusters are merged until only one large cluster remains which contains all the observations. At each stage the two nearest clusters are combined to form one larger cluster.

For method="average", the distance between two clusters is the average of the dissimilarities between the points in one cluster and the points in the other cluster.

In method="single", we use the smallest dissimilarity between a point in the first cluster and a point in the second cluster (nearest neighbor method).

When method="complete", we use the largest dissimilarity between a point in the first cluster and a point in the second cluster (furthest neighbor method).

The method = "flexible" allows (and requires) more details: The Lance-Williams formula specifies how dissimilarities are computed when clusters are agglomerated (equation (32) in K&R(1990), p.237). If clusters \( C_1 \) and \( C_2 \) are agglomerated into a new cluster, the dissimilarity between their union and another cluster \( Q \) is given by

\[
D(C_1 \cup C_2, Q) = \alpha_1 \ast D(C_1, Q) + \alpha_2 \ast D(C_2, Q) + \beta \ast D(C_1, C_2) + \gamma \ast |D(C_1, Q) - D(C_2, Q)|,
\]

where the four coefficients \((\alpha_1, \alpha_2, \beta, \gamma)\) are specified by the vector par.method, either directly as vector of length 4, or (more conveniently) if par.method is of length 1, say \( \alpha \), par.method is extended to give the “Flexible Strategy” (K&R(1990), p.236 f) with Lance-Williams coefficients \((\alpha_1 = \alpha_2 = \alpha, \beta = 1 - 2\alpha, \gamma = 0)\).

Also, if length(par.method) == 3, \( \gamma = 0 \) is set.
Care and expertise is probably needed when using method = "flexible" particularly for the case when par.method is specified of longer length than one. Since cluster version 2.0, choices leading to invalid merge structures now signal an error (from the C code already). The weighted average (method="weighted") is the same as method="flexible", par.method = 0.5. Further, method="single" is equivalent to method="flexible", par.method = c(.5, .5, 0, -.5), and method="complete" is equivalent to method="flexible", par.method = c(.5, .5, 0, +.5).

The method = "gaverage" is a generalization of "average", aka “flexible UPGMA" method, and is (a generalization of the approach) detailed in Belbin et al. (1992). As "flexible", it uses the Lance-Williams formula above for dissimilarity updating, but with $\alpha_1$ and $\alpha_2$ not constant, but proportional to the sizes $n_1$ and $n_2$ of the clusters $C_1$ and $C_2$ respectively, i.e,

$$\alpha_j = \alpha'_j \frac{n_1}{n_1 + n_2},$$

where $\alpha'_1$, $\alpha'_2$ are determined from par.method, either directly as $(\alpha_1, \alpha_2, \beta, \gamma)$ or $(\alpha_1, \alpha_2, \beta)$ with $\gamma = 0$, or (less flexibly, but more conveniently) as follows:

Belbin et al proposed “flexible beta”, i.e. the user would only specify $\beta$ (as par.method), sensibly in

$$-1 \leq \beta < 1,$$

and $\beta$ determines $\alpha'_1$ and $\alpha'_2$ as

$$\alpha'_j = 1 - \beta,$$

and $\gamma = 0$.

This $\beta$ may be specified by par.method (as length 1 vector), and if par.method is not specified, a default value of -0.1 is used, as Belbin et al recommend taking a $\beta$ value around -0.1 as a general agglomerative hierarchical clustering strategy.

Note that method = "gaverage", par.method = 0 (or par.method = c(1, 1, 0, 0)) is equivalent to the agnes() default method "average".

Value

an object of class "agnes" (which extends "twins") representing the clustering. See agnes.object for details, and methods applicable.

BACKGROUND

Cluster analysis divides a dataset into groups (clusters) of observations that are similar to each other.

Hierarchical methods like agnes, diana, and mona construct a hierarchy of clusterings, with the number of clusters ranging from one to the number of observations.

Partitioning methods like pam, clara, and fanny require that the number of clusters be given by the user.

Author(s)

Method "gaverage" has been contributed by Pierre Roudier, Landcare Research, New Zealand.

References


**See Also**

`agnes.object`, `daisy`, `diana`, `dist`, `hclust`, `plot.agnes`, `twins.object`.

**Examples**

```r
data(votes.repub)
agn1 <- agnes(votes.repub, metric = "manhattan", stand = TRUE)
agn1
plot(agn1)

op <- par(mfrow=c(2,2))
agn2 <- agnes(daisy(votes.repub), diss = TRUE, method = "complete")
plot(agn2)
## alpha = 0.625 ==> beta = -1/4 is "recommended" by some
agn5 <- agnes(votes.repub, method = "flexible", par.meth = 0.625)
plot(agn5)
par(op)

## "show" equivalence of three "flexible" special cases
d.vr <- daisy(votes.repub)
a.wgt <- agnes(d.vr, method = "weighted")
a.sing <- agnes(d.vr, method = "single")
a.comp <- agnes(d.vr, method = "complete")
iC <- -(6:7) # not using 'call' and 'method' for comparisons
stopifnot(
  all.equal(a.wgt[iC], agnes(d.vr, method="flexible", par.method = 0.5)[iC]) ,
  all.equal(a.sing[iC], agnes(d.vr, method="flex", par.method= c(.5,.5,0,-.5))[iC]),
  all.equal(a.comp[iC], agnes(d.vr, method="flex", par.method= c(.5,.5,0,.5))[iC])
)

## Exploring the dendrogram structure
(d2 <- as.dendrogram(agn2)) # two main branches
d2[[1]] # the first branch
d2[[2]] # the 2nd one { 8 + 42 = 50 }
d2[[1]][[1]][[1]] # first sub-branch of branch 1 .. and shorter form
identical(d2[[c(1,1)]], d2[[1]][[1]][[1]])

## a "textual picture" of the dendrogram :
str(d2)

data(agriculture)

## Plot similar to Figure 7 in ref
## Not run: plot(agnes(agriculture), ask = TRUE)

data(animals)
aa.a <- agnes(animals) # default method = "average"
aa.ga <- agnes(animals, method = "gaverage")
```
The objects of class "agnes" represent an agglomerative hierarchical clustering of a dataset.

A legitimate agnes object is a list with the following components:

- **order**: a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
- **order.lab**: a vector similar to `order`, but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
- **height**: a vector with the distances between merging clusters at the successive stages.
- **ac**: the agglomerative coefficient, measuring the clustering structure of the dataset. For each observation i, denote by m(i) its dissimilarity to the first cluster it is merged with, divided by the dissimilarity of the merger in the final step of the algorithm. The ac is the average of all 1 - m(i). It can also be seen as the average width (or the percentage filled) of the banner plot. Because ac grows with the number of observations, this measure should not be used to compare datasets of very different sizes.
- **merge**: an (n-1) by 2 matrix, where n is the number of observations. Row i of `merge` describes the merging of clusters at step i of the clustering. If a number j in the row is negative, then the single observation |j| is merged at this stage. If j is positive, then the merger is with the cluster formed at stage j of the algorithm.
- **diss**: an object of class "dissimilarity" (see `dissimilarity.object`), representing the total dissimilarity matrix of the dataset.
- **data**: a matrix containing the original or standardized measurements, depending on the `stand` option of the function `agnes`. If a dissimilarity matrix was given as input structure, then this component is not available.

This class of objects is returned from `agnes`. 
METHODS

The "agnes" class has methods for the following generic functions: print, summary, plot, and as.dendrogram.

In addition, cutree(x, *) can be used to "cut" the dendrogram in order to produce cluster assignments.

INHERITANCE

The class "agnes" inherits from "twins". Therefore, the generic functions pltree and as.hclust are available for agnes objects. After applying as.hclust(), all its methods are available, of course.

See Also

agnes, diana, as.hclust, hclust, plot.agnes, twins.object.
cutree.

Examples

data(agriculture)
ag.ag <- agnes(agriculture)
class(ag.ag)
pltree(ag.ag) # the dendrogram

## cut the dendrogram -> get cluster assignments:
(ck3 <- cutree(ag.ag, k = 3))
(ch6 <- cutree(as.hclust(ag.ag), h = 6))
stopifnot(identical(unname(ch6), ck3))

agriculture                      European Union Agricultural Workforces

Description

Gross National Product (GNP) per capita and percentage of the population working in agriculture for each country belonging to the European Union in 1993.

Usage

data(agriculture)

Format

A data frame with 12 observations on 2 variables:

| . [,1] x         | numeric | per capita GNP |
| . [,2] y         | numeric | percentage in agriculture |

The row names of the data frame indicate the countries.
Details

The data seem to show two clusters, the “more agricultural” one consisting of Greece, Portugal, Spain, and Ireland.

Source


References

see those in agnes.

See Also

agnes, daisy, diana.

Examples

data(animals)

## Compute the dissimilarities using Euclidean metric and without
## standardization
daisy(animals, metric = "euclidean", stand = FALSE)

## 2nd plot is similar to Figure 3 in Struyf et al (1996)
plot(pam(animals, 2))

## Plot similar to Figure 7 in Struyf et al (1996)
## Not run: plot(agnes(animals), ask = TRUE)

## Plot similar to Figure 8 in Struyf et al (1996)
## Not run: plot(diana(animals), ask = TRUE)

animals
<table>
<thead>
<tr>
<th>Attributes of Animals</th>
</tr>
</thead>
<tbody>
<tr>
<td>animals</td>
</tr>
</tbody>
</table>

Description

This data set considers 6 binary attributes for 20 animals.

Usage

data(animals)
Format

A data frame with 20 observations on 6 variables:

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
</tr>
</thead>
<tbody>
<tr>
<td>.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>.1</td>
<td>war</td>
<td>warm-blooded</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>.2</td>
<td>fly</td>
<td>can fly</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>.3</td>
<td>ver</td>
<td>vertebrate</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>.4</td>
<td>end</td>
<td>endangered</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>.5</td>
<td>gro</td>
<td>live in groups</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>.6</td>
<td>hai</td>
<td>have hair</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

All variables are encoded as 1 = 'no', 2 = 'yes'.

Details

This dataset is useful for illustrating monothetic (only a single variable is used for each split) hierarchical clustering.

Source


References

see Struyf, Hubert & Rousseeuw (1996), in *agnes*.

Examples

```r
data(animals)
apply(animals,2, table) # simple overview

ma <- mona(animals)
ma
## Plot similar to Figure 10 in Struyf et al (1996)
plot(ma)
```

---

**bannerplot**

*Plot Banner (of Hierarchical Clustering)*

Description

Draws a “banner”, i.e. basically a horizontal *barplot* visualizing the (agglomerative or divisive) hierarchical clustering or an other binary dendrogram structure.

Usage

```r
bannerplot(x, w = rev(x$height), fromLeft = TRUE,
           main=NULL, sub=NULL, xlab = "Height", adj = 0,
           col = c(2, 0), border = 0, axes = TRUE, frame.plot = axes,
           rev.xax = !fromLeft, xax.pretty = TRUE,
           labels = NULL, nmax.lab = 35, max.strlen = 5,
           yax.do = axes && length(x$order) <= nmax.lab,
           yaxRight = fromLeft, y.mar = 2.4 + max.strlen/2.5, ...)
```
Arguments

- **x**: a list with components `order`, `order.lab` and `height` when `w`, the next argument is not specified.
- **w**: non-negative numeric vector of bar widths.
- **fromLeft**: logical, indicating if the banner is from the left or not.
- **main, sub**: main and sub titles, see `title`.
- **xlab**: x axis label (with ‘correct’ default e.g. for `plot.agnes`).
- **adj**: passed to `title(main, sub)` for string adjustment.
- **col**: vector of length 2, for two horizontal segments.
- **border**: color for bar border; now defaults to background (no border).
- **axes**: logical indicating if axes (and labels) should be drawn at all.
- **frame.plot**: logical indicating the banner should be framed; mainly used when `border = 0` (as per default).
- **rev.xax**: logical indicating if the x axis should be reversed (as in `plot.diana`).
- **xax.pretty**: logical or integer indicating if `pretty()` should be used for the x axis. `xax.pretty = FALSE` is mainly for back compatibility.
- **labels**: labels to use on y-axis; the default is constructed from `x`.
- **nmax.lab**: integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
- **max.strlen**: positive integer giving the length to which strings are truncated in banner plot labeling.
- **yax.do**: logical indicating if a y axis and banner labels should be drawn.
- **yaxRight**: logical indicating if the y axis is on the right or left.
- **y.mar**: positive number specifying the margin width to use when banners are labeled (along a y-axis). The default adapts to the string width and optimally would also depend on the font.
- **...**: graphical parameters (see `par`) may also be supplied as arguments to this function.

**Note**

This is mainly a utility called from `plot.agnes`, `plot.diana` and `plot.mona`.

**Author(s)**

Martin Maechler (from original code of Kaufman and Rousseeuw).

**Examples**

```r
data(agriculture)
bannerplot(agnes(agriculture), main = "Bannerplot")```
chorSub

Subset of C-horizon of Kola Data

Description

This is a small rounded subset of the C-horizon data `chorizon` from package `mvoutlier`.

Usage

```r
data(chorSub)
```

Format

A data frame with 61 observations on 10 variables. The variables contain scaled concentrations of chemical elements.

Details

This data set was produced from `chorizon` via these statements:

```r
data(chorizon, package = "mvoutlier")
chorSub <- round(100*scale(chorizon[,101:110]))[190:250,]
storage.mode(chorSub) <- "integer"
colnames(chorSub) <- gsub("_*", ",", colnames(chorSub))
```

Source


See Also

`chorizon` in package `mvoutlier` and other Kola data in the same package.

Examples

```r
data(chorSub)
summary(chorSub)
pairs(chorSub, gap = .1)# some outliers
```
Description

Computes a "clara" object, a list representing a clustering of the data into \( k \) clusters.

Usage

```r
clara(x, k, metric = c("euclidean", "manhattan", "jaccard"),
      stand = FALSE, cluster.only = FALSE, samples = 5,
      sampsize = min(n, 40 + 2 * k), trace = 0, medoids.x = TRUE,
      keep.data = medoids.x, rngR = FALSE, pamLike = FALSE, correct.d = TRUE)
```

Arguments

- **x**: data matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed.
- **k**: integer, the number of clusters. It is required that \( 0 < k < n \) where \( n \) is the number of observations (i.e., \( n = \text{nrow}(x) \)).
- **metric**: character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean", "manhattan", and "jaccard". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences.
- **stand**: logical, indicating if the measurements in \( x \) are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable’s mean value and dividing by the variable’s mean absolute deviation.
- **cluster.only**: logical; if true, only the clustering will be computed and returned, see details.
- **samples**: integer, say \( N \), the number of samples to be drawn from the dataset. The default, \( N = 5 \), is rather small for historical (and now back compatibility) reasons and we recommend to set samples an order of magnitude larger.
- **sampsize**: integer, say \( j \), the number of observations in each sample. sampsize should be higher than the number of clusters \( (k) \) and at most the number of observations \( (n = \text{nrow}(x)) \). While computational effort is proportional to \( j^2 \), see note below, it may still be advisable to set \( j = \text{sampsize} \) to a larger value than the (historical) default.
- **trace**: integer indicating a trace level for diagnostic output during the algorithm.
- **medoids.x**: logical indicating if the medoids should be returned, identically to some rows of the input data \( x \). If FALSE, keep. data must be false as well, and the medoid indices, i.e., row numbers of the medoids will still be returned (i.e. med component), and the algorithm saves space by needing one copy less of \( x \).
- **keep.data**: logical indicating if the (scaled if stand is true) data should be kept in the result. Setting this to FALSE saves memory (and hence time), but disables clusplot()ing of the result. Use medoids.x = FALSE to save even more memory.
logical indicating if R’s random number generator should be used instead of the primitive clara()-builtin one. If true, this also means that each call to clara() returns a different result – though only slightly different in good situations.

pamLike logical indicating if the “swap” phase (see pam, in C code) should use the same algorithm as pam(). Note that from Kaufman and Rousseeuw’s description this should have been true always, but as the original Fortran code and the subsequent port to C has always contained a small one-letter change (a typo according to Martin Maechler) with respect to PAM, the default, pamLike = FALSE has been chosen to remain back compatible rather than “PAM compatible”.

correct.d logical or integer indicating that—only in the case of NAs present in x—the correct distance computation should be used instead of the wrong formula which has been present in the original Fortran code and been in use up to early 2016. Because the new correct formula is not back compatible, for the time being, a warning is signalled in this case, unless the user explicitly specifies correct.d.

Details

clara is fully described in chapter 3 of Kaufman and Rousseeuw (1990). Compared to other partitioning methods such as pam, it can deal with much larger datasets. Internally, this is achieved by considering sub-datasets of fixed size (sampsize) such that the time and storage requirements become linear in \( n \) rather than quadratic.

Each sub-dataset is partitioned into \( k \) clusters using the same algorithm as in pam. Once \( k \) representative objects have been selected from the sub-dataset, each observation of the entire dataset is assigned to the nearest medoid.

The mean (equivalent to the sum) of the dissimilarities of the observations to their closest medoid is used as a measure of the quality of the clustering. The sub-dataset for which the mean (or sum) is minimal, is retained. A further analysis is carried out on the final partition.

Each sub-dataset is forced to contain the medoids obtained from the best sub-dataset until then. Randomly drawn observations are added to this set until sampsize has been reached.

When cluster.only is true, the result is simply a (possibly named) integer vector specifying the clustering, i.e., clara(x,k, cluster.only=TRUE) is the same as clara(x,k)$clustering but computed more efficiently.

Value

If cluster.only is false (as by default), an object of class "clara" representing the clustering. See clara.object for details.

If cluster.only is true, the result is the "clustering", an integer vector of length \( n \) with entries from 1:k.

Note

By default, the random sampling is implemented with a very simple scheme (with period \( 2^{16} = 65536 \)) inside the Fortran code, independently of R’s random number generation, and as a matter of fact, deterministically. Alternatively, we recommend setting rngR = TRUE which uses R’s random number generators. Then, clara() results are made reproducible typically by using set.seed() before calling clara.

The storage requirement of clara computation (for small \( k \)) is about \( O(n \times p) + O(j^2) \) where \( j = \text{sampsize} \), and \( (n, p) = \text{dim}(x) \). The CPU computing time (again assuming small \( k \)) is about \( O(n \times p \times j^2 \times N) \), where \( N = \text{samples} \).
For “small” datasets, the function `pam` can be used directly. What can be considered small, is really a function of available computing power, both memory (RAM) and speed. Originally (1990), “small” meant less than 100 observations; in 1997, the authors said “small (say with fewer than 200 observations)”; as of 2006, you can use `pam` with several thousand observations.

Author(s)

Kaufman and Rousseeuw (see `agnes`), originally. Metric "jaccard": Kamil Kozłowski (@ownedoutcomes.com) and Kamil Jadeszko. All arguments from `trace` on, and most `R` documentation and all tests by Martin Maechler.

See Also

`agnes` for background and references; `clara.object`, `pam`, `partition.object`, `plot.partition`.

Examples

## generate 500 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(200,0,8), rnorm(200,0,8)),
cbind(rnorm(300,50,8), rnorm(300,50,8)))
clarax <- clara(x, 2, samples=50)
clarax
clarax$clusinfo
## using pamLike=TRUE gives the same (apart from the 'call'):
all.equal(clarax[-8],
clairax(x, 2, samples=50, pamLike = TRUE)[-8])
plot(clarax)
## cluster.only = TRUE -- save some memory/time :
clclus <- clara(x, 2, samples=50, cluster.only = TRUE)
stopifnot(identical(clclus, clarax$clustering))

## 'xclara' is an artificial data set with 3 clusters of 1000 bivariate
## objects each.
data(xclara)
(clx3 <- clara(xclara, 3))
## "better" number of samples
c1.3 <- clara(xclara, 3, samples=100)
## but that did not change the result here:
stopifnot(c1.3clcustering == clx3$clustering)
## Plot similar to Figure 5 in Struyf et al (1996)
## Not run: plot(clx3, ask = TRUE)
## Try 100 times *different* random samples -- for reliability:
nSim <- 100
nCl <- 3 # = no.classes
set.seed(421)# (reproducibility)
c1 <- matrix(NA,nrow(xclara), nSim)
for(i in 1:nSim)
  c1[,i] <- clara(xclara, nCl, medoids.x = FALSE, rngR = TRUE)$cluster
tcl <- apply(c1,1, tabulate, nbins = nCl)
## those that are not always in same cluster (5 out of 3000 for this seed):
(iDoubt <- which(apply(tcl,2, function(n) all(n < nSim)))
if(length(iDoubt)) { # (not for all seeds)
clara.object

Clustering Large Applications (CLARA) Object

Description

The objects of class "clara" represent a partitioning of a large dataset into clusters and are typically returned from clara.

Value

A legitimate clara object is a list with the following components:

- **sample**: labels or case numbers of the observations in the best sample, that is, the sample used by the clara algorithm for the final partition.
- **medoids**: the medoids or representative objects of the clusters. It is a matrix with in each row the coordinates of one medoid. Possibly NULL, namely when the object resulted from clara(*, medoids.x=FALSE). Use the following i.med in that case.
- **i.med**: the indices of the medoids above: medoids <- x[i.med,] where x is the original data matrix in clara(x,*)
- **clustering**: the clustering vector, see partition.object.
- **objective**: the objective function for the final clustering of the entire dataset.
- **clusinfo**: matrix, each row gives numerical information for one cluster. These are the cardinality of the cluster (number of observations), the maximal and average dissimilarity between the observations in the cluster and the cluster’s medoid. The last column is the maximal dissimilarity between the observations in the cluster and the cluster’s medoid, divided by the minimal dissimilarity between the cluster’s medoid and the medoid of any other cluster. If this ratio is small, the cluster is well-separated from the other clusters.
- **diss**: dissimilarity (maybe NULL), see partition.object.
- **silinfo**: list with silhouette width information for the best sample, see partition.object.
- **call**: generating call, see partition.object.
- **data**: matrix, possibly standardized, or NULL, see partition.object.

Methods, Inheritance

The "clara" class has methods for the following generic functions: print, summary.

The class "clara" inherits from "partition". Therefore, the generic functions plot and clusplot can be used on a clara object.

See Also

clara, dissimilarity.object, partition.object, plot.partition.
clusGap() calculates a goodness of clustering measure, the "gap" statistic. For each number of clusters \( k \), it compares \( \log(W(k)) \) with \( E^\star[\log(W(k))] \) where the latter is defined via bootstrapping, i.e., simulating from a reference \((H_0)\) distribution, a uniform distribution on the hypercube determined by the ranges of \( x \), after first centering, and then \( \text{svd} \) (aka 'PCA')-rotating them when (as by default) \( \text{spaceH0} = "scaledPCA" \).

\[ \text{maxSE}(f, SE.f) \] determines the location of the maximum of \( f \), taking a "1-SE rule" into account for the \(*SE*\) methods. The default method "firstSEmax" looks for the smallest \( k \) such that its value \( f(k) \) is not more than 1 standard error away from the first local maximum. This is similar but not the same as "Tibs2001SEmax", Tibshirani et al’s recommendation of determining the number of clusters from the gap statistics and their standard deviations.

### Usage

```r
clusGap(x, FUNcluster, K.max, B = 100, d.power = 1,
        spaceH0 = c("scaledPCA", "original"),
        verbose = interactive(), ...)
```

```r
maxSE(f, SE.f,
      method = c("firstSEmax", "Tibs2001SEmax", "globalSEmax",
                 "firstmax", "globalmax"),
      SE.factor = 1)
```

```r
## S3 method for class 'clusGap'
print(x, method = "firstSEmax", SE.factor = 1, ...)
```

```r
## S3 method for class 'clusGap'
plot(x, type = "b", xlab = "k", ylab = expression(Gap[k]),
     main = NULL, do.arrows = TRUE,
     arrowArgs = list(col="red3", length=1/16, angle=90, code=3), ...)
```

### Arguments

- **x**: numeric matrix or \texttt{data.frame}.
- **FUNcluster**: a \texttt{function} which accepts as first argument a (data) matrix like \( x \), second argument, say \( k, k \geq 2 \), the number of clusters desired, and returns a \texttt{list} with a component named (or shortened to) \texttt{cluster} which is a vector of length \( n = \text{nrow}(x) \) of integers in 1:k determining the clustering or grouping of the \( n \) observations.
- **K.max**: the maximum number of clusters to consider, must be at least two.
- **B**: integer, number of Monte Carlo ("bootstrap") samples.
- **d.power**: a positive integer specifying the power \( p \) which is applied to the euclidean distances (\texttt{dist}) before they are summed up to give \( W(k) \). The default, \( d.\text{power} = 1 \), corresponds to the “historical” \texttt{R} implementation, whereas \( d.\text{power} = 2 \) corresponds to what Tibshirani et al had proposed. This was found by Juan Gonzalez, in 2016-02.
spaceH0  a character string specifying the space of the $H_0$ distribution (of no cluster). Both “scaledPCA” and “original” use a uniform distribution in a hyper cube and had been mentioned in the reference; “original” been added after a proposal (including code) by Juan Gonzalez.

verbose  integer or logical, determining if “progress” output should be printed. The default prints one bit per bootstrap sample.

... (for clusGap():) optionally further arguments for FUNcluster(), see kmeans example below.

f  numeric vector of ‘function values’, of length $K$, whose (“1 SE respected”) maximum we want.

SE.f  numeric vector of length $K$ of standard errors of $f$.

method  character string indicating how the “optimal” number of clusters, $\hat{k}$, is computed from the gap statistics (and their standard deviations), or more generally how the location $\hat{k}$ of the maximum of $f_k$ should be determined.

"globalmax": simply corresponds to the global maximum, i.e., is which.max(f)

"firstmax": gives the location of the first local maximum.

"Tibs2001SEmax": uses the criterion, Tibshirani et al (2001) proposed: “the smallest $k$ such that $f(k) \geq f(k+1) - s_{k+1}$”. Note that this chooses $k = 1$ when all standard deviations are larger than the differences $f(k+1) - f(k)$.

"firstSEmax": location of the first $f()$ value which is not smaller than the first local maximum minus SE.factor * SE.f[], i.e, within an “f S.E.” range of that maximum (see also SE.factor).

This, the default, has been proposed by Martin Maechler in 2012, when adding clusGap() to the cluster package, after having seen the “globalSEmax” proposal (in code) and read the "Tibs2001SEmax” proposal.

"globalSEmax": (used in Dudoit and Fridlyand (2002), supposedly following Tibshirani’s proposition): location of the first $f()$ value which is not smaller than the global maximum minus SE.factor * SE.f[], i.e, within an “f S.E.” range of that maximum (see also SE.factor).

See the examples for a comparison in a simple case.

SE.factor  [When method contains ”SE”] Determining the optimal number of clusters, Tibshirani et al. proposed the “1 S.E.”-rule. Using an SE.factor $f$, the “fS.E.”-rule is used, more generally.

type, xlab, ylab, main  arguments with the same meaning as in plot.default(), with different default.

do.arrows  logical indicating if (1 SE-)”error bars” should be drawn, via arrows().

arrowArgs  a list of arguments passed to arrows(); the default, notably angle and code, provide a style matching usual error bars.

Details

The main result <res>$Tab[,”gap”] of course is from bootstrapping aka Monte Carlo simulation and hence random, or equivalently, depending on the initial random seed (see set.seed()). On the other hand, in our experience, using $B = 500$ gives quite precise results such that the gap plot is basically unchanged after an another run.
clusGap

Value

clusGap(...) returns an object of S3 class "clusGap", basically a list with components

Tab

a matrix with K.max rows and 4 columns, named "logW", "E.logW", "gap", and "SE.sim", where gap = E.logW - logW, and SE.sim corresponds to the standard error of gap, SE.sim[k] = s_k, where s_k := \sqrt{1/B sd^*(gap)} and sd^*(\cdot) is the standard deviation of the simulated ("bootstrapped") gap values.

call

the clusGap(...) call.

spaceH0

the spaceH0 argument (match.arg()ed).

n

number of observations, i.e., nrow(x).

B

input B

FUNcluster

input function FUNcluster

Author(s)

This function is originally based on the functions gap of former (Bioconductor) package SAGx by Per Broberg, gapStat() from former package SLmisc by Matthias Kohl and ideas from gap() and its methods of package lga by Justin Harrington.

The current implementation is by Martin Maechler.

The implementation of spaceH0 = "original" is based on code proposed by Juan Gonzalez.

References


See Also

silhouette for a much simpler less sophisticated goodness of clustering measure.

cluster.stats() in package fpc for alternative measures.

Examples

### --- maxSE() methods -------------------------------------------
(mets <- eval(formals(maxSE)$method))
fk <- c(2,3,5,4,7,8,5,4)
sk <- c(1,1,2,1,1,3,1,1)/2

# use plot.clusGap():
plot(structure(class="clusGap", list(Tab = cbind(gap=fk, SE.sim=sk))))

# Note that 'firstmax' and 'globalmax' are always at 3 and 6 :
sapply(c(1/4, 1,2,4), function(SEf)
    sapply(mets, function(M) maxSE(fk, sk, method = M, SE.factor = SEf)))

### --- clusGap() -------------------------------------------------
## ridiculously nicely separated clusters in 3 D :

```r
x <- rbind(matrix(rnorm(150, sd = 0.1), ncol = 3),
            matrix(rnorm(150, mean = 1, sd = 0.1), ncol = 3),
            matrix(rnorm(150, mean = 2, sd = 0.1), ncol = 3),
            matrix(rnorm(150, mean = 3, sd = 0.1), ncol = 3))
```

## Slightly faster way to use pam (see below)

```r
pam1 <- function(x, k) list(cluster = pam(x, k, cluster.only=TRUE))
```

## We do not recommend using hier.clustering here, but if you want,
## there is factoextra::hcut () or a cheap version of it

```r
hclusCut <- function(x, k, d.meth = "euclidean", ...)
  list(cluster = cutree(hclust(dist(x, method=d.meth), ...), k=k))
```

## You can manually set it before running this : doExtras <- TRUE # or FALSE

```r
if(!(exists("doExtras") && is.logical(doExtras)))
doExtras <- cluster:::doExtras()
```}

```r
if(doExtras) {
## Note we use B = 60 in the following examples to keep them "speedy".
## ---- rather keep the default B = 500 for your analysis!

## note we can pass 'nstart = 20' to kmeans() :

gskmm <- clusGap(x, FUN = kmeans, n.start = 20, B = 60)
gskmm #-> its print() method
plot(gskmm, main = "clusGap(., FUN = kmeans, n.start=20, B= 60)"

set.seed(12); system.time(
  gsPam0 <- clusGap(x, FUN = pam, K.max = 8, B = 60)
)
set.seed(12); system.time(
  gsPam1 <- clusGap(x, FUN = pam1, K.max = 8, B = 60)
)
## and show that it gives the "same":
not.eq <- c("call", "FUNcluster"); n <- names(gsPam0)
eq <- n[n %in% not.eq]
stopifnot(identical(gsPam1[eq], gsPam0[eq]))
print(gsPam1, method="globalSEmax")
print(gsPam1, method="globalmax")
plot(gsHc <- clusGap(x, FUN = hclusCut, K.max = 8, B = 60))
}
```}

```r
gs.pam.RU <- clusGap(ruspini, FUN = pam1, K.max = 8, B = 60)
gs.pam.RU
plot(gs.pam.RU, main = "Gap statistic for the 'ruspini' data")
mtext("k = 4 is best .. and k = 5 pretty close")
```

## This takes a minute..
## No clustering ==> k = 1 ("one cluster") should be optimal:

```r
Z <- matrix(rnorm(256*3), 256,3)
gsp.Z <- clusGap(Z, FUN = pam1, K.max = 8, B = 200)
```}

```r
plot(gsP.Z, main = "clusGap(<iid_rnorm_p=3>) ==> k = 1 cluster is optimal")
gsP.Z
```
clusplot

_Bivariate Cluster Plot (of a Partitioning Object)_

### Description

Draws a 2-dimensional “clusplot” (clustering plot) on the current graphics device. The generic function has a default and a partition method.

### Usage

```r
clusplot(x, ...)  
## S3 method for class 'partition'
clusplot(x, main = NULL, dist = NULL, ...)  
```

### Arguments

- **x**
  - an R object, here, specifically an object of class “partition”, e.g. created by one of the functions `pam`, `clara`, or `fanny`.
- **main**
  - title for the plot; when NULL (by default), a title is constructed, using `x$call`.
- **dist**
  - when `x` does not have a `diss` nor a `data` component, e.g., for `pam(dist(*), keep.diss=FALSE)`, `dist` must specify the dissimilarity for the clusplot.
- **...**
  - optional arguments passed to methods, notably the `clusplot.default` method (except for the `diss` one) may also be supplied to this function. Many graphical parameters (see `par`) may also be supplied as arguments here.

### Details

The `clusplot.partition()` method relies on `clusplot.default`.

If the clustering algorithms `pam`, `fanny` and `clara` are applied to a data matrix of observations-by-variables then a clusplot of the resulting clustering can always be drawn. When the data matrix contains missing values and the clustering is performed with `pam` or `fanny`, the dissimilarity matrix will be given as input to clusplot. When the clustering algorithm `clara` was applied to a data matrix with NAs then clusplot() will replace the missing values as described in `clusplot.default`, because a dissimilarity matrix is not available.

### Value

For the partition (and default) method: An invisible list with components Distances and Shading, as for `clusplot.default`, see there.

### Side Effects

A 2-dimensional clusplot is created on the current graphics device.

### See Also

- `clusplot.default` for references; `partition.object`, `pam`, `pam.object`, `clara`, `clara.object`, `fanny`, `fanny.object`, `par`.
Examples

### For more, see ?clusplot.default

```r
# generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10, 0, 0.5), rnorm(10, 0, 0.5)),
            cbind(rnorm(15, 5, 0.5), rnorm(15, 5, 0.5)))
clusplot(pam(x, 2))
# add noise, and try again :
x4 <- cbind(x, rnorm(25), rnorm(25))
clusplot(pam(x4, 2))
```

clusplot.default

Bivariate Cluster Plot (clusplot) Default Method

Description

Creates a bivariate plot visualizing a partition (clustering) of the data. All observation are represented by points in the plot, using principal components or multidimensional scaling. Around each cluster an ellipse is drawn.

Usage

```r
## Default S3 method:
clusplot(x, clus, diss = FALSE,
s.x.2d = mkCheckX(x, diss), stand = FALSE,
lines = 2, shade = FALSE, color = FALSE,
labels = 0, plotchar = TRUE,
col.p = "dark green", col.txt = col.p,
col.clus = if(color) c(2, 4, 6, 3) else 5,
cex = 1, cex.txt = cex,
span = TRUE,
add = FALSE,
xlim = NULL, ylim = NULL,
main = paste("CLUSPLOT(" , substitute(x) , ")"),
sub = paste("These two components explain",
round(100 * var.dec, digits = 2), ", % of the point variability.")
```

Arguments

- **x**: matrix or data frame, or dissimilarity matrix, depending on the value of the **diss** argument.
  
  In case of a matrix (alike), each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed. They are replaced by the median of the corresponding variable. When some variables or some observations contain only missing values, the function stops with a warning message.
  
  In case of a dissimilarity matrix, `x` is the output of `daisy` or `dist` or a symmetric matrix. Also, a vector of length `n * (n - 1) / 2` is allowed (where `n` is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.
clus
a vector of length n representing a clustering of x. For each observation the
vector lists the number or name of the cluster to which it has been assigned.
clus is often the clustering component of the output of pam, fanny or clara.

diss
logical indicating if x will be considered as a dissimilarity matrix or a matrix of
observations by variables (see x argument above).

s.x.2d
a list with components named x (a n × 2 matrix; typically something like
principal components of original data), labs and var.dec.

stand
logical flag: if true, then the representations of the n observations in the 2-
dimensional plot are standardized.

lines
integer out of 0, 1, 2, used to obtain an idea of the distances between ellipses.
The distance between two ellipses E1 and E2 is measured along the line con-
necting the centers m1 and m2 of the two ellipses.
In case E1 and E2 overlap on the line through m1 and m2, no line is drawn.
Otherwise, the result depends on the value of lines: If
lines = 0, no distance lines will appear on the plot;
lines = 1, the line segment between m1 and m2 is drawn;
lines = 2, a line segment between the boundaries of E1 and E2 is drawn (along
the line connecting m1 and m2).

shade
logical flag: if TRUE, then the ellipses are shaded in relation to their density.
The density is the number of points in the cluster divided by the area of the
ellipse.

color
logical flag: if TRUE, then the ellipses are colored with respect to their density.
With increasing density, the colors are light blue, light green, red and purple. To
see these colors on the graphics device, an appropriate color scheme should be
selected (we recommend a white background).

labels
integer code, currently one of 0,1,2,3,4 and 5. If
labels= 0, no labels are placed in the plot;
labels= 1, points and ellipses can be identified in the plot (see identify);
labels= 2, all points and ellipses are labelled in the plot;
labels= 3, only the points are labelled in the plot;
labels= 4, only the ellipses are labelled in the plot.
labels= 5, the ellipses are labelled in the plot, and points can be identified.
The levels of the vector clus are taken as labels for the clusters. The labels
of the points are the rownames of x if x is matrix like. Otherwise (diss =
TRUE), x is a vector, point labels can be attached to x as a "Labels" attribute
(attr(x,"Labels")), as is done for the output of daisy.
A possible names attribute of clus will not be taken into account.

plotchar
logical flag: if TRUE, then the plotting symbols differ for points belonging to
different clusters.

span
logical flag: if TRUE, then each cluster is represented by the ellipse with small-
est area containing all its points. (This is a special case of the minimum volume
ellipsoid.)
If FALSE, the ellipse is based on the mean and covariance matrix of the same
points. While this is faster to compute, it often yields a much larger ellipse.
There are also some special cases: When a cluster consists of only one point, a
tiny circle is drawn around it. When the points of a cluster fall on a straight line,
span=FALSE draws a narrow ellipse around it and span=TRUE gives the exact
line segment.
clusplot.default

add
logical indicating if ellipses (and labels if labels is true) should be added to an already existing plot. If false, neither a title or sub title, see sub, is written.

col.p
color code(s) used for the observation points.
col.txt
color code(s) used for the labels (if labels >= 2).
col.clus
color code for the ellipses (and their labels); only one if color is false (as per default).
cex, cex.txt
character expansion (size), for the point symbols and point labels, respectively.
xlim, ylim
numeric vectors of length 2, giving the x- and y- ranges as in plot.default.
main
main title for the plot; by default, one is constructed.
sub
sub title for the plot; by default, one is constructed.
xlab, ylab
x- and y- axis labels for the plot, with defaults.
verbose
a logical indicating, if there should be extra diagnostic output; mainly for ‘de-bugging’.
...
Further graphical parameters may also be supplied, see par.

Details
clusplot uses function calls princomp(*, cor = (ncol(x) > 2)) or cmdscale(*, add=TRUE), respectively, depending on diss being false or true. These functions are data reduction techniques to represent the data in a bivariate plot.

Ellipses are then drawn to indicate the clusters. The further layout of the plot is determined by the optional arguments.

Value
An invisible list with components:

Distances
When lines is 1 or 2 we obtain a k by k matrix (k is the number of clusters). The element in [i,j] is the distance between ellipse i and ellipse j. If lines = 0, then the value of this component is NA.

Shading
A vector of length k (where k is the number of clusters), containing the amount of shading per cluster. Let y be a vector where element i is the ratio between the number of points in cluster i and the area of ellipse i. When the cluster i is a line segment, y[i] and the density of the cluster are set to NA. Let z be the sum of all the elements of y without the NAs. Then we put shading = y/z *37 + 3.

Side Effects
a visual display of the clustering is plotted on the current graphics device.

Note
When we have 4 or fewer clusters, then the color=TRUE gives every cluster a different color. When there are more than 4 clusters, clusplot uses the function pam to cluster the densities into 4 groups such that ellipses with nearly the same density get the same color. col.clus specifies the colors used.
The col.p and col.txt arguments, added for R, are recycled to have length the number of observations. If col.p has more than one value, using color = TRUE can be confusing because of a mix of point and ellipse colors.
References


See Also

`princomp, cmdscale, pam, clara, daisy, par, identify, cov.mve, clusplot.partition`.

Examples

```r
## plotting votes.diss(dissimilarity) in a bivariate plot and
## partitioning into 2 clusters
data(votes.repub)
votes.diss <- daisy(votes.repub)
pamv <- pam(votes.diss, 2, diss = TRUE)
clusplot(pamv, shade = TRUE)
## is the same as
votes.clus <- pamv$clustering
clusplot(votes.diss, votes.clus, diss = TRUE, shade = TRUE)
## Now look at components 3 and 2 instead of 1 and 2:
str(cMDS <- cmdscale(votes.diss, k=3, add=TRUE))
clusplot(pamv, s.x.2d = list(x=cMDS$points[, c(3,2)],
                           labs=rownames(votes.repub), var.dec=NA),
          shade = TRUE, col.p = votes.clus,
          sub="", xlab = "Component 3", ylab = "Component 2")
clusplot(pamv, col.p = votes.clus, labels = 4)# color points and label ellipses
## "simple" cheap ellipses: larger than minimum volume:
## here they are *added* to the previous plot:
clusplot(pamv, span = FALSE, add = TRUE, col.clus = "midnightblue")

## Setting a small *label* size:
clusplot(votes.diss, votes.clus, diss = TRUE, labels = 3, cex.txt = 0.6)

if(dev.interactive()) { # uses identify() *interactively* :
    clusplot(votes.diss, votes.clus, diss = TRUE, shade = TRUE, labels = 1)
    clusplot(votes.diss, votes.clus, diss = TRUE, labels = 5)# ident. only points
}

## plotting iris (data frame) in a 2-dimensional plot and partitioning
## into 3 clusters.
data(iris)
iris.x <- iris[, 1:4]
c13 <- pam(iris.x, 3)$clustering
op <- par(mfrow= c(2,2))
clusplot(iris.x, c13, color = TRUE)
U <- par("usr")
## zoom in:
rect(0,-1, 2,1, border = "orange", lwd=2)
clusplot(iris.x, c13, color = TRUE, xlim = c(0,2), ylim = c(-1,1))
```
coef.hclust

Agglomerative / Divisive Coefficient for 'hclust' Objects

Description

Computes the “agglomerative coefficient” (aka “divisive coefficient” for diana), measuring the clustering structure of the dataset.

For each observation i, denote by $m(i)$ its dissimilarity to the first cluster it is merged with, divided by the dissimilarity of the merger in the final step of the algorithm. The agglomerative coefficient is the average of all $1 - m(i)$. It can also be seen as the average width (or the percentage filled) of the banner plot.

coeffHier() directly interfaces to the underlying C code, and “proves” that only object$heights is needed to compute the coefficient.

Because it grows with the number of observations, this measure should not be used to compare datasets of very different sizes.

Usage

coefHier(object)
coef.hclust(object, ...)
## S3 method for class 'hclust'
coef(object, ...)
## S3 method for class 'twins'
coef(object, ...)

Arguments

object an object of class "hclust" or "twins", i.e., typically the result of hclust(.), agnes(.), or diana(.).

Since coef.hclust only uses object$heights, and object$merge, object can be any list-like object with appropriate merge and heights components.

For coeffHier, even only object$heights is needed.

... currently unused potential further arguments

Value

a number specifying the agglomerative (or divisive for diana objects) coefficient as defined by Kaufman and Rousseeuw, see agnes.object$ac or diana.object$dc.
Examples

```r
data(iris)
aa <- agnes(iris)
coef(aa) # really just extracts aa$ac
coef(as.hclust(aa)) # recomputes
coefHier(aa) # ditto
```

---

daisy 

Dissimilarity Matrix Calculation

Description

Compute all the pairwise dissimilarities (distances) between observations in the data set. The original variables may be of mixed types. In that case, or whenever **metric = "gower"** is set, a generalization of Gower's formula is used, see 'Details' below.

Usage

```r
daisy(x, metric = c("euclidean", "manhattan", "gower"),
     stand = FALSE, type = list(), weights = rep.int(1, p),
     warnBin = warnType, warnAsym = warnType, warnConst = warnType,
     warnType = TRUE)
```

Arguments

- **x** numeric matrix or data frame, of dimension \( n \times p \), say. Dissimilarities will be computed between the rows of \( x \). Columns of mode numeric (i.e. all columns when \( x \) is a matrix) will be recognized as interval scaled variables, columns of class factor will be recognized as nominal variables, and columns of class ordered will be recognized as ordinal variables. Other variable types should be specified with the **type** argument. Missing values (\( \text{NAs} \)) are allowed.
- **metric** character string specifying the metric to be used. The currently available options are "euclidean" (the default), "manhattan" and "gower". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. “Gower’s distance” is chosen by metric "gower" or automatically if some columns of \( x \) are not numeric. Also known as Gower’s coefficient (1971), expressed as a dissimilarity, this implies that a particular standardisation will be applied to each variable, and the “distance” between two units is the sum of all the variable-specific distances, see the details section.
- **stand** logical flag: if TRUE, then the measurements in \( x \) are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable’s mean value and dividing by the variable’s mean absolute deviation. If not all columns of \( x \) are numeric, **stand** will be ignored and Gower’s standardization (based on the range) will be applied in any case, see argument **metric**, above, and the details section.
- **type** list for specifying some (or all) of the types of the variables (columns) in \( x \). The list may contain the following components:
"asymm" Asymmetric binary variable, aka "A" in result Types, see dissimilarity.object.
"symm" Symmetric binary variable, aka "S".
"factor" Nominal – the default for factor variables, aka "N".
"ordered" Ordinal – the default for ordered (factor) variables, aka "O", see dissimilarity.object.
"logratio" ratio scaled numeric variables that are to be logarithmically transformed (log10) and then treated as numeric ("I"): must be positive numeric variable.
"ordratio" "raTio"-like variable to be treated as ordered (using the factor codes unclass(as.ordered(x[,j]))), aka "T".
"numeric"/"integer" Interval scaled – the default for all numeric (incl integer) columns of x, aka "I" in result Types, see dissimilarity.object.

Each component is a (character or numeric) vector, containing either the names or the numbers of the corresponding columns of x.

Variables not mentioned in type are interpreted as usual, see argument x, and also 'default' above. Consequently, the default type = list() may often be sufficient.

weights an optional numeric vector of length p=ncol(x); to be used in “case 2” (mixed variables, or metric = "gower"), specifying a weight for each variable (x[,k]) instead of 1 in Gower's original formula.

warnBin, warnAsym, warnConst
logicals indicating if the corresponding type checking warnings should be signalled (when found).

warnType logical indicating if all the type checking warnings should be active or not.

Details

The original version of daisy is fully described in chapter 1 of Kaufman and Rousseeuw (1990). Compared to dist whose input must be numeric variables, the main feature of daisy is its ability to handle other variable types as well (e.g. nominal, ordinal, (a)symmetric binary) even when different types occur in the same data set.

The handling of nominal, ordinal, and (a)symmetric binary data is achieved by using the general dissimilarity coefficient of Gower (1971). If x contains any columns of these data-types, both arguments metric and stand will be ignored and Gower’s coefficient will be used as the metric. This can also be activated for purely numeric data by metric = "gower". With that, each variable (column) is first standardized by dividing each entry by the range of the corresponding variable, after subtracting the minimum value; consequently the rescaled variable has range [0, 1], exactly.

Note that setting the type to symm (symmetric binary) gives the same dissimilarities as using nominal (which is chosen for non-ordered factors) only when no missing values are present, and more efficiently.

Note that daisy signals a warning when 2-valued numerical variables do not have an explicit type specified, because the reference authors recommend to consider using "asymm"; the warning may be silenced by warnBin = FALSE.

In the daisy algorithm, missing values in a row of x are not included in the dissimilarities involving that row. There are two main cases,

1. If all variables are interval scaled (and metric is not "gower"), the metric is "euclidean", and n_s is the number of columns in which neither row i and j have NAs, then the dissimilarity
d(i,j) returned is $\sqrt{p/n_g}$ ($p = \text{ncol(x)}$) times the Euclidean distance between the two vectors of length $n_g$ shortened to exclude NAs. The rule is similar for the "manhattan" metric, except that the coefficient is $p/n_g$. If $n_g = 0$, the dissimilarity is NA.

2. When some variables have a type other than interval scaled, or if metric = "gower" is specified, the dissimilarity between two rows is the weighted mean of the contributions of each variable. Specifically,

$$d_{ij} = \frac{\sum_{k=1}^{p} w_k \delta_{ij}^{(k)} d_{ij}^{(k)}}{\sum_{k=1}^{p} w_k \delta_{ij}^{(k)}}.$$ 

In other words, $d_{ij}$ is a weighted mean of $d_{ij}^{(k)}$ with weights $w_k \delta_{ij}^{(k)}$, where $w_k = \text{weights}[k]$, $\delta_{ij}^{(k)}$ is 0 or 1, and $d_{ij}^{(k)}$, the k-th variable contribution to the total distance, is a distance between $x[i,k]$ and $x[j,k]$, see below.

The 0-1 weight $\delta_{ij}^{(k)}$ becomes zero when the variable $x[,k]$ is missing in either or both rows (i and j), or when the variable is asymmetric binary and both values are zero. In all other situations it is 1.

The contribution $d_{ij}^{(k)}$ of a nominal or binary variable to the total dissimilarity is 0 if both values are equal, 1 otherwise. The contribution of other variables is the absolute difference of both values, divided by the total range of that variable. Note that "standard scoring" is applied to ordinal variables, i.e., they are replaced by their integer codes 1:K. Note that this is not the same as using their ranks (since there typically are ties).

As the individual contributions $d_{ij}^{(k)}$ are in [0, 1], the dissimilarity $d_{ij}$ will remain in this range. If all weights $w_k \delta_{ij}^{(k)}$ are zero, the dissimilarity is set to NA.

Value

an object of class "dissimilarity" containing the dissimilarities among the rows of x. This is typically the input for the functions pam, fanny, agnes or diana. For more details, see dissimilarity.object.

Background

Dissimilarities are used as inputs to cluster analysis and multidimensional scaling. The choice of metric may have a large impact.

Author(s)

Anja Struyf, Mia Hubert, and Peter and Rousseeuw, for the original version.

Martin Maechler improved the NA handling and type specification checking, and extended functionality to metric = "gower" and the optional weights argument.

References


See Also
dissimilarity.object, dist, pam, fanny, clara, agnes, diana.
Examples

```r
data(agriculture)
## Example 1 in ref:
## Dissimilarities using Euclidean metric and without standardization
d.agr <- daisy(agriculture, metric = "euclidean", stand = FALSE)
d.agr
as.matrix(d.agr)[,"DK"] # via as.matrix.dist(.)
## compare with
as.matrix(daisy(agriculture, metric = "gower"))

data(flower)
## Example 2 in ref
summary(dfl1 <- daisy(flower, type = list(asymm = 3)))
summary(dfl2 <- daisy(flower, type = list(asymm = c(1, 3), ordratio = 7)))
## this failed earlier:
summary(dfl3 <- daisy(flower,
    type = list(asymm = c("V1", "V3"), symm= 2, ordratio= 7, logratio= 8)))
```

**Description**

Computes a divisive hierarchical clustering of the dataset returning an object of class `diana`.

**Usage**

```r
diana(x, diss = inherits(x, "dist"), metric = "euclidean", stand = FALSE,
    stop.at.k = FALSE,
    keep.diss = n < 100, keep.data = !diss, trace.lev = 0)
```

**Arguments**

- `x`: data matrix or data frame, or dissimilarity matrix or object, depending on the value of the `diss` argument. In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed. In case of a dissimilarity matrix, `x` is typically the output of `daisy` or `dist`. Also a vector of length n*(n-1)/2 is allowed (where n is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.
- `diss`: logical flag: if TRUE (default for `dist` or `dissimilarity` objects), then `x` will be considered as a dissimilarity matrix. If FALSE, then `x` will be considered as a matrix of observations by variables.
- `metric`: character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the
**Details**

`diana` is fully described in chapter 6 of Kaufman and Rousseeuw (1990). It is probably unique in computing a divisive hierarchy, whereas most other software for hierarchical clustering is agglomerative. Moreover, `diana` provides (a) the divisive coefficient (see `diana.object`) which measures the amount of clustering structure found; and (b) the banner, a novel graphical display (see `plot.diana`).

The `diana`-algorithm constructs a hierarchy of clusterings, starting with one large cluster containing all n observations. Clusters are divided until each cluster contains only a single observation. At each stage, the cluster with the largest diameter is selected. (The diameter of a cluster is the largest dissimilarity between any two of its observations.)

To divide the selected cluster, the algorithm first looks for its most disparate observation (i.e., which has the largest average dissimilarity to the other observations of the selected cluster). This observation initiates the "splinter group". In subsequent steps, the algorithm reassigns observations that are closer to the "splinter group" than to the "old party". The result is a division of the selected cluster into two new clusters.

**Value**

an object of class "diana" representing the clustering; this class has methods for the following generic functions: print, summary, plot.

Further, the class "diana" inherits from "twins". Therefore, the generic function `pltree` can be used on a `diana` object, and `as.hclust` and `as.dendrogram` methods are available.

A legitimate `diana` object is a list with the following components:

- **order**
  - a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.

- **order.lab**
  - a vector similar to `order`, but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.

- **height**
  - a vector with the diameters of the clusters prior to splitting.

- **dc**
  - the divisive coefficient, measuring the clustering structure of the dataset. For each observation i, denote by \(d(i)\) the diameter of the last cluster to which it
belongs (before being split off as a single observation), divided by the diameter of the whole dataset. The dc is the average of all $1 - d(i)$. It can also be seen as the average width (or the percentage filled) of the banner plot. Because dc grows with the number of observations, this measure should not be used to compare datasets of very different sizes.

merge an (n-1) by 2 matrix, where n is the number of observations. Row i of merge describes the split at step n-i of the clustering. If a number j in row r is negative, then the single observation $|j|$ is split off at stage n-r. If j is positive, then the cluster that will be splitted at stage n-j (described by row j), is split off at stage n-r.

diss an object of class "dissimilarity", representing the total dissimilarity matrix of the dataset.

data a matrix containing the original or standardized measurements, depending on the stand option of the function agnes. If a dissimilarity matrix was given as input structure, then this component is not available.

See Also

agnes also for background and references; cutree (and as.hclust) for grouping extraction; daisy, dist, plot.diana, twins.object.

Examples

data(votes.repub)
dv <- diana(votes.repub, metric = "manhattan", stand = TRUE)
print(dv)
plot(dv)

# Cut into 2 groups:
dv2 <- cutree(as.hclust(dv), k = 2)
table(dv2) # 8 and 42 group members
rownames(votes.repub)[dv2 == 1]

# For two groups, does the metric matter?
dv0 <- diana(votes.repub, stand = TRUE) # default: Euclidean
dv.2 <- cutree(as.hclust(dv0), k = 2)
table(dv2 == dv.2) # identical group assignments
str(as.dendrogram(dv0)) # (via as.dendrogram.twins() method)

data(agriculture)
# Plot similar to Figure 8 in ref
# Not run: plot(diana(agriculture), ask = TRUE)
Value

The dissimilarity matrix is symmetric, and hence its lower triangle (column wise) is represented as a vector to save storage space. If the object, is called do, and n the number of observations, i.e., $n \leftarrow attr(do, \text{"Size"})$, then for $i < j <= n$, the dissimilarity between (row) i and j is $d_{ij} = do[n*(i-1) - i*(i-1)/2 + j-i]$. The length of the vector is $n * (n - 1)/2$, i.e., of order $n^2$.

"dissimilarity" objects also inherit from class dist and can use dist methods, in particular, as.matrix, such that $d_{ij}$ from above is just as.matrix(do)[i,j].

The object has the following attributes:

Size the number of observations in the dataset.

Metric the metric used for calculating the dissimilarities. Possible values are "euclidean", "manhattan", "mixed" (if variables of different types were present in the dataset), and "unspecified".

Labels optionally, contains the labels, if any, of the observations of the dataset.

NA.message optionally, if a dissimilarity could not be computed, because of too many missing values for some observations of the dataset.

Types when a mixed metric was used, the types for each variable as one-letter codes, see also type in daisy():
A: Asymmetric binary
S: Symmetric binary
N: Nominal (factor)
O: Ordinal (ordered factor)
I: Interval scaled, possibly after log transform "logratio" (numeric)
T: ratio treated as ordered

GENERATION

daisy returns this class of objects. Also the functions pam, clara, fanny, agnes, and diana return a dissimilarity object, as one component of their return objects.

METHODS

The "dissimilarity" class has methods for the following generic functions: print, summary.

See Also
daisy, dist, pam, clara, fanny, agnes, diana.

dissimilarity

ellipsoidhull

Compute the Ellipsoid Hull or Spanning Ellipsoid of a Point Set

Description

Compute the “ellipsoid hull” or “spanning ellipsoid”, i.e. the ellipsoid of minimal volume (‘area’ in 2D) such that all given points lie just inside or on the boundary of the ellipsoid.
ellipsoidhull

Usage

```
ellipsoidhull(x, tol=0.01, maxit=5000,
    ret.wt = FALSE, ret.sqdist = FALSE, ret.pr = FALSE)
```

## S3 method for class 'ellipsoid'
```
print(x, digits = max(1,getOption("digits") - 2), ...)
```

Arguments

- **x**: the \( n \times p \) matrix.
- **tol**: convergence tolerance for Titterington’s algorithm. Setting this to much smaller values may drastically increase the number of iterations needed, and you may want to increase `maxit` as well.
- **maxit**: integer giving the maximal number of iteration steps for the algorithm.
- **ret.wt**, **ret.sqdist**, **ret.pr**: logicals indicating if additional information should be returned, `ret.wt` specifying the weights, `ret.sqdist` the squared distances and `ret.pr` the final probabilities in the algorithms.
- **digits,...**: the usual arguments to print methods.

Details

The "spanning ellipsoid" algorithm is said to stem from Titterington(1976), in Pison et al (1999) who use it for `clusplot.default`. The problem can be seen as a special case of the "Min.V ol." ellipsoid of which a more more flexible and general implementation is `cov.mve` in the MASS package.

Value

an object of class "ellipsoid", basically a list with several components, comprising at least

- **cov**: \( p \times p \) covariance matrix description the ellipsoid.
- **loc**: \( p \)-dimensional location of the ellipsoid center.
- **d2**: average squared radius. Further, \( d^2 = t^2 \), where \( t \) is "the value of a t-statistic on the ellipse boundary" (from `ellipse` in the `ellipse` package), and hence, more usefully, \( d^2 = qchisq(alpha, df = p) \), where alpha is the confidence level for \( p \)-variate normally distributed data with location and covariance `loc` and `cov` to lie inside the ellipsoid.
- **wt**: the vector of weights iff `ret.wt` was true.
- **sqdist**: the vector of squared distances iff `ret.sqdist` was true.
- **prob**: the vector of algorithm probabilities iff `ret.pr` was true.
- **it**: number of iterations used.
- **tol, maxit**: just the input argument, see above.
- **eps**: the achieved tolerance which is the maximal squared radius minus \( p \).
- **ierr**: error code as from the algorithm; 0 means `ok`.
- **conv**: logical indicating if the converged. This is defined as `it < maxit && ierr == 0`.

Author(s)

Martin Maechler did the present class implementation; Rousseeuw et al did the underlying original code.
References


See Also

predict.ellipsoid which is also the predict method for ellipsoid objects.  
volume.ellipsoid for an example of 'manual' ellipsoid object construction;  
 further ellipse from package ellipse and ellipsePoints from package sfsmisc.  
chull for the convex hull, clusplot which makes use of this; cov.mve.

Examples

x <- rnorm(100)  
xy <- unname(cbind(x, rnorm(100) + 2*x + 10))  
exy. <- ellipsoidhull(xy)  
exy. # >> calling print.ellipsoid()  
plot(xy, main = "ellipsoidhull(<Gauss data>) -- 'spanning points'")  
lines(predict(exy.), col="blue")  
points(rbind(exy.$loc), col = "red", cex = 3, pch = 13)  
exy <- ellipsoidhull(xy, tol = 1e-7, ret.wt = TRUE, ret.sq = TRUE)  
str(exy) # had small 'tol', hence many iterations  
(ii <- which(zapsmall(exy $ wt) > 1e-6))  
## --> only about 4 to 6 "spanning ellipsoid" points  
round(exy$wt[ii],3); sum(exy$wt[ii]) # weights summing to 1  
points(xy[ii,], pch = 21, cex = 2,  
col="blue", bg = adjustcolor("blue",0.25))

fanny  

Fuzzy Analysis Clustering

Description

Computes a fuzzy clustering of the data into k clusters.

Usage

fanny(x, k, diss = inherits(x, "dist"), memb.exp = 2,  
metric = c("euclidean", "manhattan", "SqEuclidean"),  
stand = FALSE, iniMem.p = NULL, cluster.only = FALSE,  
keep.diss = !diss & & !cluster.only & & n < 100,  
keep.data = !diss & & !cluster.only,  
maxit = 500, tol = 1e-15, trace.lev = 0)
Arguments

**x**
data matrix or data frame, or dissimilarity matrix, depending on the value of the **diss** argument.

In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed.

In case of a dissimilarity matrix, **x** is typically the output of **daisy** or **dist**. Also a vector of length \( n(n-1)/2 \) is allowed (where \( n \) is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.

**k**
integer giving the desired number of clusters. It is required that \( 0 < k < n/2 \) where \( n \) is the number of observations.

**diss**
logical flag: if TRUE (default for **dist** or dissimilarity objects), then **x** is assumed to be a dissimilarity matrix. If FALSE, then **x** is treated as a matrix of observations by variables.

**memb.exp**
number \( r \) strictly larger than 1 specifying the membership exponent used in the fit criterion; see the ‘Details’ below. Default: 2 which used to be hardwired inside FANNY.

**metric**
character string specifying the metric to be used for calculating dissimilarities between observations. Options are "euclidean" (default), "manhattan", and "SqEuclidean". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences, and "SqEuclidean", the squared euclidean distances are sum-of-squares of differences. Using this last option is equivalent (but somewhat slower) to computing so called “fuzzy C-means”.

If **x** is already a dissimilarity matrix, then this argument will be ignored.

**stand**
logical; if true, the measurements in **x** are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable’s mean value and dividing by the variable’s mean absolute deviation. If **x** is already a dissimilarity matrix, then this argument will be ignored.

**iniMem.p**
numeric \( n \times k \) matrix or NULL (by default); can be used to specify a starting membership matrix, i.e., a matrix of non-negative numbers, each row summing to one.

**cluster.only**
logical; if true, no silhouette information will be computed and returned, see details.

**keep.diss, keep.data**
lógicos indicando si las dissimilaridades y/o datos de entrada **x** deben ser conservados en el resultado. Configurar estos a **FALSE** puede dar resultados más pequeños y ahorra tiempo de almacén de memoria.

**maxit, tol**
maximal number of iterations and default tolerance for convergence (relative convergence of the fit criterion) for the FANNY algorithm. The defaults maxit = 500 and tol = 1e-15 used to be hardwired inside the algorithm.

**trace.lev**
integer specifying a trace level for printing diagnostics during the C-internal algorithm. Default \( 0 \) does not print anything; higher values print increasingly more.
Details

In a fuzzy clustering, each observation is “spread out” over the various clusters. Denote by $u_{iv}$ the membership of observation $i$ to cluster $v$.

The memberships are nonnegative, and for a fixed observation $i$ they sum to 1. The particular method fanny stems from chapter 4 of Kaufman and Rousseeuw (1990) (see the references in daisy) and has been extended by Martin Maechler to allow user specified memb.exp, iniMem.p, maxit, tol, etc.

Fanny aims to minimize the objective function

$$
\sum_{v=1}^{k} \frac{\sum_{i=1}^{n} \sum_{j=1}^{n} u_{iv}^{r} u_{jv}^{r} d(i,j)}{2 \sum_{j=1}^{n} u_{jv}^{r}}
$$

where $n$ is the number of observations, $k$ is the number of clusters, $r$ is the membership exponent memb.exp and $d(i,j)$ is the dissimilarity between observations $i$ and $j$.

Note that $r \to 1$ gives increasingly crisper clusterings whereas $r \to \infty$ leads to complete fuzzyness. K&R(1990), p.191 note that values too close to 1 can lead to slow convergence. Further note that even the default, $r = 2$ can lead to complete fuzzyness, i.e., memberships $u_{iv} \equiv 1/k$. In that case a warning is signalled and the user is advised to chose a smaller memb.exp ($= r$).

Compared to other fuzzy clustering methods, fanny has the following features: (a) it also accepts a dissimilarity matrix; (b) it is more robust to the spherical cluster assumption; (c) it provides a novel graphical display, the silhouette plot (see plot.partition).

Value

an object of class "fanny" representing the clustering. See fanny.object for details.

See Also

agees for background and references; fanny.object, partition.object, plot.partition, daisy, dist.

Examples

```r
## generate 10+15 objects in two clusters, plus 3 objects lying
## between those clusters.
x <- rbind(cbind(rnorm(10, 0, 0.5), rnorm(10, 0, 0.5)),
            cbind(rnorm(15, 5, 0.5), rnorm(15, 5, 0.5)),
            cbind(rnorm( 3,3.2,0.5), rnorm( 3,3.2,0.5)))
fannyx <- fanny(x, 2)
## Note that observations 26:28 are "fuzzy" (closer to # 2):
fannyx
summary(fannyx)
plot(fannyx)

(fan.x.15 <- fanny(x, 2, memb.exp = 1.5)) # 'crisper' for obs. 26:28
(fanny(x, 2, memb.exp = 3)) # more fuzzy in general

data(ruspini)
f4 <- fanny(ruspini, 4)
stopifnot(rle(f4$clustering)$lengths == c(20,23,17,15))
plot(f4, which = 1)
## Plot similar to Figure 6 in Stryuf et al (1996)
plot(fanny(ruspini, 5))
```
Description

The objects of class "fanny" represent a fuzzy clustering of a dataset.

Value

A legitimate fanny object is a list with the following components:

- **membership**: matrix containing the memberships for each pair consisting of an observation and a cluster.
- **memb.exp**: the membership exponent used in the fitting criterion.
- **coeff**: Dunn’s partition coefficient \( F(k) \) of the clustering, where \( k \) is the number of clusters. \( F(k) \) is the sum of all squared membership coefficients, divided by the number of observations. Its value is between \( 1/k \) and 1.
  
  The normalized form of the coefficient is also given. It is defined as \( (F(k) - 1/k)/(1 - 1/k) \), and ranges between 0 and 1. A low value of Dunn's coefficient indicates a very fuzzy clustering, whereas a value close to 1 indicates a near-crisp clustering.
- **clustering**: the clustering vector of the nearest crisp clustering, see `partition.object`.
- **k.crisp**: integer (\( \leq k \)) giving the number of crisp clusters; can be less than \( k \), where it’s recommended to decrease memb.exp.
- **objective**: named vector containing the minimal value of the objective function reached by the FANNY algorithm and the relative convergence tolerance `tol` used.
- **convergence**: named vector with iterations, the number of iterations needed and converged indicating if the algorithm converged (in `maxit` iterations within convergence tolerance `tol`).
- **diss**: an object of class "dissimilarity", see `partition.object`.
- **call**: generating call, see `partition.object`.
- **silinfo**: list with silhouette information of the nearest crisp clustering, see `partition.object`.
- **data**: matrix, possibly standardized, or NULL, see `partition.object`.

GENERATION

These objects are returned from `fanny`.

METHODS

The "fanny" class has methods for the following generic functions: `print`, `summary`.

INHERITANCE

The class "fanny" inherits from "partition". Therefore, the generic functions `plot` and `clusplot` can be used on a fanny object.

See Also

`fanny`, `print.fanny`, `dissimilarity.object`, `partition.object`, `plot.partition`.
flower

**Flower Characteristics**

**Description**

8 characteristics for 18 popular flowers.

**Usage**

data(flower)

**Format**

A data frame with 18 observations on 8 variables:

- **V1** winters, is binary and indicates whether the plant may be left in the garden when it freezes.
- **V2** shadow, is binary and shows whether the plant needs to stand in the shadow.
- **V3** tubers, is asymmetric binary and distinguishes between plants with tubers and plants that grow in any other way.
- **V4** color, is nominal and specifies the flower’s color (1 = white, 2 = yellow, 3 = pink, 4 = red, 5 = blue).
- **V5** soil, is ordinal and indicates whether the plant grows in dry (1), normal (2), or wet (3) soil.
- **V6** preference, is ordinal and gives someone’s preference ranking going from 1 to 18.
- **V7** height, is interval scaled, the plant’s height in centimeters.
- **V8** distance, is interval scaled, the distance in centimeters that should be left between the plants.

**References**

Struyf, Hubert and Rousseeuw (1996), see agnes.

**Examples**

data(flower)

## Example 2 in ref
daisy(flower, type = list(asymm = 3))
daisy(flower, type = list(asymm = c(1, 3), ordratio = 7))
lower.to.upper.tri.inds

*Permute Indices for Triangular Matrices*

**Description**

Compute index vectors for extracting or reordering of lower or upper triangular matrices that are stored as contiguous vectors.

**Usage**

```r
lower.to.upper.tri.inds(n)
upper.to.lower.tri.inds(n)
```

**Arguments**

- `n` integer larger than 1.

**Value**

integer vector containing a permutation of `1:N` where \( N = n(n - 1)/2 \).

**See Also**

`upper.tri`, `lower.tri` with a related purpose.

**Examples**

```r
m5 <- matrix(NA,5,5)
m <- m5; m[lower.tri(m)] <- upper.to.lower.tri.inds(5); m
m <- m5; m[upper.tri(m)] <- lower.to.upper.tri.inds(5); m

stopifnot(lower.to.upper.tri.inds(2) == 1,
          lower.to.upper.tri.inds(3) == 1:3,
          upper.to.lower.tri.inds(3) == 1:3,
          sort(upper.to.lower.tri.inds(5)) == 1:10,
          sort(lower.to.upper.tri.inds(6)) == 1:15)
```

medoids

*Compute pam-consistent Medoids from Clustering*

**Description**

Given a data matrix or dissimilarity `x` for say \( n \) observational units and a clustering, compute the `pam()`-consistent medoids.

**Usage**

```r
medoids(x, clustering, diss = inherits(x, "dist"), USE.NAMES = FALSE, ...)
```
Arguments

x
clustering

either a data matrix or data frame, or dissimilarity matrix or object, see also pam.
an integer vector of length n, the number of observations, giving for each observation the number ('id') of the cluster to which it belongs. In other words, clustering has values from 1:k where k is the number of clusters, see also partition.object and cutree(), for examples where such clustering vectors are computed.
diss
see also pam.
USE.NAMES
a logical, typical false, passed to the vapply() call computing the medoids.
...
optimal further argument passed to pam(xj, k=1,...), notably metric, or
variant="f_5" to use a faster algorithm, or trace.lev = k.

Value

a numeric vector of length

Author(s)

Martin Maechler, after being asked how pam() could be used instead of kmeans(), starting from a previous clustering.

See Also

pam, kmeans. Further, cutree() and agnes (or hclust).

Examples

## From example(agnes):
data(votes.repub)
agn1 <- agnes(votes.repub, metric = "manhattan", stand = TRUE)
agn2 <- agnes(daisy(votes.repub), diss = TRUE, method = "complete")
agnS <- agnes(votes.repub, method = "flexible", par.meth = 0.625)
for(k in 2:11) {
  print(table(cl.k <- cutree(agnS, k=k)))
  stopifnot(length(cl.k) == nrow(votes.repub), 1 <= cl.k, cl.k <= k, table(cl.k) >= 2)
  m.k <- medoids(votes.repub, cl.k)
  cat("k =", k, "; sort(medoids) = "); dput(sort(m.k), control={})
}

mona

MONothetic Analysis Clustering of Binary Variables

Description

Returns a list representing a divisive hierarchical clustering of a dataset with binary variables only.

Usage

mona(x, trace.lev = 0)
Arguments

\textbf{x} \hspace{1cm} \text{data matrix or data frame in which each row corresponds to an observation, and each column corresponds to a variable. All variables must be binary. A limited number of missing values (NAs) is allowed. Every observation must have at least one value different from NA. No variable should have half of its values missing. There must be at least one variable which has no missing values. A variable with all its non-missing values identical is not allowed.}

\textbf{trace.lev} \hspace{1cm} \text{logical or integer indicating if (and how much) the algorithm should produce progress output.}

Details

\texttt{mona} is fully described in chapter 7 of Kaufman and Rousseeuw (1990). It is “monothetic” in the sense that each division is based on a single (well-chosen) variable, whereas most other hierarchical methods (including \texttt{agnes} and \texttt{diana}) are “polythetic”, i.e. they use all variables together.

The \texttt{mona}-algorithm constructs a hierarchy of clusterings, starting with one large cluster. Clusters are divided until all observations in the same cluster have identical values for all variables. At each stage, all clusters are divided according to the values of one variable. A cluster is divided into one cluster with all observations having value 1 for that variable, and another cluster with all observations having value 0 for that variable.

The variable used for splitting a cluster is the variable with the maximal total association to the other variables, according to the observations in the cluster to be splitted. The association between variables \(f\) and \(g\) is given by \((a(f,g)d(f,g) - b(f,g)c(f,g))\), where \(a(f,g), b(f,g), c(f,g),\) and \(d(f,g)\) are the numbers in the contingency table of \(f\) and \(g\). [That is, \(a(f,g)\) (resp. \(d(f,g)\)) is the number of observations for which \(f\) and \(g\) both have value 0 (resp. value 1); \(b(f,g)\) (resp. \(c(f,g)\)) is the number of observations for which \(f\) has value 0 (resp. 1) and \(g\) has value 1 (resp. 0).] The total association of a variable \(f\) is the sum of its associations to all variables.

Value

an object of class “\texttt{mona}” representing the clustering. See \texttt{mona.object} for details.

Missing Values (NAs)

The \texttt{mona}-algorithm requires “pure” 0-1 values. However, \texttt{mona(x)} allows \texttt{x} to contain (not too many) NAs. In a preliminary step, these are “imputed”, i.e., all missing values are filled in. To do this, the same measure of association between variables is used as in the algorithm. When variable \(f\) has missing values, the variable \(g\) with the largest absolute association to \(f\) is looked up. When the association between \(f\) and \(g\) is positive, any missing value of \(f\) is replaced by the value of \(g\) for the same observation. If the association between \(f\) and \(g\) is negative, then any missing value of \(f\) is replaced by the value of \(1-g\) for the same observation.

Note

In \texttt{cluster} versions before 2.0.6, the algorithm entered an infinite loop in the boundary case of one variable, i.e., \texttt{ncol(x) == 1}, which currently signals an error (because the algorithm now in C, has not correctly taken account of this special case).

See Also

\texttt{agnes} for background and references; \texttt{mona.object}, \texttt{plot.mona}. 

Examples

```r
data(animals)
ma <- mona(animals)
ma
## Plot similar to Figure 10 in Struyf et al (1996)
plot(ma)
```

```r
## One place to see if/how error messages are *translated* (to 'de' / 'pl'):
ani.NA <- animals; ani.NA[4,] <- NA
aniNA <- within(animals, { end[2:9] <- NA })
aniN2 <- animals; aniN2[cbind(1:6, c(3, 1, 4:6, 2))] <- NA
ani.non2 <- within(animals, end[7] <- 3 )
ani.idNA <- within(animals, end[!is.na(end)] <- 1 )
try( mona(ani.NA) ) ## error: .. object with all values missing
try( mona(aniNA) ) ## error: .. more than half missing values
try( mona(aniN2) ) ## error: all have at least one missing
try( mona(ani.non2) ) ## error: all must be binary
try( mona(ani.idNA) ) ## error: ditto
```

mona.object

**Monothetic Analysis (MONA) Object**

Description

The objects of class "mona" represent the divisive hierarchical clustering of a dataset with only binary variables (measurements). This class of objects is returned from `mona`.

Value

A legitimate mona object is a list with the following components:

- `data` matrix with the same dimensions as the original data matrix, but with factors coded as 0 and 1, and all missing values replaced.
- `order` a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
- `order.lab` a vector similar to `order`, but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
- `variable` vector of length n-1 where n is the number of observations, specifying the variables used to separate the observations of `order`.
- `step` vector of length n-1 where n is the number of observations, specifying the separation steps at which the observations of `order` are separated.

METHODS

The "mona" class has methods for the following generic functions: `print`, `summary`, `plot`.

See Also

`mona` for examples etc, `plot.mona`.
Partitioning Around Medoids

Description

Partitioning (clustering) of the data into k clusters “around medoids”, a more robust version of \textit{K-means}.

Usage

\begin{verbatim}
pam(x, k, diss = inherits(x, "dist"),
   metric = c("euclidean", "manhattan"),
   medoids = if(is.numeric(nstart)) "random",
   nstart = if(variant == "faster") 1 else NA,
   stand = FALSE, cluster.only = FALSE,
   do.swap = TRUE,
   keep.diss = !diss && !cluster.only && n < 100,
   keep.data = !diss && !cluster.only,
   variant = c("original", "o_1", "o_2", "f_3", "f_4", "f_5", "faster"),
   pamonce = FALSE, trace.lev = 0)
\end{verbatim}

Arguments

- **x**: data matrix or data frame, or dissimilarity matrix or object, depending on the value of the diss argument.
  - In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (\texttt{NAs}) are allowed—as long as every pair of observations has at least one case not missing.
  - In case of a dissimilarity matrix, \texttt{x} is typically the output of \texttt{daisy} or \texttt{dist}. Also a vector of length \texttt{n*(n-1)/2} is allowed (where \texttt{n} is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (\texttt{NAs}) are not allowed.

- **k**: positive integer specifying the number of clusters, less than the number of observations.

- **diss**: logical flag: if TRUE (default for \texttt{dist} or dissimilarity objects), then \texttt{x} will be considered as a dissimilarity matrix. If FALSE, then \texttt{x} will be considered as a matrix of observations by variables.

- **metric**: character string specifying the metric to be used for calculating dissimilarities between observations.
  - The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. If \texttt{x} is already a dissimilarity matrix, then this argument will be ignored.

- **medoids**: NULL (default) or length-k vector of integer indices (in 1:n) specifying initial medoids instead of using the ‘build’ algorithm.

- **nstart**: used only when medoids = "random": specifies the \texttt{number} of random “starts”; this argument corresponds to the one of \texttt{kmeans()} (from R’s package \texttt{stats}).
stand logical; if true, the measurements in \( x \) are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable’s mean value and dividing by the variable’s mean absolute deviation. If \( x \) is already a dissimilarity matrix, then this argument will be ignored.

cluster.only logical; if true, only the clustering will be computed and returned, see details.

do.swap logical indicating if the swap phase should happen. The default, TRUE, correspond to the original algorithm. On the other hand, the swap phase is much more computer intensive than the build one for large \( n \), so can be skipped by do.swap = FALSE.

keep.diss, keep.data logicals indicating if the dissimilarities and/or input data \( x \) should be kept in the result. Setting these to FALSE can give much smaller results and hence even save memory allocation time.

pamonce logical or integer in 0:6 specifying algorithmic short cuts as proposed by Reynolds et al. (2006), and Schubert and Rousseeuw (2019, 2021) see below.

variant a character string denoting the variant of PAM algorithm to use; a more self-documenting version of pamonce which should be used preferably; note that “faster” not only uses pamonce = 6 but also nstart = 1 and hence medoids = "random" by default.

trace.lev integer specifying a trace level for printing diagnostics during the build and swap phase of the algorithm. Default 0 does not print anything; higher values print increasingly more.

Details

The basic pam algorithm is fully described in chapter 2 of Kaufman and Rousseeuw(1990). Compared to the k-means approach in kmeans, the function pam has the following features: (a) it also accepts a dissimilarity matrix; (b) it is more robust because it minimizes a sum of dissimilarities instead of a sum of squared euclidean distances; (c) it provides a novel graphical display, the silhouette plot (see plot.partition) (d) it allows to select the number of clusters using \( \text{mean(silhouette(pr[, "sil_width"])} \) on the result \( \text{pr <- pam(\ldots)} \), or directly its component \( \text{pr$silinfo$avg.width} \), see also pam.object.

When cluster.only is true, the result is simply a (possibly named) integer vector specifying the clustering, i.e., \( \text{pam(x,k, cluster.only=TRUE)} \) is the same as \( \text{pam(x,k)$clustering} \) but computed more efficiently.

The pam-algorithm is based on the search for \( k \) representative objects or medoids among the observations of the dataset. These observations should represent the structure of the data. After finding a set of \( k \) medoids, \( k \) clusters are constructed by assigning each observation to the nearest medoid. The goal is to find \( k \) representative objects which minimize the sum of the dissimilarities of the observations to their closest representative object.

By default, when medoids are not specified, the algorithm first looks for a good initial set of medoids (this is called the build phase). Then it finds a local minimum for the objective function, that is, a solution such that there is no single switch of an observation with a medoid (i.e. a ‘swap’) that will decrease the objective (this is called the swap phase).

When the medoids are specified (or randomly generated), their order does not matter; in general, the algorithms have been designed to not depend on the order of the observations.

The pamonce option, new in cluster 1.14.2 (Jan. 2012), has been proposed by Matthias Studer, University of Geneva, based on the findings by Reynolds et al. (2006) and was extended by Erich Schubert, TU Dortmund, with the FastPAM optimizations.
The default FALSE (or integer 0) corresponds to the original “swap” algorithm, whereas pamonce = 1 (or TRUE), corresponds to the first proposal .... and pamonce = 2 additionally implements the second proposal as well.

The key ideas of ‘FastPAM’ (Schubert and Rousseeuw, 2019) are implemented except for the linear approximate build as follows:

pamonce = 3: reduces the runtime by a factor of O(k) by exploiting that points cannot be closest to all current medoids at the same time.

pamonce = 4: additionally allows executing multiple swaps per iteration, usually reducing the number of iterations.

pamonce = 5: adds minor optimizations copied from the pamonce = 2 approach, and is expected to be the fastest of the ‘FastPam’ variants included.

‘FasterPAM’ (Schubert and Rousseeuw, 2021) is implemented via

pamonce = 6: execute each swap which improves results immediately, and hence typically multiple swaps per iteration; this swapping algorithm runs in \( O(n^2) \) rather than \( O(n(n - k)k) \) time which is much faster for all but small \( k \).

In addition, ‘FasterPAM’ uses random initialization of the medoids (instead of the ‘build’ phase) to avoid the \( O(n^2k) \) initialization cost of the build algorithm. In particular for large \( k \), this yields a much faster algorithm, while preserving a similar result quality.

One may decide to use repeated random initialization by setting \( n_{\text{start}} > 1 \).

Value

an object of class “pam” representing the clustering. See ?pam.object for details.

Note

For large datasets, pam may need too much memory or too much computation time since both are \( O(n^2) \). Then, clara() is preferable, see its documentation.

There is hard limit currently, \( n \leq 65536 \), at \( 2^{16} \) because for larger \( n \), \( n(n - 1)/2 \) is larger than the maximal integer (.Machine$integer.max = 2^{31} - 1 \).

Author(s)

Kaufman and Rousseeuw’s orginal Fortran code was translated to C and augmented in several ways, e.g. to allow cluster.only=TRUE or do.swap=FALSE, by Martin Maechler.

Matthias Studer, Univ.Geneva provided the pamonce (1 and 2) implementation.

Erich Schubert, TU Dortmund contributed the pamonce (3 to 6) implementation.

References


See Also

agnes for background and references; pam.object, clara, daisy, partition.object, plot.partition, dist.

Examples

## generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
        cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
pamx <- pam(x, 2)
pamx # Medoids: '7' and '25' ...
summary(pamx)
plot(pamx)

## use obs. 1 & 16 as starting medoids -- same result (typically)
(p2m <- pam(x, 2, medoids = c(1,16)))

## no _build_ *and* no _swap_ phase: just cluster all obs. around (1, 16):
p2.s <- pam(x, 2, medoids = c(1,16), do.swap = FALSE)
p2.s

p3m <- pam(x, 3, trace = 2)

## rather stupid initial medoids:
(p3m. <- pam(x, 3, medoids = 3:1, trace = 1))

pam(daisy(x, metric = "manhattan"), 2, diss = TRUE)
data(ruspini)

## Plot similar to Figure 4 in Stryuf et al (1996)
## Not run: plot(pam(ruspini, 4), ask = TRUE)

pam.object

Partitioning Around Medoids (PAM) Object

Description

The objects of class "pam" represent a partitioning of a dataset into clusters.

Value

A legitimate pam object is a list with the following components:

medoids the medoids or representative objects of the clusters. If a dissimilarity matrix was given as input to pam, then a vector of numbers or labels of observations is given, else medoids is a matrix with in each row the coordinates of one medoid.
id.med integer vector of indices giving the medoid observation numbers.
clustering the clustering vector, see partition.object.
ojective the objective function after the first and second step of the pam algorithm.
isolation vector with length equal to the number of clusters, specifying which clusters are isolated clusters (L- or L*-clusters) and which clusters are not isolated.
A cluster is an L*-cluster iff its diameter is smaller than its separation. A cluster is an L-cluster iff for each observation i the maximal dissimilarity between i and
any other observation of the cluster is smaller than the minimal dissimilarity between i and any observation of another cluster. Clearly each L*-cluster is also an L-cluster.

clusinfo matrix, each row gives numerical information for one cluster. These are the cardinality of the cluster (number of observations), the maximal and average dissimilarity between the observations in the cluster and the cluster’s medoid, the diameter of the cluster (maximal dissimilarity between two observations of the cluster), and the separation of the cluster (minimal dissimilarity between an observation of the cluster and an observation of another cluster).

silinfo list with silhouette width information, see \texttt{partition.object}.

diss dissimilarity (maybe NULL), see \texttt{partition.object}.

call generating call, see \texttt{partition.object}.

data (possibly standardized) see \texttt{partition.object}.

\textbf{GENERATION}

These objects are returned from \texttt{pam}.

\textbf{METHODS}

The "pam" class has methods for the following generic functions: \texttt{print}, \texttt{summary}.

\textbf{INHERITANCE}

The class "pam" inherits from "partition". Therefore, the generic functions \texttt{plot} and \texttt{clusplot} can be used on a \texttt{pam} object.

\textbf{See Also}

\texttt{pam, dissimilarity.object, partition.object, plot.partition}.

\textbf{Examples}

```r
## Use the silhouette widths for assessing the best number of clusters,
## following a one-dimensional example from Christian Hennig:
##
x <- c(rnorm(50), rnorm(50, mean=5), rnorm(30, mean=15))
asw <- numeric(20)
for (k in 2:20)
asw[k] <- pam(x, k) \$ silinfo \$ avg.width
k.best <- which.max(asw)
cat("silhouette-optimal number of clusters:", k.best, "\n")

plot(1:20, asw, type= "h", main = "pam() clustering assessment",
xlab= "k (\# clusters)", ylab = "average silhouette width")
axis(1, k.best, paste("best",k.best,sep="\n"), col = "red", col.axis = "red")
```
**Description**

The objects of class "partition" represent a partitioning of a dataset into clusters.

**Value**

A "partition" object is a list with the following (and typically more) components:

- **clustering**: the clustering vector. An integer vector of length \(n\), the number of observations, giving for each observation the number ('id') of the cluster to which it belongs.
- **call**: the matched call generating the object.
- **silinfo**: a list with all silhouette information, only available when the number of clusters is non-trivial, i.e., \(1 < k < n\) and then has the following components, see silhouette
  - **widths**: an \((n \times 3)\) matrix, as returned by \texttt{silhouette()}\), with for each observation \(i\) the cluster to which \(i\) belongs, as well as the neighbor cluster of \(i\) (the cluster, not containing \(i\), for which the average dissimilarity between its observations and \(i\) is minimal), and the silhouette width \(s(i)\) of the observation.
  - **clus.avg.widths**: the average silhouette width per cluster.
  - **avg.width**: the average silhouette width for the dataset, i.e., simply the average of \(s(i)\) over all observations \(i\).

This information is also needed to construct a silhouette plot of the clustering, see \texttt{plot.partition}.

Note that \texttt{avg.width} can be maximized over different clusterings (e.g. with varying number of clusters) to choose an optimal clustering.

- **objective**: value of criterion maximized during the partitioning algorithm, may more than one entry for different stages.
- **diss**: an object of class "dissimilarity", representing the total dissimilarity matrix of the dataset (or relevant subset, e.g. for \texttt{clara}).
- **data**: a matrix containing the original or standardized data. This might be missing to save memory or when a dissimilarity matrix was given as input structure to the clustering method.

**GENERATION**

These objects are returned from \texttt{pam}, \texttt{clara} or \texttt{fanny}.

**METHODS**

The "partition" class has a method for the following generic functions: \texttt{plot}, \texttt{clusplot}.

**INHERITANCE**

The following classes inherit from class "partition": "pam","clara" and "fanny".

See \texttt{pam.object}, \texttt{clara.object} and \texttt{fanny.object} for details.
See Also

pam, clara, fanny.

plantTraits

---

**Plant Species Traits Data**

**Description**

This dataset constitutes a description of 136 plant species according to biological attributes (morphological or reproductive).

**Usage**

```r
data(plantTraits)
```

**Format**

A data frame with 136 observations on the following 31 variables.

- `pdias` Diaspore mass (mg)
- `longindex` Seed bank longevity
- `durflow` Flowering duration
- `height` Plant height, an ordered factor with levels 1 < 2 < ... < 8.
- `begflow` Time of first flowering, an ordered factor with levels 1 < 2 < 3 < 4 < 5 < 6 < 7 < 8 < 9
- `mycor` Mycorrhizas, an ordered factor with levels 0:never < 1:sometimes < 2:always
- `vegaer` Aerial vegetative propagation, an ordered factor with levels 0:never < 1:present but limited < 2:important.
- `vegsout` Underground vegetative propagation, an ordered factor with 3 levels identical to `vegaer` above.
- `autopoll` Selfing pollination, an ordered factor with levels 0:never < 1:rare < 2:often < 3:the rule
- `insects` Insect pollination, an ordered factor with 5 levels 0 < ... < 4.
- `wind` Wind pollination, an ordered factor with 5 levels 0 < ... < 4.
- `lign` A binary factor with levels 0:1, indicating if plant is woody.
- `piq` A binary factor indicating if plant is thorny.
- `ros` A binary factor indicating if plant is rosette.
- `semiros` Semi-rosette plant, a binary factor (0: no; 1: yes).
- `leafy` Leafy plant, a binary factor.
- `suman` Summer annual, a binary factor.
- `winan` Winter annual, a binary factor.
- `monocarp` Monocarpic perennial, a binary factor.
- `polycarp` Polycarpic perennial, a binary factor.
- `seasaes` Seasonal aestival leaves, a binary factor.
- `seashiv` Seasonal hibernal leaves, a binary factor.
- `seasver` Seasonal vernal leaves, a binary factor.
everalw leaves always evergreen, a binary factor.
everparti leaves partially evergreen, a binary factor.
elaio fruits with an elaiosome (dispersed by ants), a binary factor.
endoo endoochorous fruits, a binary factor.
epizoo epizoochorous fruits, a binary factor.
aquat aquatic dispersal fruits, a binary factor.
windgl wind dispersed fruits, a binary factor.
unsp unspecialized mechanism of seed dispersal, a binary factor.

Details
Most of factor attributes are not disjunctive. For example, a plant can be usually pollinated by insects but sometimes self-pollination can occurred.

Source

Examples

data(plantTraits)

## Calculation of a dissimilarity matrix
library(cluster)
dai.b <- daisy(plantTraits,
type = list(ordratio = 4:11, symm = 12:13, asymm = 14:31))

## Hierarchical classification
agn.trts <- agnes(dai.b, method="ward")
plot(agn.trts, which.plots = 2, cex= 0.6)
plot(agn.trts, which.plots = 1)
cutree6 <- cutree(agn.trts, k=6)
cutree6

## Principal Coordinate Analysis
cmds.dai.b <- cmdscale(dai.b, k=6)
plot(cmds.dai.b[, 1:2], asp = 1, col = cutree6)

---

**plot.agnes**

*Plots of an Agglomerative Hierarchical Clustering*

**Description**

Creates plots for visualizing an agnes object.

**Usage**

```r
## S3 method for class 'agnes'
plot(x, ask = FALSE, which.plots = NULL, main = NULL,
    sub = paste("Agglomerative Coefficient = ",round(x$ac, digits = 2)),
    adj = 0, nmax.lab = 35, max.strlen = 5, xax.pretty = TRUE, ...)
```
Arguments

x
an object of class "agnes", typically created by \texttt{agnes(.)}.

ask
logical; if true and which.plots is NULL, \texttt{plot.agnes} operates in interactive mode, via menu.

which.plots
integer vector or NULL (default), the latter producing both plots. Otherwise, which.plots must contain integers of 1 for a banner plot or 2 for a dendrogram or "clustering tree".

main, sub
main and sub title for the plot, with convenient defaults. See documentation for these arguments in \texttt{plot.default}.

adj
for label adjustment in \texttt{bannerplot()}. 

nmax.lab
integer indicating the number of labels which is considered too large for single-name labelling the banner plot.

max.strlen
positive integer giving the length to which strings are truncated in banner plot labeling.

xax.pretty
logical or integer indicating if \texttt{pretty(*, n = xax.pretty)} should be used for the x axis. \texttt{xax.pretty = FALSE} is for back compatibility.

...
graphical parameters (see \texttt{par}) may also be supplied and are passed to \texttt{bannerplot()} or \texttt{pltree()} (see \texttt{pltree.twins}), respectively.

Details

When \texttt{ask = TRUE}, rather than producing each plot sequentially, \texttt{plot.agnes} displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted one must set \texttt{par(ask= TRUE)} before invoking the plot command.

The banner displays the hierarchy of clusters, and is equivalent to a tree. See Rousseeuw (1986) or chapter 5 of Kaufman and Rousseeuw (1990). The banner plots distances at which observations and clusters are merged. The observations are listed in the order found by the agnes algorithm, and the numbers in the height vector are represented as bars between the observations.

The leaves of the clustering tree are the original observations. Two branches come together at the distance between the two clusters being merged.

For more customization of the plots, rather call \texttt{bannerplot} and \texttt{pltree()}, i.e., its method \texttt{pltree.twins}, respectively.

directly with corresponding arguments, e.g., \texttt{xlab} or \texttt{ylab}.

Side Effects

Appropriate plots are produced on the current graphics device. This can be one or both of the following choices:

Banner
Clustering tree

Note

In the banner plot, observation labels are only printed when the number of observations is limited less than \texttt{nmax.lab} (35, by default), for readability. Moreover, observation labels are truncated to maximally \texttt{max.strlen} (5) characters.

For the dendrogram, more flexibility than via \texttt{pltree()} is provided by \texttt{dg <- as.dendrogram(x)} and plotting \texttt{dg} via \texttt{plot.dendrogram}. 

plot.agnes
plot.diana

Plots of a Divisive Hierarchical Clustering

Description

Creates plots for visualizing a diana object.

Usage

## S3 method for class 'diana'
plot(x, ask = FALSE, which.plots = NULL, main = NULL,
     sub = paste("Divisive Coefficient = ", round(x$dc, digits = 2)),
     adj = 0, nmax.lab = 35, max.strlen = 5, xax.pretty = TRUE, ...)

Arguments

x  an object of class "diana", typically created by diana(.).
ask logical; if true and which.plots is NULL, plot.diana operates in interactive mode, via menu.
which.plots  integer vector or NULL (default), the latter producing both plots. Otherwise, which.plots must contain integers of 1 for a banner plot or 2 for a dendrogram or "clustering tree".
main, sub  main and sub title for the plot, each with a convenient default. See documentation for these arguments in plot.default.
adj  for label adjustment in bannerplot().

Examples

## Can also pass 'labels' to pltree() and bannerplot():
data(iris)
cS <- as.character(Sp <- iris$Species)
cS[Sp == "setosa"] <- "S"
cS[Sp == "versicolor"] <- "V"
cS[Sp == "virginica"] <- "g"
ai <- agnes(iris[, 1:4])
plot(ai, labels = cS, nmax = 150)# bannerplot labels are mess
nmax.lab  integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
max.strlen  positive integer giving the length to which strings are truncated in banner plot labeling.
xax.pretty  logical or integer indicating if pretty(*, n = xax.pretty) should be used for the x axis. xax.pretty = FALSE is for back compatibility.

Details

When ask = TRUE, rather than producing each plot sequentially, plot.diana displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted one must set par(ask = TRUE) before invoking the plot command.

The banner displays the hierarchy of clusters, and is equivalent to a tree. See Rousseeuw (1986) or chapter 6 of Kaufman and Rousseeuw (1990). The banner plots the diameter of each cluster being splitted. The observations are listed in the order found by the diana algorithm, and the numbers in the height vector are represented as bars between the observations.

The leaves of the clustering tree are the original observations. A branch splits up at the diameter of the cluster being splitted.

Side Effects

An appropriate plot is produced on the current graphics device. This can be one or both of the following choices:
Banner
Clustering tree

Note

In the banner plot, observation labels are only printed when the number of observations is limited less than nmax.lab (35, by default), for readability. Moreover, observation labels are truncated to maximally max.strlen (5) characters.

References

see those in plot.agnes.

See Also
diana, diana.object, twins.object, par.

Examples

example(diana)# -> dv <- diana(....)
plot(dv, which = 1, nmax.lab = 100)

## wider labels :
op <- par(mar = par("mar") + c(0, 2, 0,0))
plot(dv, which = 1, nmax.lab = 100, max.strlen = 12)
par(op)
plot.mona

Banner of Monothetic Divisive Hierarchical Clusterings

Description

Creates the banner of a mona object.

Usage

```r
## S3 method for class 'mona'
plot(x, main = paste("Banner of ", deparse1(x$call)),
     sub = NULL, xlab = "Separation step",
     col = c(2,0), axes = TRUE, adj = 0,
     nmax.lab = 35, max.strlen = 5, ...)
```

Arguments

- `x`: an object of class "mona", typically created by `mona(.)`.
- `main,sub`: main and sub titles for the plot, with convenient defaults. See documentation in `plot.default`.
- `xlab`: x axis label, see `title`.
- `col,adj`: graphical parameters passed to `bannerplot()`.
- `axes`: logical, indicating if (labeled) axes should be drawn.
- `nmax.lab`: integer indicating the number of labels which is considered too large for labeling.
- `max.strlen`: positive integer giving the length to which strings are truncated in labeling.
- `...`: further graphical arguments are passed to `bannerplot()` and `text`.

Details

Plots the separation step at which clusters are splitted. The observations are given in the order found by the mona algorithm, the numbers in the step vector are represented as bars between the observations.

When a long bar is drawn between two observations, those observations have the same value for each variable. See chapter 7 of Kaufman and Rousseeuw (1990).

Side Effects

A banner is plotted on the current graphics device.

Note

In the banner plot, observation labels are only printed when the number of observations is limited less than `nmax.lab` (35, by default), for readability. Moreover, observation labels are truncated to maximally `max.strlen` (5) characters.

References

see those in `plot.agnes`.
plot.partition

Plot of a Partition of the Data Set

Description

Creates plots for visualizing a partition object.

Usage

```r
## S3 method for class 'partition'
plot(x, ask = FALSE, which.plots = NULL,
nmax.lab = 40, max.strlen = 5, data = x$data, dist = NULL,
stand = FALSE, lines = 2,
shade = FALSE, color = FALSE, labels = 0, plotchar = TRUE,
span = TRUE, xlim = NULL, ylim = NULL, main = NULL, ...)
```

Arguments

- `x`: an object of class "partition", typically created by the functions `pam, clara,` or `fanny`.
- `ask`: logical; if true and which.plots is NULL, plot.partition operates in interactive mode, via menu.
- `which.plots`: integer vector or NULL (default), the latter producing both plots. Otherwise, which.plots must contain integers of 1 for a clusplot or 2 for silhouette.
- `nmax.lab`: integer indicating the number of labels which is considered too large for single-name labeling the silhouette plot.
- `max.strlen`: positive integer giving the length to which strings are truncated in silhouette plot labeling.
- `data`: numeric matrix with the scaled data; per default taken from the partition object x, but can be specified explicitly.
- `dist`: when x does not have a diss component as for pam(*, keep.diss=FALSE), dist must be the dissimilarity if a clusplot is desired.
- `stand`, `lines`, `shade`, `color`, `labels`, `plotchar`, `span`, `xlim`, `ylim`, `main`, ...: All optional arguments available for the clusplot.default function (except for the diss one) and graphical parameters (see par) may also be supplied as arguments to this function.

Details

When ask= TRUE, rather than producing each plot sequentially, plot.partition displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted, call par (ask= TRUE) before invoking the plot command.

The clusplot of a cluster partition consists of a two-dimensional representation of the observations, in which the clusters are indicated by ellipses (see clusplot.partition for more details).
The silhouette plot of a nonhierarchical clustering is fully described in Rousseeuw (1987) and in chapter 2 of Kaufman and Rousseeuw (1990). For each observation i, a bar is drawn, representing its silhouette width s(i), see silhouette for details. Observations are grouped per cluster, starting with cluster 1 at the top. Observations with a large s(i) (almost 1) are very well clustered, a small s(i) (around 0) means that the observation lies between two clusters, and observations with a negative s(i) are probably placed in the wrong cluster.

A clustering can be performed for several values of k (the number of clusters). Finally, choose the value of k with the largest overall average silhouette width.

Side Effects

An appropriate plot is produced on the current graphics device. This can be one or both of the following choices:

- Clusplot
- Silhouette plot

Note

In the silhouette plot, observation labels are only printed when the number of observations is less than nmax.lab (40, by default), for readability. Moreover, observation labels are truncated to maximally max.strlen (5) characters.

For more flexibility, use plot(silhouette(x), ...), see plot.silhouette.

References


Further, the references in plot.agnes.

See Also

partition.object, clusplot.partition, clusplot.default, pam, pam.object, clara, clara.object, fanny, fanny.object, par.

Examples

```r
## generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
           cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
plot(pam(x, 2))

## Save space not keeping data in clus.object, and still clusplot() it:
data(xclara)
x <- clara(xclara, 3, keep.data = FALSE)
x$data # is NULL
plot(cx, data = xclara)
```
Description

`pltree()` Draws a clustering tree (“dendrogram”) on the current graphics device. We provide the `twins` method draws the tree of a `twins` object, i.e., hierarchical clustering, typically resulting from `agnes()` or `diana()`.

Usage

```r
pltree(x, ...) 
## S3 method for class 'twins'
pltree(x, main = paste("Dendrogram of ", deparse1(x$call)),
       labels = NULL, ylab = "Height", ...)
```

Arguments

- `x` in general, an R object for which a `pltree` method is defined; specifically, an object of class "twins", typically created by either `agnes()` or `diana()`.
- `main` main title with a sensible default.
- `labels` labels to use; the default is constructed from `x`.
- `ylab` label for y-axis.
- `...` graphical parameters (see `par`) may also be supplied as arguments to this function.

Details

Creates a plot of a clustering tree given a `twins` object. The leaves of the tree are the original observations. In case of an agglomerative clustering, two branches come together at the distance between the two clusters being merged. For a divisive clustering, a branch splits up at the diameter of the cluster being splitted.

Note that currently the method function simply calls `plot(as.hclust(x), ...)`, which dispatches to `plot.hclust(...)`. If more flexible plots are needed, consider `xx <- as.dendrogram(as.hclust(x))` and plotting `xx`, see `plot.dendrogram`.

Value

a NULL value is returned.

See Also

`agnes`, `agnes.object`, `diana`, `diana.object`, `hclust`, `par`, `plot.agnes`, `plot.diana`. 
Examples

data(votes.repub)
agn <- agnes(votes.repub)
pltree(agn)

dagn <- as.dendrogram(as.hclust(agn))
dagn2 <- as.dendrogram(as.hclust(agn), hang = 0.2)
op <- par(mar = par("mar") + c(0,0,0, 2)) # more space to the right
plot(dagn2, horiz = TRUE)
plot(dagn, horiz = TRUE, center = TRUE,
     nodePar = list(lab.cex = 0.6, lab.col = "forest green", pch = NA),
     main = deparse(agn$call))
par(op)

---

pluton Isotopic Composition Plutonium Batches

Description

The `pluton` data frame has 45 rows and 4 columns, containing percentages of isotopic composition of 45 Plutonium batches.

Usage

data(pluton)

Format

This data frame contains the following columns:

- **Pu238** the percentages of $^{238}Pu$, always less than 2 percent.
- **Pu239** the percentages of $^{239}Pu$, typically between 60 and 80 percent (from neutron capture of Uranium, $^{238}U$).
- **Pu240** percentage of the plutonium 240 isotope.
- **Pu241** percentage of the plutonium 241 isotope.

Details

Note that the percentage of plutonium~242 can be computed from the other four percentages, see the examples.

In the reference below it is explained why it is very desirable to combine these plutonium patches in three groups of similar size.

Source

Available as `pluton.dat` from the archive of the University of Antwerpen, `../datasets/clusplot-examples.tar.gz`, no longer available.

References

Examples

```r
data(pluton)

hist(apply(pluton, 1, sum), col = "gray") # between 94% and 100%
pu5 <- pluton
pu5$Pu242 <- 100 - apply(pluton, 1, sum) # the remaining isotope.
pairs(pu5)
```

predict.ellipsoid

### Predict Method for Ellipsoid Objects

#### Description

Compute points on the ellipsoid boundary, mostly for drawing.

#### Usage

```r
predict.ellipsoid(object, n.out = 201, ...) 
## S3 method for class 'ellipsoid'
predict(object, n.out = 201, ...)
ellipsoidPoints(A, d2, loc, n.half = 201)
```

#### Arguments

- `object`: an object of class `ellipsoid`, typically from `ellipsoidhull()`; alternatively any list-like object with proper components, see details below.
- `n.out`, `n.half`: half the number of points to create.
- `A`, `d2`, `loc`: arguments of the auxiliary `ellipsoidPoints`, see below.
- `...`: passed to and from methods.

#### Details

Note `ellipsoidPoints` is the workhorse function of `predict.ellipsoid` a standalone function and method for `ellipsoid` objects, see `ellipsoidhull`. The class of `object` is not checked; it must solely have valid components `loc` (length `p`), the `p x p` matrix `cov` (corresponding to `A`) and `d2` for the center, the shape ("covariance") matrix and the squared average radius (or distance) or `qchisq(*, p)` quantile.

Unfortunately, this is only implemented for `p = 2`, currently; contributions for `p ≥ 3` are very welcome.

#### Value

A numeric matrix of dimension `2*n.out` times `p`.

#### See Also

`ellipsoidhull`, `volume.ellipsoid`.
## see also example(ellipsoidhull)

## Robust vs. L.S. covariance matrix

```r
set.seed(143)
x <- rt(200, df=3)
y <- 3*x + rt(200, df=2)
plot(x,y, main="non-normal data (N=200)"
 mtext("with classical and robust cov.matrix ellipsoids")
 X <- cbind(x,y)
 C.ls <- cov(X) ; m.ls <- colMeans(X)
d2.99 <- qchisq(0.99, df = 2)
lines(ellipsoidPoints(C.ls, d2.99, loc=m.ls), col="green")
if(require(MASS)) {
 Cxy <- cov.rob(cbind(x,y))
 lines(ellipsoidPoints(Cxy$cov, d2 = d2.99, loc=Cxy$center), col="red")
}
```

# MASS

---

### Description

Prints the call, agglomerative coefficient, ordering of objects and distances between merging clusters ('Height') of an agnes object.

This is a method for the generic print() function for objects inheriting from class agnes, see agnes.object.

### Usage

```r
## S3 method for class 'agnes'
print(x, ...)
```

### Arguments

- `x` an agnes object.
- `...` potential further arguments (required by generic).

### See Also

summary.agnes producing more output; agnes.agnes.object, print.print.default.
print.clara  

Print Method for CLARA Objects

Description

Prints the best sample, medoids, clustering vector and objective function of clara object. This is a method for the function print() for objects inheriting from class clara.

Usage

```r
## S3 method for class 'clara'
print(x, ...)
```

Arguments

- `x`: a clara object.

- `...`: potential further arguments (require by generic).

See Also

summary.clara producing more output; clara, clara.object, print, print.default.

print.diana  

Print Method for DIANA Objects

Description

Prints the ordering of objects, diameters of splitted clusters, and divisive coefficient of a diana object. This is a method for the function print() for objects inheriting from class diana.

Usage

```r
## S3 method for class 'diana'
print(x, ...)
```

Arguments

- `x`: a diana object.

- `...`: potential further arguments (require by generic).

See Also

diana, diana.object, print, print.default.
print.dissimilarity  

Print and Summary Methods for Dissimilarity Objects

Description

Print or summarize the distances and the attributes of a dissimilarity object.

These are methods for the functions print() and summary() for dissimilarity objects. See print, print.default, or summary for the general behavior of these.

Usage

## S3 method for class 'dissimilarity'
print(x, diag = NULL, upper = NULL,
digits =getOption("digits"), justify = "none", right = TRUE, ...)
## S3 method for class 'dissimilarity'
summary(object,
digits = max(3,getOption("digits") - 2), ...)
## S3 method for class 'summary.dissimilarity'
print(x, ...)

Arguments

x, object  a dissimilarity object or a summary.dissimilarity one for print.summary.dissimilarity().
digits  the number of digits to use, see print.default.
diag, upper, justify, right  optional arguments specifying how the triangular dissimilarity matrix is printed; see print.dist.
...  potential further arguments (require by generic).

See Also
daisy, dissimilarity.object, print, print.default, print.dist.

Examples

## See example(daisy)

sd <- summary(daisy(matrix(rnorm(100), 20,5)))
 sd # -> print.summary.dissimilarity(.)
str(sd)
### print.fanny

**Print and Summary Methods for FANNY Objects**

**Description**

Prints the objective function, membership coefficients and clustering vector of `fanny` object. This is a method for the function `print()` for objects inheriting from class `fanny`.

**Usage**

```r
## S3 method for class 'fanny'
print(x, digits = getOption("digits"), ...)
## S3 method for class 'fanny'
summary(object, ...)
## S3 method for class 'summary.fanny'
print(x, digits = getOption("digits"), ...)
```

**Arguments**

- `x, object` - a `fanny` object.
- `digits` - number of significant digits for printing. see `print.default`.
- `...` - potential further arguments (required by generic).

**See Also**

`fanny, fanny.object, print, print.default`.

### print.mona

**Print Method for MONA Objects**

**Description**

Prints the ordering of objects, separation steps, and used variables of a `mona` object. This is a method for the function `print()` for objects inheriting from class `mona`.

**Usage**

```r
## S3 method for class 'mona'
print(x, ...)
```

**Arguments**

- `x` - a `mona` object.
- `...` - potential further arguments (require by generic).

**See Also**

`mona, mona.object, print, print.default`.
**print.pam**  
*Print Method for PAM Objects*

**Description**
Prints the medoids, clustering vector and objective function of pam object.  
This is a method for the function `print()` for objects inheriting from class pam.

**Usage**
```r
## S3 method for class 'pam'
prompt(x, ...)
```

**Arguments**
- `x` a pam object.
- `...` potential further arguments (require by generic).

**See Also**
`pam`, `pam.object`, `print`, `print.default`.

---

**ruspini**  
*Ruspini Data*

**Description**
The Ruspini data set, consisting of 75 points in four groups that is popular for illustrating clustering techniques.

**Usage**
```r
data(ruspini)
```

**Format**
A data frame with 75 observations on 2 variables giving the x and y coordinates of the points, respectively.

**Source**

**References**
see those in agnes.
Examples

```r
data(ruspini)

## Plot similar to Figure 4 in Stryuf et al (1996)
## Not run: plot(pam(ruspini, 4), ask = TRUE)

## Plot similar to Figure 6 in Stryuf et al (1996)
plot(fanny(ruspini, 5))
```

silhouette

**Compute or Extract Silhouette Information from Clustering**

Description

Compute silhouette information according to a given clustering in \( k \) clusters.

Usage

```r
silhouette(x, ...)
```

## Default S3 method:

```r
silhouette(x, dist, dmatrix, ...)
```

## S3 method for class 'partition'

```r
silhouette(x, ...)
```

## S3 method for class 'clara'

```r
silhouette(x, full = FALSE, subset = NULL, ...)
```

```r
sortSilhouette(object, ...)
```

## S3 method for class 'silhouette'

```r
summary(object, FUN = mean, ...)
```

## S3 method for class 'silhouette'

```r
plot(x, nmax.lab = 40, max.strlen = 5,
main = NULL, sub = NULL, xlab = expression("Silhouette width "* s[i]),
col = "gray", do.col.sort = length(col) > 1, border = 0,
cex.names = par("cex.axis"), do.n.k = TRUE, do.clus.stat = TRUE, ...)
```

Arguments

- **x**: an object of appropriate class; for the default method an integer vector with \( k \) different integer cluster codes or a list with such an x$clustering component. Note that silhouette statistics are only defined if \( 2 \leq k \leq n - 1 \).
- **dist**: a dissimilarity object inheriting from class `dist` or coercible to one. If not specified, `dmatrix` must be.
- **dmatrix**: a symmetric dissimilarity matrix \( (n \times n) \), specified instead of `dist`, which can be more efficient.
- **full**: logical or number in \([0,1]\) specifying if a full silhouette should be computed for `clara` object. When a number, say \( f \), for a random `sample.int(n, size = f*n)` of the data the silhouette values are computed. This requires \( O((f * n)^2) \) memory, since the full dissimilarity of the (sub)sample (see `daisy`) is needed internally.
subset a subset from \(1:n\), specified instead of full to specify the indices of the observations to be used for the silhouette computations.

object an object of class silhouette.

... further arguments passed to and from methods.

FUN function used to summarize silhouette widths.

nmax.lab integer indicating the number of labels which is considered too large for single-name labeling the silhouette plot.

max.strlen positive integer giving the length to which strings are truncated in silhouette plot labeling.

main, sub, xlab arguments to title; have a sensible non-NULL default here.

col, border, cex.names arguments passed barplot(); note that the default used to be \(\text{col} = \text{heat.colors}(n), \text{border} = \text{par("fg")}\) instead.

col can also be a color vector of length \(k\) for clusterwise coloring, see also do.col.sort:

do.col.sort logical indicating if the colors \(\text{col}\) should be sorted “along” the silhouette; this is useful for casewise or clusterwise coloring.

do.n.k logical indicating if \(n\) and \(k\) “title text” should be written.

do.clus.stat logical indicating if cluster size and averages should be written right to the silhouettes.

Details

For each observation \(i\), the silhouette width \(s(i)\) is defined as follows:

Put \(a(i) = \text{average dissimilarity between } i \text{ and all other points of the cluster to which } i \text{ belongs (if } i \text{ is the only observation in its cluster, } s(i) := 0 \text{ without further calculations). For all other clusters } C, \text{ put } d(i, C) = \text{average dissimilarity of } i \text{ to all observations of } C. \text{ The smallest of these } d(i, C) \text{ is } b(i) := \min_C d(i, C), \text{ and can be seen as the dissimilarity between } i \text{ and its “neighbor” cluster, i.e., the nearest one to which it does not belong. Finally,}

\[
s(i) := \frac{b(i) - a(i)}{\max(a(i), b(i))}
\]

silhouette.default() is now based on C code donated by Romain Francois (the R version being still available as \text{cluster::silhouette.default.R}).

Observations with a large \(s(i)\) (almost 1) are very well clustered, a small \(s(i)\) (around 0) means that the observation lies between two clusters, and observations with a negative \(s(i)\) are probably placed in the wrong cluster.

Value

silhouette() returns an object, \(\text{sil}\), of class silhouette which is an \(n \times 3\) matrix with attributes. For each observation \(i\), \(\text{sil}[i,]\) contains the cluster to which \(i\) belongs as well as the neighbor cluster of (the cluster, not containing \(i\), for which the average dissimilarity between its observations and \(i\) is minimal), and the silhouette width \(s(i)\) of the observation. The \text{colnames} correspondingly are \text{c("cluster", "neighbor", "sil_width").}

summary(sil) returns an object of class \text{summary.silhouette}, a list with components

si.summary: numerical \text{summary} of the individual silhouette widths \(s(i)\).
clus.avg.widths: numeric (rank 1) array of clusterwise means of silhouette widths where mean = FUN is used.

avg.width: the total mean FUN(s) where s are the individual silhouette widths.

clus.sizes: table of the k cluster sizes.

call: if available, the call creating sil.

Ordered: logical identical to attr(sil, "Ordered"), see below.

sortSilhouette(sil) orders the rows of sil as in the silhouette plot, by cluster (increasingly) and decreasing silhouette width s(i).

attr(sil, "Ordered") is a logical indicating if sil is ordered as by sortSilhouette(). In that case, rownames(sil) will contain case labels or numbers, and attr(sil, "iOrd") the ordering index vector.

Note

While silhouette() is intrinsic to the partition clusterings, and hence has a (trivial) method for these, it is straightforward to get silhouettes from hierarchical clusterings from silhouette.default() with cutree() and distance as input.

By default, for clara() partitions, the silhouette is just for the best random subset used. Use full = TRUE to compute (and later possibly plot) the full silhouette.

References


chapter 2 of Kaufman and Rousseeuw (1990), see the references in plot.agnes.

See Also

partition.object, plot.partition.

Examples

data(ruspini)
pr4 <- pam(ruspini, 4)
str(si <- silhouette(pr4))
(ssi <- summary(si))
plot(si) # silhouette plot
plot(si, col = c("red", "green", "blue", "purple"))# with cluster-wise coloring

si2 <- silhouette(pr4$clustering, dist(ruspini, "canberra"))
summary(si2) # has small values: "canberra"'s fault
plot(si2, nmax= 80, cex.names=0.6)

op <- par(mfrow= c(3,2), oma= c(0,0, 3, 0),
  mgp= c(1.6,.8,0), mar= .1+c(4,2,2,2))
for(k in 2:6)
  plot(silhouette(pam(ruspini, k=k)), main = paste("k = ",k), do.n.k=FALSE)
  mtext("PAM(Ruspini) as in Kaufman & Rousseeuw, p.101",
    outer = TRUE, font = par("font.main"), cex = par("cex.main"); frame()

  # the same with cluster-wise colours:
c6 <- c("tomato", "forest green", "dark blue", "purple2", "goldenrod4", "gray20")
  for(k in 2:6)
## silhouette(pam(ruspini, k=k)), main = paste("k = ",k), do.n.k=FALSE,
col = c6[1:k])

par(op)

## clara(): standard silhouette is just for the best random subset
data(xclara)
set.seed(7)
str(xc1k <- xclara[ sample(nrow(xclara), size = 1000) ,]) # rownames == indices
c13 <- clara(xc1k, 3)
plot(silhouette(c13))# only of the "best" subset of 46
## The full silhouette: internally needs large (36 MB) dist object:
sf <- silhouette(c13, full = TRUE) ## this is the same as
s.full <- silhouette(c13$clustering, daisy(xc1k))
stopifnot(all.equal(sf, s.full, check.attributes = FALSE, tolerance = 0))
## color dependent on original "3 groups of each 1000": % __FIXME ??__
plot(sf, col = 2+ as.integer(names(c13$clustering) ) %/% 1000,
main ="plot(silhouette(clara(.), full = TRUE))")

## Silhouette for a hierarchical clustering:
ar <- agnes(ruspini)
si3 <- silhouette(cutree(ar, k = 5), # k = 4 gave the same as pam() above
daisy(ruspini))
stopifnot(is.data.frame(di3 <- as.data.frame(si3)))
plot(si3, mmax = 80, cex.names = 0.5)
## 2 groups: agnes() wasn't too good:
si4 <- silhouette(cutree(ar, k = 2), daisy(ruspini))
plot(si4, mmax = 80, cex.names = 0.5)

---

### sizeDiss

**Sample Size of Dissimilarity Like Object**

**Description**

Returns the number of observations (sample size) corresponding to a dissimilarity like object, or equivalently, the number of rows or columns of a matrix when only the lower or upper triangular part (without diagonal) is given.

It is nothing else but the inverse function of \( f(n) = n(n-1)/2 \).

**Usage**

```r
sizeDiss(d)
```

**Arguments**

- `d` any R object with length (typically) \( n(n-1)/2 \).

**Value**

- a number; \( n \) if `length(d) == n(n-1)/2`, NA otherwise.

**See Also**

`dissimilarity.object` and also `as.dist` for class dissimilarity and dist objects which have a `Size` attribute.
Examples

sizeDiss(1:10) # 5, since 10 == 5 * (5 - 1) / 2
sizeDiss(1:9) # NA

n <- 1:100
stopifnot(n == sapply(n*(n-1)/2, function(n) sizeDiss(logical(n))))

summary.agnes  
Summary Method for 'agnes' Objects

Description
Returns (and prints) a summary list for an agnes object. Printing gives more output than the corresponding print.agnes method.

Usage

## S3 method for class 'agnes'
summary(object, ...)

## S3 method for class 'summary.agnes'
print(x, ...)

Arguments

x, object  a agnes object.
...
potential further arguments (require by generic).

See Also

agnes, agnes.object.

Examples

data(agriculture)
summary(agnes(agriculture))

summary.clara  
Summary Method for 'clara' Objects

Description
Returns (and prints) a summary list for a clara object. Printing gives more output than the corresponding print.clara method.

Usage

## S3 method for class 'clara'
summary(object, ...)

## S3 method for class 'summary.clara'
print(x, ...)
Arguments

x, object  a clara object.

...  potential further arguments (require by generic).

See Also

clara.object

Examples

## generate 2000 objects, divided into 5 clusters.
set.seed(47)
x <- rbind(cbind(rnorm(400, 0, 4), rnorm(400, 0, 4)),
            cbind(rnorm(400, 10, 8), rnorm(400, 40, 6)),
            cbind(rnorm(400, 30, 4), rnorm(400, 0, 4)),
            cbind(rnorm(400, 40, 4), rnorm(400, 20, 2)),
            cbind(rnorm(400, 50, 4), rnorm(400, 50, 4)))

clx5 <- clara(x, 5)
## Mis'classification' table:

table(rep(1:5, rep(400,5)), clx5$clust) # -> 1 "error"
summary(clx5)
## Graphically:
par(mfrow = c(3,1), mgp = c(1.5, 0.6, 0), mar = par("mar") - c(0,0,2,0))
plot(x, col = rep(2:6, rep(400,5)))
plot(clx5)}

summary.diana Summary Method for 'diana' Objects

Description

Returns (and prints) a summary list for a diana object.

Usage

## S3 method for class 'diana'
summary(object, ...)
## S3 method for class 'summary.diana'
print(x, ...)

Arguments

x, object  a diana object.

...  potential further arguments (require by generic).

See Also
diana, diana.object.
Summary Method for 'mona' Objects

Description

Returns (and prints) a summary list for a mona object.

Usage

```r
## S3 method for class 'mona'
summary(object, ...)
## S3 method for class 'summary.mona'
print(x, ...)
```

Arguments

- `x, object` a mona object.
- `...` potential further arguments (require by generic).

See Also

mona, mona.object.

Summary Method for PAM Objects

Description

Summarize a pam object and return an object of class summary.pam. There's a print method for the latter.

Usage

```r
## S3 method for class 'pam'
summary(object, ...)
## S3 method for class 'summary.pam'
print(x, ...)
```

Arguments

- `x, object` a pam object.
- `...` potential further arguments (require by generic).

See Also

pam, pam.object.
twins.object

Hierarchical Clustering Object

Description

The objects of class "twins" represent an agglomerative or divisive (polythetic) hierarchical clustering of a dataset.

Value

See agnes.object and diana.object for details.

GENERATION

This class of objects is returned from agnes or diana.

METHODS

The "twins" class has a method for the following generic function: pltree.

INHERITANCE

The following classes inherit from class "twins": "agnes" and "diana".

See Also

agnes, diana.

----------

volume.ellipsoid

Compute the Volume (of an Ellipsoid)

Description

Compute the volume of geometric R object. This is a generic function and has a method for ellipsoid objects (typically resulting from ellipsoidhull()).

Usage

volume(object, ...)  
## S3 method for class 'ellipsoid'  
volume(object, log = FALSE, ...)

Arguments

object

an R object the volume of which is wanted; for the ellipsoid method, an object of that class (see ellipsoidhull or the example below).

log

logical indicating if the volume should be returned in log scale. Maybe needed in largish dimensions.

...

potential further arguments of methods, e.g. log.
Value

a number, the volume \( V \) (or \( \log(V) \) if \( \log = \text{TRUE} \)) of the given object.

Author(s)

Martin Maechler (2002, extracting from former \texttt{clusplot} code); Keefe Murphy (2019) provided code for dimensions \( d > 2 \).

See Also

\texttt{ellipsoidhull} for spanning ellipsoid computation.

Examples

```r
## example(ellipsoidhull) # which defines 'ellipsoid' object <namefoo>
myEl <- structure(list(cov = rbind(c(3,1),1:2), loc = c(0,0), d2 = 10),
                     class = "ellipsoid")
volume(myEl)# i.e. "area" here (d = 2)
myEl # also mentions the "volume"
set.seed(1)
d5 <- matrix(rt(500, df=3), 100,5)
e5 <- ellipsoidhull(d5)
```

Description

A data frame with the percents of votes given to the republican candidate in presidential elections from 1856 to 1976. Rows represent the 50 states, and columns the 31 elections.

Usage

data(votes.repub)

Source


Data from 1964 to 1976 is from R. M. Scammon, \textit{American Votes 12}, Congressional Quarterly.
Bivariate Data Set with 3 Clusters

Description
An artificial data set consisting of 3000 points in 3 quite well-separated clusters.

Usage
data(xclara)

Format
A data frame with 3000 observations on 2 numeric variables (named V1 and V2) giving the x and y coordinates of the points, respectively.

Note
Our version of the xclara is slightly more rounded than the one from read.table("xclara.dat") and the relative difference measured by all.equal is 1.15e-7 for V1 and 1.17e-7 for V2 which suggests that our version has been the result of a options(digits = 7) formatting.

Previously (before May 2017), it was claimed the three cluster were each of size 1000, which is clearly wrong. pam(*, 3) gives cluster sizes of 899, 1149, and 952, which apart from seven "outliers" (or "mislabellings") correspond to observation indices {1 : 900}, {901 : 2050}, and {2051 : 3000}, see the example.

Source
Sample data set accompanying the reference below (file 'xclara.dat' in side 'clus_examples.tar.gz').

References

Examples
## Visualization: Assuming groups are defined as {1:1000}, {1001:2000}, {2001:3000}
plot(xclara, cex = 3/4, col = rep(1:3, each=1000))
p.ID <- c(78, 1411, 2535) ## PAM’s medoid indices  == pam(xclara, 3)$id.med
text(xclara[p.ID,], labels = 1:3, cex=2, col=1:3)

px <- pam(xclara, 3) ## takes ~2 seconds
cxcl <- px$clustering ; iCl <- split(seq_along(cxcl), cxcl)
boxplot(iCl, range = 0.7, horizontal=TRUE,
main = "Indices of the 3 clusters of pam(xclara, 3)"
)

## Look more closely now:
bxCl <- boxplot(iCl, range = 0.7, plot=FALSE)
## We see 3 + 2 + 2 = 7 clear "outlier"s or "wrong group" observations:
with(bxCl, rbind(out, group))
## out  1038 1451 1610  30 327 562  770
Apart from these, what are the robust ranges of indices? -- Robust range:

```r
t(iR <- bxCI$stats[c(1,5),])
```

900

901 2050

2051 3000

gc <- adjustcolor("gray20", 1/2)
abline(v = iR, col = gc, lty=3)
axis(3, at = c(0, iR[2,]), padj = 1.2, col=gc, col.axis=gc)
Chapter 21

The codetools package

---

**checkUsage**  
*Check R Code for Possible Problems*

**Description**
Check R code for possible problems.

**Usage**
```
checkUsage(fun, name = "<anonymous>", report = cat, all = FALSE,  
suppressLocal = FALSE, suppressParamAssigns = !all,  
suppressParamUnused = !all, suppressFundefMismatch = FALSE,  
suppressLocalUnused = FALSE, suppressNoLocalFun = !all,  
skipWith = FALSE, suppressUndefined = dfltSuppressUndefined,  
suppressPartialMatchArgs = TRUE)
```

```
checkUsageEnv(env, ...)
```

```
checkUsagePackage(pack, ...)
```

**Arguments**
- **fun** closure.
- **name** character; name of closure.
- **env** environment containing closures to check.
- **pack** character naming package to check.
- **...** options to be passed to checkUsage.
- **report** function to use to report possible problems.
- **all** logical; report all possible problems if TRUE.
- **suppressLocal** suppress all local variable warnings.
- **suppressParamAssigns** suppress warnings about assignments to formal parameters.
- **suppressParamUnused** suppress warnings about unused formal parameters.

2699
suppressFundefMismatch

suppress warnings about multiple local function definitions with different formal argument lists

suppressLocalUnused

suppress warnings about unused local variables

suppressNoLocalFun

suppress warnings about using local variables as functions with no apparent local function definition

skipWith

logical; if true, do no examine code portion of with expressions.
suppressUndefined

suppress warnings about undefined global functions and variables.
suppressPartialMatchArgs

suppress warnings about partial argument matching

Details

checkUsage checks a single R closure. Options control which possible problems to report. The default settings are moderately verbose. A first pass might use suppressLocal=TRUE to suppress all information related to local variable usage. The suppressXYZ values can either be scalar logicals or character vectors; then they are character vectors they only suppress problem reports for the variables with names in the vector.

checkUsageEnv and checkUsagePackage are convenience functions that apply checkUsage to all closures in an environment or a package. checkUsagePackage requires that the package be loaded. If the package has a name space then the internal name space frame is checked.

Author(s)

Luke Tierney

Examples

checkUsage(checkUsage)
checkUsagePackage("codetools", all=TRUE)
## Not run: checkUsagePackage("base", suppressLocal=TRUE)

Description

These functions provide some tools for analysing R code. Mainly intended to support the other tools in this package and byte code compilation.

Usage

collectLocals(e, collect)
collectUsage(fun, name = "<anonymous>", ...)
constantFold(e, env = NULL, fail = NULL)
findFuncLocals(formals, body)
findLocals(e, envir = .BaseEnv)
findLocalsList(elist, envir = .BaseEnv)
flattenAssignment(e)
getAssignedVar(e)
isConstantValue(v, w)
makeCodeWalker(..., handler, call, leaf)
makeConstantFolder(..., leaf, handler, call, exit, isLocal, foldable, isConstant, signal)
makeLocalsCollector(..., leaf, handler, isLocal, exit, collect)
makeUsageCollector(fun, ..., name, enterLocal, enterGlobal, enterInternal, startCollectLocals, finishCollectLocals, warn, signal)
walkCode(e, w = makeCodeWalker())

Arguments

- **e**: R expression.
- **elist**: list of R expressions.
- **v**: R object.
- **fun**: closure.
- **formals**: formal arguments of a closure.
- **body**: body of a closure.
- **name**: character.
- **env**: character.
- **envir**: environment.
- **w**: code walker.
- **...**: extra elements for code walker.
- **collect**: function.
- **fail**: function.
- **handler**: function.
- **call**: function.
- **leaf**: function.
- **isLocal**: function.
- **exit**: function.
- **enterLocal**: function.
- **enterGlobal**: function.
- **enterInternal**: function.
- **startCollectLocals**: function.
- **finishCollectLocals**: function.
- **warn**: function.
- **signal**: function.
- **isConstant**: function.
- **foldable**: function.

Author(s)

Luke Tierney
findGlobals  

Find Global Functions and Variables Used by a Closure

Description
Finds global functions and variables used by a closure.

Usage
findGlobals(fun, merge = TRUE)

Arguments
fun function object; usually a closure.
merge logical

Details
The result is an approximation. R semantics only allow variables that might be local to be identified (and event that assumes no use of assign and rm).

Value
Character vector if merge is true; otherwise, a list with functions and variables character vector components. Character vectors are of length zero for non-closures.

Author(s)
Luke Tierney

Examples
findGlobals(findGlobals)
findGlobals(findGlobals, merge = FALSE)

showTree  

Print Lisp-Style Representation of R Expression

Description
Prints a Lisp-style representation of R expression. This can be useful for understanding how some things are parsed.

Usage
showTree(e, write = cat)

Arguments
e R expression.
write function of one argument to write the result.
showTree

Author(s)
Luke Tierney

Examples
- showTree(quote(-3))
- showTree(quote("x"<1))
- showTree(quote("f"(x)))
Chapter 22

The foreign package

---

lookup.xport  
Lookup Information on a SAS XPORT Format Library

Description
Scans a file as a SAS XPORT format library and returns a list containing information about the SAS library.

Usage
lookup.xport(file)

Arguments
file  
character variable with the name of the file to read. The file must be in SAS XPORT format.

Value
A list with one component for each dataset in the XPORT format library.

Author(s)
Saikat DebRoy

References

See Also
read.xport
Examples

## Not run: ## no XPORT file is installed.
lookup.xport("test.xpt")

## End(Not run)

read.arff  
Read Data from ARFF Files

Description

Reads data from Weka Attribute-Relation File Format (ARFF) files.

Usage

read.arff(file)

Arguments

file  
a character string with the name of the ARFF file to read from, or a connection which will be opened if necessary, and if so closed at the end of the function call.

Value

A data frame containing the data from the ARFF file.

References

Attribute-Relation File Format  

See Also

write.arff; functions write.arff and read.arff in package RWeka which provide some support for logicals via conversion to or from factors.

read.dbf  
Read a DBF File

Description

The function reads a DBF file into a data frame, converting character fields to factors, and trying to respect NULL fields.

The DBF format is documented but not much adhered to. There is no guarantee this will read all DBF files.

Usage

read.dbf(file, as.is = FALSE)
Arguments

- `file`: name of input file
- `as.is`: should character vectors not be converted to factors?

Details

DBF is the extension used for files written for the ‘XBASE’ family of database languages, ‘covering the dBase, Clipper, FoxPro, and their Windows equivalents Visual dBase, Visual Objects, and Visual FoxPro, plus some older products’ ([https://www.clicketyclick.dk/databases/xbase/format/](https://www.clicketyclick.dk/databases/xbase/format/)). Most of these follow the file structure used by Ashton-Tate’s dBase II, III or 4 (later owned by Borland).

`read.dbf` is based on C code from [http://shapelib.maptools.org/](http://shapelib.maptools.org/) which implements the ‘XBASE’ specification. It can convert fields of type "L" (logical), "N" and "F" (numeric and float) and "D" (dates): all other field types are read as-is as character vectors. A numeric field is read as an `R` integer vector if it is encoded to have no decimals, otherwise as a numeric vector. However, if the numbers are too large to fit into an integer vector, it is changed to numeric. Note that is possible to read integers that cannot be represented exactly even as doubles: this sometimes occurs if IDs are incorrectly coded as numeric.

Value

A data frame of data from the DBF file; note that the field names are adjusted to use in R using `make.names(unique=TRUE)`.

There is an attribute "data_type" giving the single-character dBase types for each field.

Note

Not to be able to read a particular ‘DBF’ file is not a bug: this is a convenience function especially for shapefiles.

Author(s)

Nicholas Lewin-Koh and Roger Bivand; shapelib by Frank Warmerdam

References


See Also

`write.dbf`

Examples

```r
x <- read.dbf(system.file("files/sids.dbf", package="foreign")[1])
str(x)
summary(x)
```
**Description**

Reads a file in Stata version 5–12 binary format into a data frame.

Frozen: will not support Stata formats after 12.

**Usage**

```r
read.dta(file, convert.dates = TRUE, convert.factors = TRUE, missing.type = FALSE, convert.underscore = FALSE, warn.missing.labels = TRUE)
```

**Arguments**

- `file` a filename or URL as a character string.
- `convert.dates` Convert Stata dates to `Date` class, and date-times to `POSIXct` class?
- `convert.factors` Use Stata value labels to create factors? (Version 6.0 or later).
- `missing.type` For version 8 or later, store information about different types of missing data?
- `convert.underscore` Convert "\_" in Stata variable names to "." in R names?
- `warn.missing.labels` Warn if a variable is specified with value labels and those value labels are not present in the file.

**Details**

If the filename appears to be a URL (of schemes ‘http:’, ‘ftp:’ or ‘https:’) the URL is first downloaded to a temporary file and then read. (‘https:’ is only supported on some platforms.)

The variables in the Stata data set become the columns of the data frame. Missing values are correctly handled. The data label, variable labels, timestamp, and variable/dataset characteristics are stored as attributes of the data frame.

By default Stata dates (%d and %td formats) are converted to R’s `Date` class, and variables with Stata value labels are converted to factors. Ordinarily, `read.dta` will not convert a variable to a factor unless a label is present for every level. Use `convert.factors = NA` to override this. In any case the value label and format information is stored as attributes on the returned data frame. Stata’s date formats are sketchily documented: if necessary use `convert.dates = FALSE` and examine the attributes to work out how to post-process the dates.

Stata 8 introduced a system of 27 different missing data values. If `missing.type` is `TRUE` a separate list is created with the same variable names as the loaded data. For string variables the list value is `NULL`. For other variables the value is `NA` where the observation is not missing and 0–26 when the observation is missing. This is attached as the “missing” attribute of the returned value.

The default file format for Stata 13, `format-115`, is substantially different from those for Stata 5–12.
Value

A data frame with attributes. These will include "datalabel", "time.stamp", "formats", "types", "val.labels", "var.labels" and "version" and may include "label.table" and "expansion.table". Possible versions are 5, 6, 7, -7 (Stata 7SE, ‘format-111’), 8 (Stata 8 and 9, ‘format-113’), 10 (Stata 10 and 11, ‘format-114’) and 12 (Stata 12, ‘format-115’).

The value labels in attribute "val.labels" name a table for each variable, or are an empty string. The tables are elements of the named list attribute "label.table": each is an integer vector with names.

Author(s)

Thomas Lumley and R-core members: support for value labels by Brian Quistorff.

References

Stata Users Manual (versions 5 & 6), Programming manual (version 7), or online help (version 8 and later) describe the format of the files. Or directly at https://www.stata.com/help.cgi?dta_114 and https://www.stata.com/help.cgi?dta_113, but note that these have been changed since first published.

See Also

Different approaches are available in package memisc (see its help for Stata.file), function read_dta in package haven and package readstata13.

write.dta, attributes, Date.factor

Examples

write.dta(swiss,swissfile <- tempfile())
read.dta(swissfile)
Arguments

file  A filename, URL, or connection.
read.deleted  Deleted records are read if TRUE, omitted if FALSE or replaced with NA if NA.
guess.broken.dates  Attempt to convert dates with 0 or 2 digit year information (see ‘Details’).
thisyear  A 4-digit year to use for dates with no year. Defaults to the current year.
lower.case.names  Convert variable names to lowercase?

Details

Epi Info allows dates to be specified with no year or with a 2 or 4 digits. Dates with four-digit years are always converted to Date class. With the guess.broken.dates option the function will attempt to convert two-digit years using the operating system’s default method (see Date) and will use the current year or the thisyear argument for dates with no year information.

If read.deleted is TRUE the "deleted" attribute of the data frame indicates the deleted records.

Value

A data frame.

Note

Some later versions of Epi Info use the Microsoft Access file format to store data. That may be readable with the RODBC package.

References

https://www.cdc.gov/epiinfo/, http://www.epidata.dk

See Also

DateTimeClasses

Examples

## Not run: ## That file is not available
read.epiinfo("oswego.rec", guess.broken.dates = TRUE, thisyear = "1972")

## End(Not run)
Arguments

file character variable with the name of the file to read. The file must be in Minitab Portable Worksheet format.

Value

A list with one component for each column, matrix, or constant stored in the Minitab worksheet.

Note

This function was written around 1990 for the format current then. Later versions of Minitab appear to have added to the format.

Author(s)

Douglas M. Bates

References

https://www.minitab.com/

Examples

## Not run:
read.mtp("ex1-10.mtp")
## End(Not run)

Description

Read a file in Octave text data format into a list.

Usage

read.octave(file)

Arguments

file a character string with the name of the file to read.

Details

This function is used to read in files in Octave text data format, as created by `save -text` in Octave. It knows about most of the common types of variables, including the standard atomic (real and complex scalars, matrices, and N-d arrays, strings, ranges, and boolean scalars and matrices) and recursive (structs, cells, and lists) ones, but has no guarantee to read all types. If a type is not recognized, a warning indicating the unknown type is issued, it is attempted to skip the unknown entry, and NULL is used as its value. Note that this will give incorrect results, and maybe even errors, in the case of unknown recursive data types.

As Octave can read MATLAB binary files, one can make the contents of such files available to R by using Octave’s `load` and `save` (as text) facilities as an intermediary step.
Value

A list with one named component for each variable in the file.

Author(s)

Stephen Eglen <stephen@gnu.org> and Kurt Hornik

References

https://octave.org/

---

**read.spss**  
*Read an SPSS Data File*

**Description**

`read.spss` reads a file stored by the SPSS `save` or `export` commands. This was originally written in 2000 and has limited support for changes in SPSS formats since (which have not been many).

**Usage**

```r
read.spss(file, use.value.labels = TRUE, to.data.frame = FALSE,  
max.value.labels = Inf, trim.factor.names = FALSE,  
trim_values = TRUE, reencode = NA, use.missings = to.data.frame,  
sub = ".", add.undeclared.levels = c("sort", "append", "no"),  
duplicated.value.labels = c("append", "condense"),  
duplicated.value.labels.infix = ".duplicated_", ...)```

**Arguments**

- `file`: character string: the name of the file or URL to read.
- `use.value.labels`: logical: convert variables with value labels into R factors with those levels? This is only done if there are at least as many labels as values of the variable (when values without a matching label are returned as NA).
- `to.data.frame`: logical: return a data frame?
- `max.value.labels`: logical: only variables with value labels and at most this many unique values will be converted to factors if TRUE.
- `trim.factor.names`: logical: trim trailing spaces from factor levels?
- `trim_values`: logical: should values and value labels have trailing spaces ignored when matching for use.value.labels = TRUE?
- `reencode`: logical: should character strings be re-encoded to the current locale. The default, NA, means to do so in UTF-8 or latin-1 locales, only. Alternatively a character string specifying an encoding to assume for the file.
- `use.missings`: logical: should information on user-defined missing values be used to set the corresponding values to NA?
read.spss

sub character string: If not NA it is used by iconv to replace any non-convertible bytes in character/factor input. Default is ".". For back compatibility with foreign versions <= 0.8-68 use sub=NA.

add.undeclared.levels character: specify how to handle variables with at least one value label and further non-missing values that have no value label (like a factor levels in R). For "sort" (the default) it adds undeclared factor levels to the already declared levels (and labels) and sort them according to level, for "append" it appends undeclared factor levels to declared levels (and labels) without sorting, and for "no" this does not convert to factor in case of numeric SPSS levels (not labels), and still converts to factor if the SPSS levels are characters and to.data.frame=TRUE. For back compatibility with foreign versions <= 0.8-68 use add.undeclared.levels="no" (not recommended as this may convert some values with missing corresponding value labels to NA).

duplicated.value.labels character: what to do with duplicated value labels for different levels. For "append" (the default), the first original value label is kept while further duplicated labels are renamed to paste0(label, duplicated.value.labels.infix, level), for "condense", all levels with identical labels are condensed into exactly the first of these levels in R. Back compatibility with foreign versions <= 0.8-68 is not given as R versions >= 3.4.0 no longer support duplicated factor labels.

duplicated.value.labels.infix character: the infix used for labels of factor levels with duplicated value labels in SPSS (default "._duplicated_") if duplicated.value.labels="append".

... passed to as.data.frame if to.data.frame = TRUE.

Details

This uses modified code from the PSPP project (http://www.gnu.org/software/pspp/) for reading the SPSS formats.

If the filename appears to be a URL (of schemes 'http:', 'ftp:' or 'https:') the URL is first downloaded to a temporary file and then read. ('https:' is supported where supported by download.file with its current default method.)

Occasionally in SPSS, value labels will be added to some values of a continuous variable (e.g. to distinguish different types of missing data), and you will not want these variables converted to factors. By setting max.value.labels you can specify that variables with a large number of distinct values are not converted to factors even if they have value labels.

If SPSS variable labels are present, they are returned as the "variable.labels" attribute of the answer.

Fixed length strings (including value labels) are padded on the right with spaces by SPSS, and so are read that way by R. The default argument trim.values=TRUE causes trailing spaces to be ignored when matching to value labels, as examples have been seen where the strings and the value labels had different amounts of padding. See the examples for sub for ways to remove trailing spaces in character data.

URL https://learn.microsoft.com/en-us/windows/win32/intl/code-page-identifiers provides a list of translations from Windows codepage numbers to encoding names that iconv is likely to know about and so suitable values for reencode. Automatic re-encoding is attempted for apparent codepages of 200 or more in a UTF-8 or latin-1 locale: some other high-numbered codepages can be re-encoded on most systems, but the encoding names are platform-dependent (see iconvlist).
Value

A list (or optionally a data frame) with one component for each variable in the saved data set.

If what looks like a Windows codepage was recorded in the SPSS file, it is attached (as a number) as attribute "codepage" to the result.

There may be attributes "label.table" and "variable.labels". Attribute "label.table" is a named list of value labels with one element per variable, either NULL or a named character vector. Attribute "variable.labels" is a named character vector with names the short variable names and elements the long names.

If there are user-defined missing values, there will be a attribute "Missings". This is a named list with one list element per variable. Each element has an element type, a length-one character vector giving the type of missingness, and may also have an element value with the values corresponding to missingness. This is a complex subject (where the R and C source code for read.spss is the main documentation), but the simplest cases are types "one", "two" and "three" with a corresponding number of (real or string) values whose labels can be found from the "label.table" attribute. Other possibilities are a finite or semi-infinite range, possibly plus a single value. See also http://www.gnu.org/software/pspp/manual/html_node/Missing-Observations.html#Missing-Observations.

Note

If SPSS value labels are converted to factors the underlying numerical codes will not in general be the same as the SPSS numerical values, since the numerical codes in R are always 1, 2, 3, ....

You may see warnings about the file encoding for SPSS save files: it is possible such files contain non-ASCII character data which need re-encoding. The most common occurrence is Windows codepage 1252, a superset of Latin-1. The encoding is recorded (as an integer) in attribute "codepage" of the result if it looks like a Windows codepage. Automatic re-encoding is done only in UTF-8 and latin-1 locales: see argument reencode.

Author(s)
Saikat DebRoy and the R-core team

See Also
A different interface also based on the PSPP codebase is available in package memisc: see its help for spss.system.file.

Examples

```r
(sav <- system.file("files", "electric.sav", package = "foreign"))
dat <- read.spss(file=sav)
str(dat)  # list structure with attributes
dat <- read.spss(file=sav, to.data.frame=TRUE)
str(dat)  # now a data.frame
```

### Now we use an example file that is not very well structured and hence may need some special treatment with appropriate argument settings.

### Expect lots of warnings as value labels (corresponding to R factor labels) are uncomplete, and an unsupported long string variable is present in the data

```r
(sav <- system.file("files", "testdata.sav", package = "foreign"))
```
### Examples for add.undeclared.levels:
## add.undeclared.levels = "sort" (default):
x.sort <- read.spss(file=sav, to.data.frame = TRUE)
## add.undeclared.levels = "append":
x.append <- read.spss(file=sav, to.data.frame = TRUE,
    add.undeclared.levels = "append")
## add.undeclared.levels = "no":
x.no <- read.spss(file=sav, to.data.frame = TRUE,
    add.undeclared.levels = "no")

levels(x.sort$factor_n_undeclared)
levels(x.append$factor_n_undeclared)
str(x.no$factor_n_undeclared)

### Examples for duplicated.value.labels:
## duplicated.value.labels = "append" (default)
x.append <- read.spss(file=sav, to.data.frame=TRUE)
## duplicated.value.labels = "condense"
x.condense <- read.spss(file=sav, to.data.frame=TRUE,
    duplicated.value.labels = "condense")

levels(x.append$factor_n_duplicated)
levels(x.condense$factor_n_duplicated)
as.numeric(x.append$factor_n_duplicated)
as.numeric(x.condense$factor_n_duplicated)

## Long Strings (>255 chars) are imported in consecutive separate variables
## (see warning about subtype 14):
x <- read.spss(file=sav, to.data.frame=TRUE, stringsAsFactors=FALSE)

cat.long.string <- function(x, w=70) cat(paste(strwrap(x, width=w), "\n"))

## first part: x$string_500:
cat.long.string(x$string_500)
## second part: x$STRIN0:
cat.long.string(x$STRIN0)
## complete long string:
long.string <- apply(x[,c("string_500", "STRIN0")], 1, paste, collapse="")
cat.long.string(long.string)

---

**read.ssd**

*Obtain a Data Frame from a SAS Permanent Dataset, via read.xport*

**Description**

Generates a SAS program to convert the ssd contents to SAS transport format and then uses `read.xport` to obtain a data frame.

**Usage**

```r
read.ssd(libname, sectionnames, 
tmpXport=tempfile(), tmpProglLoc=tempfile(), sascmd="sas")
```
Arguments

libname character string defining the SAS library (usually a directory reference)

sectionnames character vector giving member names. These are files in the libname directory. They will usually have a .ssd0x or .sas7bdat extension, which should be omitted. Use of ASCII names of at most 8 characters is strongly recommended.

tmpXport character string: location where temporary xport format archive should reside – defaults to a randomly named file in the session temporary directory, which will be removed.

tmpProgLoc character string: location where temporary conversion SAS program should reside – defaults to a randomly named file in session temporary directory, which will be removed on successful operation.

sascmd character string giving full path to SAS executable.

Details

Creates a SAS program and runs it.

Error handling is primitive.

Value

A data frame if all goes well, or NULL with warnings and some enduring side effects (log file for auditing)

Note

This requires SAS to be available. If you have a SAS dataset without access to SAS you will need another product to convert it to a format such as .csv, for example ‘Stat/Transfer’ or ‘DBMS/Copy’ or the ‘SAS System Viewer’ (Windows only).

SAS requires section names to be no more than 8 characters. This is worked by the use of symbolic links: these are barely supported on Windows.

Author(s)

For Unix: VJ Carey <stvjc@channing.harvard.edu>

See Also

read.xport

Examples

## if there were some files on the web we could get a real
## runnable example
## Not run:
R> list.files("trialdata")
[1] "baseline.sas7bdat"  "form11.sas7bdat"  "form12.sas7bdat"
[4] "form13.sas7bdat"  "form22.sas7bdat"  "form23.sas7bdat"
[7] "form3.sas7bdat"  "form4.sas7bdat"  "form48.sas7bdat"
[10] "form58.sas7bdat"  "form51.sas7bdat"  "form71.sas7bdat"
[13] "form72.sas7bdat"  "form8.sas7bdat"  "form9.sas7bdat"
[16] "form90.sas7bdat"  "form91.sas7bdat"
R> baseline <- read.ssd("trialdata", "baseline")
read.systat

Obtain a Data Frame from a Systat File

Description

read.systat reads a rectangular data file stored by the Systat SAVE command as (legacy) *.sys or more recently *.syd files.

Usage

read.systat(file, to.data.frame = TRUE)

Arguments

file character variable with the name of the file to read
to.data.frame return a data frame (otherwise a list)

Details

The function only reads those Systat files that are rectangular data files (mtype = 1), and warns when files have non-standard variable name codings. The files tested were produced on MS-DOS and Windows: files for the Mac version of Systat have a completely different format.

The C code was originally written for an add-on module for Systat described in Bivand (1992 paper). Variable names retain the trailing dollar in the list returned when to.data.frame is FALSE, and in that case character variables are returned as is and filled up to 12 characters with blanks on the right. The original function was limited to reading Systat files with up to 256 variables (a Systat limitation); it will now read up to 8192 variables.

If there is a user comment in the header this is returned as attribute "comment". Such comments are always a multiple of 72 characters (with a maximum of 720 chars returned), normally padded with trailing spaces.

Value

A data frame (or list) with one component for each variable in the saved data set.

Author(s)

Roger Bivand
**read.xport**

**Read a SAS XPORT Format Library**

**Description**

Reads a file as a SAS XPORT format library and returns a list of data.frames.

**Usage**

```r
read.xport(file, ...)  
```

**Arguments**

- `file` character variable with the name of the file to read. The file must be in SAS XPORT format.
- `...` passed to `as.data.frame` when creating the data frames.

**Value**

If there is a more than one dataset in the XPORT format library, a named list of data frames, otherwise a data frame. The columns of the data frames will be either numeric (corresponding to numeric in SAS) or factor (corresponding to character in SAS). All SAS numeric missing values (including special missing values represented by ._, .A to .Z by SAS) are mapped to \texttt{NA}.

Trailing blanks are removed from character columns before conversion to a factor. Some sources claim that character missing values in SAS are represented by `'` or `''`; these are not treated as \texttt{NA} missing values.

**Author(s)**

Saikat DebRoy <saikat@stat.wisc.edu>

**References**


---

**Examples**

```r
summary(iris)
iris.s <- read.systat(system.file("files/Iris.syd", package="foreign")[[1]])
str(iris.s)
summary(iris.s)
```
S3 read functions

See Also

lookup.xport

Examples

## Not run: ## no XPORT file is installed
read.xport("test.xpt")

## End(Not run)

S3 read functions

Read an S3 Binary or data.dump File

Description

Reads binary data files or data.dump files that were produced in S version 3.

Usage

data.restore(file, print = FALSE, verbose = FALSE, env = .GlobalEnv)
read.S(file)

Arguments

  file    the filename of the S-PLUS data.dump or binary file.
  print   whether to print the name of each object as read from the file.
  verbose whether to print the name of every subitem within each object.
  env     environment within which to create the restored object(s).

Details

read.S can read the binary files produced in some older versions of S-PLUS on either Windows (versions 3.x, 4.x, 2000) or Unix (version 3.x with 4 byte integers). It automatically detects whether the file was produced on a big- or little-endian machine and adapts itself accordingly.

data.restore can read a similar range of files produced by data.dump and for newer versions of S-PLUS, those from data.dump(..., oldStyle=TRUE).

Not all S3 objects can be handled in the current version. The most frequently encountered exceptions are functions and expressions; you will also have trouble with objects that contain model formulas. In particular, comments will be lost from function bodies, and the argument lists of functions will often be changed.

Value

For read.S, an R version of the S3 object.
For data.restore, the name of the file.

Author(s)

Duncan Murdoch
write.arff

Write Data into ARFF Files

Description

Writes data into Weka Attribute-Relation File Format (ARFF) files.

Usage

write.arff(x, file, eol = "\n", relation = deparse(substitute(x)))

Arguments

x    the data to be written, preferably a matrix or data frame. If not, coercion to a
data frame is attempted.

file  either a character string naming a file, or a connection. "" indicates output to
the standard output connection.

eol    the character(s) to print at the end of each line (row).

relation The name of the relation to be written in the file.

Details

relation will be passed through make.names before writing to the file, in an attempt to it them
acceptable to Weka, and column names what do not start with an alphabetic character will have X
prepended.

However, the references say that ARFF files are ASCII files, and that encoding is not enforced.

References

Attribute-Relation File Format https://waikato.github.io/weka-wiki/formats_and_processing/arff/

See Also

read.arff; functions write.arff and read.arff in package RWeka which provide some support
for logics via conversion to or from factors.

Examples

write.arff(iris, file = "")
Description

The function tries to write a data frame to a DBF file.

Usage

write.dbf(dataframe, file, factor2char = TRUE, max_nchar = 254)

Arguments

dataframe a data frame object.
file a file name to be written to.
factor2char logical, default TRUE, convert factor columns to character: otherwise they are written as the internal integer codes.
max_nchar The maximum number of characters allowed in a character field. Strings which exceed this will be truncated with a warning. See Details.

Details

Dots in column names are replaced by underlines in the DBF file, and names are truncated to 11 characters.

Only vector columns of classes "logical", "numeric", "integer", "character", "factor" and "Date" can be written. Other columns should be converted to one of these.

Maximum precision (number of digits including minus sign and decimal sign) for numeric is 19 - scale (digits after the decimal sign) which is calculated internally based on the number of digits before the decimal sign.

The original DBASE format limited character fields to 254 bytes. It is said that Clipper and FoxPro can read up to 32K, and it is possible to write a reader that could accept up to 65535 bytes. (The documentation suggests that only ASCII characters can be assumed to be supported.) Readers expecting the older standard (which includes Excel 2003, Access 2003 and OpenOffice 2.0) will truncate the field to the maximum width modulo 256, so increase max_nchar only if you are sure the intended reader supports wider character fields.

Value

Invisible NULL.

Note

Other applications have varying abilities to read the data types used here. Microsoft Access reads "numeric", "integer", "character" and "Date" fields, including recognizing missing values, but not "logical" (read as 0,-1). Microsoft Excel understood all possible types but did not interpret missing values in character fields correctly (showing them as character nuls).

Author(s)

Nicholas J. Lewin-Koh, modified by Roger Bivand and Brian Ripley; shapelib by Frank Warmerdam.
write.dta

References

http://shapelib.maptools.org/
https://www.clicketyclick.dk/databases/xbase/format/data_types.html

See Also

read.dbf

Examples

str(warpbreaks)
try1 <- paste(tempfile(), ".dbf", sep = "")
write.dbf(warpbreaks, try1, factor2char = FALSE)
in1 <- read.dbf(try1)
str(in1)
try2 <- paste(tempfile(), ".dbf", sep = "")
write.dbf(warpbreaks, try2, factor2char = TRUE)
in2 <- read.dbf(try2)
str(in2)
unlink(c(try1, try2))

write.dta

Write Files in Stata Binary Format

Description

Writes the data frame to file in the Stata binary format. Does not write array variables unless they can be drop-ed to a vector.

Frozen: will not support Stata formats after 10 (also used by Stata 11).

Usage

write.dta(dataframe, file, version = 7L,
         convert.dates = TRUE, tz = "GMT",
         convert.factors = c("labels", "string", "numeric", "codes"))

Arguments

dataframe

file

version

convert.dates

tz

convert.factors

Write Files in Stata Binary Format

Description

Writes the data frame to file in the Stata binary format. Does not write array variables unless they can be drop-ed to a vector.

Frozen: will not support Stata formats after 10 (also used by Stata 11).

Usage

write.dta(dataframe, file, version = 7L,
         convert.dates = TRUE, tz = "GMT",
         convert.factors = c("labels", "string", "numeric", "codes"))

Arguments

dataframe

file

version

convert.dates

tz

convert.factors

character string giving filename.

integer: Stata version: 6, 7, 8 and 10 are supported, and 9 is mapped to 8, 11 to 10.

logical: convert Date and POSIXct objects: see section ‘Dates’.

timezone for date conversion.

how to handle factors.
Details

The major difference between supported file formats in Stata versions is that version 7.0 and later allow 32-character variable names (5 and 6 were restricted to 8-character names). The `abbreviate` function is used to trim variable names to the permitted length. A warning is given if this is needed and it is an error for the abbreviated names not to be unique. Each version of Stata is claimed to be able to read all earlier formats.

The columns in the data frame become variables in the Stata data set. Missing values are handled correctly.

There are four options for handling factors. The default is to use Stata ‘value labels’ for the factor levels. With `convert.factors = "string"`, the factor levels are written as strings (the name of the value label is taken from the "val.labels" attribute if it exists or the variable name otherwise). With `convert.factors = "numeric"` the numeric values of the levels are written, or NA if they cannot be coerced to numeric. Finally, `convert.factors = "codes"` writes the underlying integer codes of the factors. This last used to be the only available method and is provided largely for backwards compatibility.

If the "label.table" attribute contains value labels with names not already attached to a variable (not the variable name or name from "val.labels") then these will be written out as well.

If the "datalabel" attribute contains a string, it is written out as the dataset label otherwise the dataset label is "Written by R."

If the "expansion.table" attribute exists expansion fields are written. This attribute should contain a list where each element is character vector of length three. The first vector element contains the name of a variable or "_dta" (meaning the dataset). The second element contains the characteristic name. The third contains the associated data.

If the "val.labels" attribute contains a character vector with a string label for each value then this is written as the value labels. Otherwise the variable names are used.

If the "var.labels" attribute contains a character vector with a string label for each variable then this is written as the variable labels. Otherwise the variable names are repeated as variable labels.

For Stata 8 or later use the default `version = 7` – the only advantage of Stata 8 format over 7 is that it can represent multiple different missing value types, and R doesn’t have them. Stata 10/11 allows longer format lists, but R does not make use of them.

Note that the Stata formats are documented to use ASCII strings – R does not enforce this, but use of non-ASCII character strings will not be portable as the encoding is not recorded. Up to 244 bytes are allowed in character data, and longer strings will be truncated with a warning.

Stata uses some large numerical values to represent missing values. This function does not currently check, and hence integers greater than 2147483620 and doubles greater than 8.988e+307 may be misinterpreted by Stata.

Value

NULL

Dates

Unless disabled by argument `convert.dates = FALSE`, R date and date-time objects (POSIXt classes) are converted into the Stata date format, the number of days since 1960-01-01. (For date-time objects this may lose information.) Stata can be told that these are dates by

```
format xdate %td;
```
It is possible to pass objects of class POSIXct to Stata to be treated as one of its versions of dates-
times. Stata uses the number of milliseconds since 1960-01-01, either excluding (format %tc) or
counting (format %tC) leap seconds. So either an object of class POSIXct can be passed to Stata with
convert.dates = FALSE and converted in Stata, or 315619200 should be added and then multiplied
by 1000 before passing to write.dta and assigning format %tc. Stata’s comments on the first
route are at https://www.stata.com/manuals13/ddatetime.pdf, but at the time of writing were
wrong: R uses POSIX conventions and hence does not count leap seconds.

Author(s)

Thomas Lumley and R-core members: support for value labels by Brian Quistorff.

References

Stata 6.0 Users Manual, Stata 7.0 Programming manual, Stata online help (version 8 and
cgi?dta_113) describe the file formats.

See Also

read.dta, attributes, DateTimeClasses, abbreviate

Examples

write.dta(swiss, swissfile <- tempfile())
read.dta(swissfile)

write.foreign
Write Text Files and Code to Read Them

Description

This function exports simple data frames to other statistical packages by writing the data as free-
format text and writing a separate file of instructions for the other package to read the data.

Usage

write.foreign(df, datafile, codefile,
               package = c("SPSS", "Stata", "SAS"), ...)

Arguments

df A data frame
datafile Name of file for data output
codefile Name of file for code output
package Name of package
... Other arguments for the individual writeForeign functions
Details

The work for this function is done by `foreign:::writeForeignStata`, `foreign:::writeForeignSAS` and `foreign:::writeForeignSPSS`. To add support for another package, e.g. Systat, create a function `writeForeignSystat` with the same first three arguments as `write.foreign`. This will be called from `write.foreign` when `package="Systat"`.

Numeric variables and factors are supported for all packages: dates and times (`Date`, `dates`, `date`, and `POSIXt` classes) and logical vectors are also supported for SAS and characters are supported for SPSS.

For `package="SAS"` there are optional arguments `dataname = "rdata"` taking a string that will be the SAS data set name, `validvarname` taking either "V6" or "V7", and `libpath = NULL` taking a string that will be the directory where the target SAS datset will be written when the generated SAS code have been run.

For `package="SPSS"` there is an optional argument `maxchars = 32L` taking an integer that causes the variable names (not variable labels) to be abbreviated to not more than `maxchars` chars. For compatibility with SPSS version 12 and before, change this to `maxchars = 8L`. In single byte locales with SPSS versions 13 or later, this can be set to `maxchars = 64L`.

For `package="SPSS"`, as a side effect, the decimal indicator is always set by `SET DECIMAL=DOT`. which may override user settings of the indicator or its default derived from the current locale.

Value

Invisible `NULL`.

Author(s)

Thomas Lumley and Stephen Weigand

Examples

```r
## Not run:
datafile <- tempfile()
codefile <- tempfile()
write.foreign(esoph, datafile, codefile, package="SPSS")
file.show(datafile)
file.show(codefile)
unlink(datafile)
unlink(codefile)

## End(Not run)
```
Chapter 23

The lattice package

Description

The lattice add-on package is an implementation of Trellis graphics for R. It is a powerful and elegant high-level data visualization system with an emphasis on multivariate data. It is designed to meet most typical graphics needs with minimal tuning, but can also be easily extended to handle most nonstandard requirements.

Details

Trellis Graphics, originally developed for S and S-PLUS at the Bell Labs, is a framework for data visualization developed by R. A. Becker, W. S. Cleveland, et al, extending ideas presented in Cleveland's 1993 book Visualizing Data. The Lattice API is based on the original design in S, but extends it in many ways.

The Lattice user interface primarily consists of several 'high-level' generic functions (listed below in the “See Also” section), each designed to create a particular type of display by default. Although the functions produce different output, they share many common features, reflected in several common arguments that affect the resulting displays in similar ways. These arguments are extensively (sometimes only) documented in the help page for xyplot, which also includes a discussion of the important topics of conditioning and control of the Trellis layout. Features specific to other high-level functions are documented in their respective help pages.

Lattice employs an extensive system of user-controllable settings to determine the look and feel of the displays it produces. To learn how to use and customize the graphical parameters used by lattice, see trellis.par.set. For other settings, see lattice.options. The default graphical settings are (potentially) different for different graphical devices. To learn how to initialize new devices with the desired settings or change the settings of the current device, see trellis.device.

It is usually unnecessary, but sometimes important to be able to plot multiple lattice plots on a single page. Such capabilities are described in the print.trellis help page. See update.trellis to learn about manipulating a "trellis" object. Tools to augment lattice plots after they are drawn (including locator-like functionality) are described in the trellis.focus help page.

The online documentation accompanying the package is complete, and effort has been made to present the help pages in a logical sequence, so that one can learn how to use lattice by reading
the PDF reference manual available at https://cran.r-project.org/package=lattice. However, the format in which the online documentation is written and the breadth of topics covered necessarily makes it somewhat terse and less than ideal as a first introduction. For a more gentle introduction, a book on lattice is available as part of Springer’s ‘Use R’ series; see the “References” section below.

Note

High-level lattice functions like `xyplot` are different from traditional R graphics functions in that they do not perform any plotting themselves. Instead, they return an object, of class “trellis”, which has to be then print-ed or plot-ed to create the actual plot. Due to R’s automatic printing rule, it is usually not necessary to explicitly carry out the second step, and lattice functions appear to behave like their traditional counterparts. However, the automatic plotting is suppressed when the high-level functions are called inside another function (most often source) or in other contexts where automatic printing is suppressed (e.g., for or while loops). In such situations, an explicit call to print or plot is required.

The lattice package is based on the Grid graphics engine and requires the grid add-on package. One consequence of this is that it is not (readily) compatible with traditional R graphics tools. In particular, changing par() settings usually has no effect on Lattice plots; lattice provides its own interface for querying and modifying an extensive set of graphical and non-graphical settings.

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References


Bell Lab’s Trellis Page contains several documents outlining the use of Trellis graphics; these provide a holistic introduction to the Trellis paradigm: http://web.archive.org/web/20081020164041/http://cm.bell-labs.com/cm/ms/departments/sia/project/trellis/display.writing.html

See Also

The following is a list of high-level functions in the lattice package and their default displays. In all cases, the actual display is produced by the so-called “panel” function, which has a suitable default, but can be substituted by an user defined function to create customized displays. In many cases, the default panel function will itself have many optional arguments to customize its output. The default panel functions are named as “panel_” followed by the name of the corresponding high-level function; i.e., the default panel function for `xyplot` is `panel.xyplot`, the one for `histogram` is `panel.histogram`, etc. Each default panel function has a separate help page, linked from the help pages of the corresponding high-level function. Although documented separately, arguments to these panel functions can be supplied directly to the high-level functions, which will pass on the arguments appropriately.

Univariate:

*barchart*: Bar plots.
bwplot: Box-and-whisker plots.
densityplot: Kernel density estimates.
dotplot: Cleveland dot plots.
histogram: Histograms.
qqmath: Theoretical quantile plots.
stripplot: One-dimensional scatterplots.

Bivariate:

qq: Quantile plots for comparing two distributions.
xyplot: Scatterplots and time-series plots (and potentially a lot more).

Trivariate:

levelplot: Level plots (similar to image plots).
contourplot: Contour plots.
cloud: Three-dimensional scatter plots.
wireframe: Three-dimensional surface plots (similar to persp plots).

Hypervariate:

splom: Scatterplot matrices.
parallel: Parallel coordinate plots.

Miscellaneous:

rfs: Residual and fitted value plots (also see oneway).
tmd: Tukey Mean-Difference plots.

In addition, there are several panel functions that do little by themselves, but can be useful components of custom panel functions. These are documented in panel.functions. Lattice also provides a collection of convenience functions that correspond to the traditional graphics primitives lines, points, etc. These are implemented using Grid graphics, but try to be as close to the traditional versions as possible in terms of their argument list. These functions have names like llines or panel.lines and are often useful when writing (or porting from S-PLUS code) nontrivial panel functions.

Finally, many useful enhancements that extend the Lattice system are available in the latticeExtra package.

Examples

## Not run:

## Show brief history of changes to lattice, including
## a summary of new features.
RShowDoc("NEWS", package = "lattice")

## End(Not run)
Description

This help page documents several commonly used high-level Lattice functions. `xyplot` produces bivariate scatterplots or time-series plots, `bwplot` produces box-and-whisker plots, `dotplot` produces Cleveland dot plots, `barchart` produces bar plots, and `stripplot` produces one-dimensional scatterplots. All these functions, along with other high-level Lattice functions, respond to a common set of arguments that control conditioning, layout, aspect ratio, legends, axis annotation, and many other details in a consistent manner. These arguments are described extensively in this help page, and should be used as the reference for other high-level functions as well.

For control and customization of the actual display in each panel, the help page of the respective default panel function will often be more informative. In particular, these help pages describe many arguments commonly used when calling the corresponding high-level function but are specific to them.

Usage

```r
xyplot(x, data, ...)
dotplot(x, data, ...)
barchart(x, data, ...)
stripplot(x, data, ...)
bwplot(x, data, ...)

## S3 method for class 'formula'
xyplot(x, data,
       allow.multiple = is.null(groups) || outer,
       outer = !is.null(groups),
       auto.key = lattice.getOption("default.args")$auto.key,
       aspect = "fill",
       panel = lattice.getOption("panel.xyplot"),
       prepanel = NULL,
       scales = list(),
       strip = TRUE,
       groups = NULL,
       xlab,
       xlim,
       ylab,
       ylim,
       drop.unused.levels = lattice.getOption("drop.unused.levels"),
       ...
       lattice.options = NULL,
       default.scales,
       default.prepanel = lattice.getOption("prepanel.default.xyplot"),
       subscripts = !is.null(groups),
       subset = TRUE)

## S3 method for class 'data.frame'
```

---

**B_00_xyplot**

*Common Bivariate Trellis Plots*

---
B_00_xyplot

xyplot(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
dotplot(x, 
data,
panel = lattice.getOption("panel.dotplot"),
default.prepanel = lattice.getOption("prepanel.default.dotplot"),
...
)

## S3 method for class 'data.frame'
dotplot(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
barchart(x, 
data,
panel = lattice.getOption("panel.barchart"),
default.prepanel = lattice.getOption("prepanel.default.barchart"),
box.ratio = 2,
...
)

## S3 method for class 'data.frame'
barchart(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
stripplot(x, 
data,
panel = lattice.getOption("panel.stripplot"),
default.prepanel = lattice.getOption("prepanel.default.stripplot"),
...
)

## S3 method for class 'data.frame'
stripplot(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
bwplot(x, 
data,
allow.multiple = is.null(groups) || outer,
outer = FALSE,
auto.key = lattice.getOption("default.args")$auto.key,
aspect = "fill",
panel = lattice.getOption("panel.bwplot"),
prepanel = NULL,
scales = list(),
strip = TRUE,
groups = NULL,
xlab,
xlim,
ylab,
ylim,
box.ratio = 1,
horizontal = NULL,
drop.unused.levels = lattice.getOption("drop.unused.levels"),
...
...,
lattice.options = NULL,
default.scales,
default.prepanel = lattice.getOption("prepanel.default.bwplot"),
subscripts = !is.null(groups),
subset = TRUE)

## S3 method for class 'data.frame'
bwplot(x, data = NULL, formula = data, ...)

Arguments

x All high-level function in lattice are generic. x is the object on which method dispatch is carried out.

For the “formula” methods, x must be a formula describing the primary variables (used for the per-panel display) and the optional conditioning variables (which define the subsets plotted in different panels) to be used in the plot. Conditioning is described in the “Details” section below.

For the functions documented here, the formula is generally of the form y ~ x | g1 * g2 * ... (or equivalently, y ~ x | g1 + g2 + ...), indicating that plots of y (on the y-axis) versus x (on the x-axis) should be produced conditional on the variables g1, g2, ... Here x and y are the primary variables, and g1, g2, ... are the conditioning variables. The conditioning variables may be omitted to give a formula of the form y ~ x, in which case the plot will consist of a single panel with the full dataset. The formula can also involve expressions, e.g., sqrt(), log(), etc. See the data argument below for rules regarding evaluation of the terms in the formula.

With the exception of xyplot, the functions documented here may also be supplied a formula of the form ~ x | g1 * g2 * .... In that case, y defaults to names(x) if x is named, and a factor with a single level otherwise.

Cases where x is not a formula is handled by appropriate methods. The numeric methods are equivalent to a call with no left hand side and no conditioning variables in the formula. For barchart and dotplot, non-trivial methods exist for tables and arrays, documented at barchart.table.

The conditioning variables g1, g2, ... must be either factors or shingles. Shin-gles provide a way of using numeric variables for conditioning; see the help page of shingle for details. Like factors, they have a "levels" attribute, which is used in producing the conditional plots. If necessary, numeric conditioning variables are converted to shingles using the shingle function; however, using equal.count may be more appropriate in many cases. Character variables are coerced to factors.

Extended formula interface: As a useful extension of the interface described above, the primary variable terms (both the LHS y and RHS x) may consist of multiple terms separated by a ‘+’ sign, e.g., y1 + y2 ~ x | a * b. This formula would be taken to mean that the user wants to plot both y1 ~ x | a * b and y2 ~ x | a * b, but with the y1 ~ x and y2 ~ x superposed in each panel. The two groups will be distinguished by different graphical parameters. This is essentially what the groups argument (see below) would produce, if y1 and y2 were concatenated to produce a longer vector, with the groups argument being an indicator of which rows come from which variable. In fact, this is exactly what
is done internally using the reshape function. This feature cannot be used in conjunction with the groups argument.

To interpret y1 + y2 as a sum, one can either set allow.multiple=FALSE or use I(y1+y2).

A variation on this feature is when the outer argument is set to TRUE. In that case, the plots are not superposed in each panel, but instead separated into different panels (as if a new conditioning variable had been added).

**Primary variables:** The x and y variables should both be numeric in xyplot, and an attempt is made to coerce them if not. However, if either is a factor, the levels of that factor are used as axis labels. In the other four functions documented here, exactly one of x and y should be numeric, and the other a factor or shingle. Which of these will happen is determined by the horizontal argument — if horizontal=TRUE, then y will be coerced to be a factor or shingle, otherwise x. The default value of horizontal is FALSE if x is a factor or shingle, TRUE otherwise. (The functionality provided by horizontal=FALSE is not S-compatible.)

Note that the x argument used to be called formula in earlier versions (when the high-level functions were not generic and the formula method was essentially the only method). This is no longer allowed. It is recommended that this argument not be named in any case, but instead be the first (unnamed) argument.

**data**

For the formula methods, a data frame (or more precisely, anything that is a valid envir argument in eval, e.g., a list or an environment) containing values for any variables in the formula, as well as groups and subset if applicable. If not found in data, or if data is unspecified, the variables are looked for in the environment of the formula. For other methods (where x is not a formula), data is usually ignored, often with a warning if it is explicitly specified.

**allow.multiple**

Logical flag specifying whether the extended formula interface described above should be in effect. Defaults to TRUE whenever sensible.

**outer**

Logical flag controlling what happens with formulas using the extended interface described above (see the entry for x for details). Defaults to FALSE, except when groups is explicitly specified or grouping does not make sense for the default panel function.

**box.ratio**

Applicable to barchart and bwplot. Specifies the ratio of the width of the rectangles to the inter-rectangle space. See also the box.width argument in the respective default panel functions.

**horizontal**

Logical flag applicable to bwplot, dotplot, barchart, and stripplot. Determines which of x and y is to be a factor or shingle (y if TRUE, x otherwise). Defaults to FALSE if x is a factor or shingle, TRUE otherwise. This argument is used to process the arguments to these high-level functions, but more importantly, it is passed as an argument to the panel function, which is expected to use it as appropriate.

A potentially useful component of scales in this case may be abbreviate = TRUE, in which case long labels which would usually overlap will be abbreviated. scales could also contain a minlength argument in this case, which would be passed to the abbreviate function.

**Common arguments:** The following arguments are common to all the functions documented here, as well as most other high-level Trellis functions. These are not documented elsewhere, except to override the usage given here.
Once the subset of rows defined by each unique combination of the levels of the grouping variables are obtained (see “Details”), the corresponding x and y variables (or other variables, as appropriate, in the case of other high-level functions) are passed on to be plotted in each panel. The actual plotting is done by the function specified by the \texttt{panel} argument. The argument may be a function object or a character string giving the name of a predefined function. Each high-level function has its own default panel function, named as “\texttt{panel}.” followed by the name of the corresponding high-level function (e.g., \texttt{panel.xyplot}, \texttt{panel.barchart}, etc).

Much of the power of Trellis Graphics comes from the ability to define customized panel functions. A panel function appropriate for the functions described here would usually expect arguments named \texttt{x} and \texttt{y}, which would be provided by the conditioning process. It can also have other arguments. It is useful to know in this context that all arguments passed to a high-level Lattice function (such as \texttt{xyplot}) that are not recognized by it are passed through to the panel function. It is thus generally good practice when defining panel functions to allow \texttt{\ldots} argument. Such extra arguments typically control graphical parameters, but other uses are also common. See documentation for individual panel functions for specifics.

Note that unlike in S-PLUS, it is not guaranteed that panel functions will be supplied only numeric vectors for the \texttt{x} and \texttt{y} arguments; they can be factors as well (but not shingles). Panel functions need to handle this case, which in most cases can be done by simply coercing them to numeric.

Technically speaking, panel functions must be written using Grid graphics functions. However, knowledge of Grid is usually not necessary to construct new custom panel functions, as there are several predefined panel functions which can help; for example, \texttt{panel.grid}, \texttt{panel.loess}, etc. There are also some grid-compatible replacements of commonly used traditional graphics functions useful for this purpose. For example, \texttt{lines} can be replaced by \texttt{llines} (or equivalently, \texttt{panel.lines}). Note that traditional graphics functions like \texttt{lines} will not work in a lattice panel function.

One case where a bit more is required of the panel function is when the \texttt{groups} argument is not \texttt{NULL}. In that case, the panel function should also accept arguments named \texttt{groups} and \texttt{subscripts} (see below for details). A useful panel function predefined for use in such cases is \texttt{panel.superpose}, which can be combined with different \texttt{panel.groups} functions to determine what is plotted for each group. See the “Examples” section for an interaction plot constructed in this way. Several other panel functions can also handle the \texttt{groups} argument, including the default ones for \texttt{xyplot}, \texttt{barchart}, \texttt{dotplot}, and \texttt{stripplot}.

Even when \texttt{groups} is not present, the panel function can have \texttt{subscripts} as a formal argument. In either case, the \texttt{subscripts} argument passed to the panel function are the indices of the \texttt{x} and \texttt{y} data for that panel in the original data, BEFORE taking into account the effect of the subset argument. Note that \texttt{groups} remains unaffected by any subsetting operations, so \texttt{groups[subscripts]} gives the values of \texttt{groups} that correspond to the data in that panel.

This interpretation of \texttt{subscripts} does not hold when the extended formula interface is in use (i.e., when \texttt{allow.multiple} is in effect). A comprehensive description would be too complicated (details can be found in the source code of the function \texttt{latticeParseFormula}), but in short, the extended interface works by creating an artificial grouping variable that is longer than the original data frame, and consequently, \texttt{subscripts} needs to refer to rows beyond those in
the original data. To further complicate matters, the artificial grouping variable is created after any effect of subset, in which case subscripts may have no relationship with corresponding rows in the original data frame.

One can also use functions called \texttt{panel.number} and \texttt{packet.number}, representing panel order and packet order respectively, inside the panel function (as well as the strip function or while interacting with a lattice display using \texttt{trellis.focus} etc). Both provide a simple integer index indicating which panel is currently being drawn, but differ in how the count is calculated. The panel number is a simple incremental counter that starts with 1 and is incremented each time a panel is drawn. The packet number on the other hand indexes the combination of levels of the conditioning variables that is represented by that panel. The two indices coincide unless the order of conditioning variables is permuted and/or the plotting order of levels within one or more conditioning variables is altered (using \texttt{perm.cond} and \texttt{index.cond} respectively), in which case \texttt{packet.number} gives the index corresponding to the ‘natural’ ordering of that combination of levels of the conditioning variables.

\texttt{panel.xyplot} has an argument called \texttt{type} which is worth mentioning here because it is quite frequently used (and as mentioned above, can be passed to \texttt{xyplot} directly). In the event that a \texttt{groups} variable is used, \texttt{panel.xyplot} calls \texttt{panel.superpose}, arguments of which can also be passed directly to \texttt{xyplot}. Panel functions for \texttt{bwplot} and friends should have an argument called \texttt{horizontal} to account for the cases when \texttt{x} is the factor or shingle.

\textbf{aspect}  
This argument controls the physical aspect ratio of the panels, which is usually the same for all the panels. It can be specified as a ratio (vertical size/horizontal size) or as a character string. In the latter case, legitimate values are "fill" (the default) which tries to make the panels as big as possible to fill the available space; "xy", which computes the aspect ratio based on the 45 degree banking rule (see \texttt{banking}); and "iso" for isometric scales, where the relation between physical distance on the device and distance in the data scale are forced to be the same for both axes.

If a \texttt{prepanel} function is specified and it returns components \texttt{dx} and \texttt{dy}, these are used for banking calculations. Otherwise, values from the default \texttt{prepanel} function are used. Not all default \texttt{prepanel} functions produce sensible banking calculations.

\textbf{groups}  
A variable or expression to be evaluated in \texttt{data}, expected to act as a grouping variable within each panel, typically used to distinguish different groups by varying graphical parameters like color and line type. Formally, if \texttt{groups} is specified, then \texttt{groups} along with \texttt{subscripts} is passed to the panel function, which is expected to handle these arguments. For high level functions where grouping is appropriate, the default panel functions can handle grouping.

It is very common to use a key (legend) when a grouping variable is specified. See entries for \texttt{key}, \texttt{auto.key} and \texttt{simpleKey} for how to draw a key.

\textbf{auto.key}  
A logical, or a list containing components to be used as arguments to \texttt{simpleKey}. The default can be set using \texttt{lattice.options}.

\texttt{auto.key = TRUE} is equivalent to \texttt{auto.key = list()}, in which case \texttt{simpleKey} is called with a set of default arguments (which may depend on the relevant high-level function). Most valid components to the key argument can be specified in this manner, as \texttt{simpleKey} will simply add unrecognized arguments to the list it produces.

\texttt{auto.key} is typically used to automatically produce a suitable legend in conjunction with a grouping variable. If \texttt{auto.key = TRUE}, a suitable legend will
be drawn if a `groups` argument is also provided, and not otherwise. In list form, `auto.key` will modify the default legend thus produced. For example, `auto.key=list(columns = 2)` will create a legend split into two columns (columns is documented in the entry for key).

More precisely, if `auto.key` is not `FALSE`, `groups` is non-null, and there is no key or legend argument specified in the call, a key is created with `simpleKey` with `levels(groups)` as the first (text) argument. (Note: this may not work in all high-level functions, but it does work for the ones where grouping makes sense with the default panel function). If `auto.key` is provided as a list and includes a `text` component, then that is used instead as the text labels in the key, and the key is drawn even if `groups` is not specified.

Note that `simpleKey` uses the default settings (see `trellis.par.get`) to determine the graphical parameters in the key, so the resulting legend will be meaningful only if the same settings are used in the plot as well. The `par.settings` argument, possibly in conjunction with `simpleTheme`, may be useful to temporarily modify the default settings for this purpose.

One disadvantage to using key (or even `simpleKey`) directly is that the graphical parameters used in the key are absolutely determined at the time when the "trellis" object is created. Consequently, if a plot once created is re-plotted with different settings, the original parameter settings will be used for the key even though the new settings are used for the actual display. However, with `auto.key`, the key is actually created at plotting time, so the settings will match.

A function that takes the same arguments as the panel function and returns a list, possibly containing components named `xlim`, `ylim`, `dx`, and `dy` (and less frequently, `xat` and `yat`). The return value of a user-supplied prepanel function need not contain all these components; in case some are missing, they are replaced by the component-wise defaults.

The `xlim` and `ylim` components are similar to the high level `xlim` and `ylim` arguments (i.e., they are usually a numeric vector of length 2 defining a range, or a character vector representing levels of a factor). If the `xlim` and `ylim` arguments are not explicitly specified (possibly as components in `scales`) in the high-level call, then the actual limits of the panels are guaranteed to include the limits returned by the prepanel function. This happens globally if the `relation` component of `scales` is "same", and on a per-panel basis otherwise.

The `dx` and `dy` components are used for banking computations in case `aspect` is specified as "xy". See documentation of `banking` for details.

If `xlim` or `ylim` is a character vector (which is appropriate when the corresponding variable is a factor), this implicitly indicates that the scale should include the first `n` integers, where `n` is the length of `xlim` or `ylim`, as the case may be. The elements of the character vector are used as the default labels for these `n` integers. Thus, to make this information consistent between panels, the `xlim` or `ylim` values should represent all the levels of the corresponding factor, even if some are not used within that particular panel.

In such cases, an additional component `xat` or `yat` may be returned by the prepanel function, which should be a subset of `1:n`, indicating which of the `n` values (levels) are actually represented in the panel. This is useful when calculating the limits with `relation="free"` or `relation="sliced"` in `scales`.

The prepanel function is responsible for providing a meaningful return value when the `x`, `y` (etc.) variables are zero-length vectors. When nothing else is appropriate, values of `NA` should be returned for the `xlim` and `ylim` components.

A logical flag or function. If `FALSE`, strips are not drawn. Otherwise, strips...
are drawn using the `strip` function, which defaults to `strip.default`. See documentation of `strip.default` to see the arguments that are available to the `strip` function. This description also applies to the `strip.left` argument (see ... below), which can be used to draw strips on the left of each panel (useful for wide short panels, e.g., in time-series plots).

**xlab**
Character or expression (or a "grob") giving label(s) for the x-axis. Generally defaults to the expression for x in the formula defining the plot. Can be specified as `NULL` to omit the label altogether. Finer control is possible, as described in the entry for `main`, with the modification that if the `label` component is omitted from the list, it is replaced by the default `xlab`.

**ylab**
Character or expression (or "grob") giving label for the y-axis. Generally defaults to the expression for y in the formula defining the plot. Finer control is possible, see entries for `main` and `xlab`.

**scales**
Generally a list determining how the x- and y-axes (tick marks and labels) are drawn. The list contains parameters in `name=value` form, and may also contain two other lists called `x` and `y` of the same form (described below). Components of `x` and `y` affect the respective axes only, while those in `scales` affect both. When parameters are specified in both lists, the values in `x` or `y` are used. Note that certain high-level functions have defaults that are specific to a particular axis (e.g., `bwplot` has `alternating=FALSE` for the categorical axis only); these can only be overridden by an entry in the corresponding component of `scales`. As a special exception, `scales` (or its `x` and `y` components) can also be a character string, in which case it is interpreted as the relation component.

The possible components are:

- **relation**
A character string that determines how axis limits are calculated for each panel. Possible values are "same" (default), "free" and "sliced". For `relation="same"`, the same limits, usually large enough to encompass all the data, are used for all the panels. For `relation="free"`, limits for each panel is determined by just the points in that panel. Behavior for `relation="sliced"` is similar, except that the length (max - min) of the scales are constrained to remain the same across panels. The determination of what axis limits are suitable for each panel can be controlled by the `prepanel` function, which can be overridden by `xlim`, `ylim` or `scales$limits` (except when `relation="sliced"`, in which case explicitly specified limits are ignored with a warning). When `relation` is "free", `xlim` or `ylim` can be a list, in which case it is treated as if its components were the limit values obtained from the prepanel calculations for each panel (after being replicated if necessary).

- **tick.number**
An integer, giving the suggested number of intervals between ticks. This is ignored for a factor, shingle, or character vector, for in these cases there is no natural rule for leaving out some of the labels. But see `xlim`.

- **draw**
A logical flag, defaulting to `TRUE`, that determines whether to draw the axis (i.e., tick marks and labels) at all.

- **alternating**
Usually a logical flag specifying whether axis labels should alternate from one side of the group of panels to the other. For finer control, `alternating` can also be a vector (replicated to be as long as the number of rows or columns per page) consisting of the following numbers
  - 0: do not draw tick labels
  - 1: bottom/left
• 2: top/right
• 3: both.

alternating applies only when relation="same". The default is TRUE, or equivalently, c(1, 2)

limits Same as xlim and ylim.

at The location of tick marks along the axis (in native coordinates), or a list as long as the number of panels describing tick locations for each panel.

labels Vector of labels (characters or expressions) to go along with at. Can also be a list like at.

cex A numeric multiplier to control character sizes for axis labels. Can be a vector of length 2, to control left/bottom and right/top labels separately.

font, fontface, fontfamily Specifies the font to be used for axis labels.

lineheight Specifies the line height parameter (height of line as a multiple of the size of text); relevant for multi-line labels. (This is currently ignored for cloud.)

tck Usually a numeric scalar controlling the length of tick marks. Can also be a vector of length 2, to control the length of left/bottom and right/top tick marks separately.

col Color of tick marks and labels.

rot Angle (in degrees) by which the axis labels are to be rotated. Can be a vector of length 2, to control left/bottom and right/top axes separately.

abbreviate A logical flag, indicating whether to abbreviate the labels using the abbreviate function. Can be useful for long labels (e.g., in factors), especially on the x-axis.

minlength Argument passed to abbreviate if abbreviate=TRUE.

log Controls whether the corresponding variable (x or y) will be log transformed before being passed to the panel function. Defaults to FALSE, in which case the data are not transformed. Other possible values are any number that works as a base for taking logarithm, TRUE (which is equivalent to 10), and "e" (for the natural logarithm). As a side effect, the corresponding axis is labeled differently. Note that this is in reality a transformation of the data, not the axes. Other than the axis labeling, using this feature is no different than transforming the data in the formula; e.g., scales=list(x = list(log = 2)) is equivalent to y ~ log2(x).

See entry for equispaced.log below for details on how to control axis labeling.

equispaced.log A logical flag indicating whether tick mark locations should be equispaced when 'log scales' are in use. Defaults to TRUE.

Tick marks are always labeled in the original (untransformed) scale, but this makes the choice of tick mark locations nontrivial. If equispaced.log is FALSE, the choice made is similar to how log scales are annotated in traditional graphics. If TRUE, tick mark locations are chosen as 'pretty' equispaced values in the transformed scale, and labeled in the form "base^loc", where base is the base of the logarithm transformation, and loc are the locations in the transformed scale.

See also xscale.components.logpower in the latticeExtra package.

format The format to use for POSIXct variables. See strftime for description of valid values.

axs A character string, "r" (default) or "i". In the latter case, the axis limits are calculated as the exact data range, instead of being padded on either side. (May not always work as expected.)
Note that much of the function of scales is accomplished by pscales in splom.

**subscripts**
A logical flag specifying whether or not a vector named subscripts should be passed to the panel function. Defaults to FALSE, unless groups is specified, or if the panel function accepts an argument named subscripts. This argument is useful if one wants the subscripts to be passed on even if these conditions do not hold; a typical example is when one wishes to augment a Lattice plot after it has been drawn, e.g., using panel.identify.

**subset**
An expression that evaluates to a logical or integer indexing vector. Like groups, it is evaluated in data. Only the resulting rows of data are used for the plot. If subscripts is TRUE, the subscripts provided to the panel function will be indices referring to the rows of data prior to the subsetting. Whether levels of factors in the data frame that are unused after the subsetting will be dropped depends on the drop.unused.levels argument.

**xlim**
Normally a numeric vector (or a DateTime object) of length 2 giving left and right limits for the x-axis, or a character vector, expected to denote the levels of x. The latter form is interpreted as a range containing c(1, length(xlim)), with the character vector determining labels at tick positions 1:length(xlim).

xlim could also be a list, with as many components as the number of panels (recycled if necessary), with each component as described above. This is meaningful only when scales$x$relation is "free", in which case these are treated as if they were the corresponding limit components returned by prepanel calculations.

**ylim**
Similar to xlim, applied to the y-axis.

**drop.unused.levels**
A logical flag indicating whether the unused levels of factors will be dropped, usually relevant when a subsetting operation is performed or an interaction is created. Unused levels are usually dropped, but it is sometimes appropriate to suppress dropping to preserve a useful layout. For finer control, this argument could also be list containing components cond and data, both logical, indicating desired behavior for conditioning variables and primary variables respectively. The default is given by lattice.getOption("drop.unused.levels"), which is initially set to TRUE for both components. Note that this argument does not control dropping of levels of the groups argument.

**default.scales**
A list giving the default values of scales for a particular high-level function. This is rarely of interest to the end-user, but may be helpful when defining other functions that act as a wrapper to one of the high-level Lattice functions.

**default.prepanel**
A function or character string giving the name of a function that serves as the (component-wise) fallback prepanel function when the prepanel argument is not specified, or does not return all necessary components. The main purpose of this argument is to enable the defaults to be overridden through the use of lattice.options.

**lattice.options**
A list that could be supplied to lattice.options. These options are applied temporarily for the duration of the call, after which the settings revert back to what they were before. The options are retained along with the object and reused during plotting. This enables the user to attach options settings to the trellis object itself rather than change the settings globally. See also the par.settings argument described below for a similar treatment of graphical settings.

... Further arguments, usually not directly processed by the high-level functions documented here, but instead passed on to other functions. Such arguments can
be broadly categorized into two types: those that affect all high-level Lattice functions in a similar manner, and those that are meant for the specific panel function being used.

The first group of arguments are processed by a common, unexported function called `trellis.skeleton`. These arguments affect all high-level functions, but are only documented here (except to override the behaviour described here). All other arguments specified in a high-level call, specifically those neither described here nor in the help page of the relevant high-level function, are passed unchanged to the panel function used. By convention, the default panel function used for any high-level function is named as “`panel`.” followed by the name of the high-level function; for example, the default panel function for `bwplot` is `panel.bwplot`. In practical terms, this means that in addition to the help page of the high-level function being used, the user should also consult the help page of the corresponding panel function for arguments that may be specified in the high-level call.

The effect of the first group of common arguments are as follows:

- **as.table**: A logical flag that controls the order in which panels should be displayed: if `FALSE` (the default), panels are drawn left to right, bottom to top (as in a graph); if `TRUE`, left to right, top to bottom (as in a table).
- **between**: A list with components `x` and `y` (both usually 0 by default), numeric vectors specifying the space between the panels (units are character heights). `x` and `y` are repeated to account for all panels in a page and any extra components are ignored. The result is used for all pages in a multi page display. In other words, it is not possible to use different `between` values for different pages.
- **key**: A list that defines a legend to be drawn on the plot. This list is used as an argument to the `draw.key` function, which produces a "grob" (grid object) eventually plotted by the print method for "trellis" objects. The structure of the legend is constrained in the ways described below. Although such a list can be and often is created explicitly, it is also possible to generate such a list using the `simpleKey` function; the latter is more convenient but less flexible. The `auto.key` argument can be even more convenient for the most common situation where legends are used, namely, in conjunction with a grouping variable. To use more than one legend, or to have arbitrary legends not constrained by the structure imposed by key, use the `legend` argument.

The position of the key can be controlled in either of two possible ways. If a component called `space` is present, the key is positioned outside the plot region, in one of the four sides, determined by the value of `space`, which can be one of "top", "bottom", "left" and "right". Alternatively, the key can be positioned inside the plot region by specifying components `x`, `y` and `corner`. `x` and `y` determine the location of the corner of the key given by `corner`, which is usually one of `c(0,0)`, `c(1,0)`, `c(1,1)` and `c(0,1)`, which denote the corners of the unit square. Fractional values are also allowed, in which case `x` and `y` determine the position of an arbitrary point inside (or outside for values outside the unit interval) the key. `x` and `y` should be numbers between 0 and 1, giving coordinates with respect to the "display area". Depending on the value of the "legend.bbox" option (see `lattice.getOption`), this can be either the full figure region ("full"), or just the region that bounds the panels and strips ("panel").

The key essentially consists of a number of columns, possibly divided into blocks, each containing some rows. The contents of the key are deter-
mined by (possibly repeated) components named "rectangles", "lines", "points" or "text". Each of these must be lists with relevant graphical parameters (see later) controlling their appearance. The key list itself can contain graphical parameters, these would be used if relevant graphical components are omitted from the other components.

The length (number of rows) of each such column (except "text"s) is taken to be the largest of the lengths of the graphical components, including the ones specified outside (see the entry for rep below for details on this). The "text" component must have a character or expression vector as its first component, to be used as labels. The length of this vector determines the number of rows.

The graphical components that can be included in key and also in the components named "text", "lines", "points" and "rectangles" (as appropriate) are:

- **cex=1** (text, lines, points)
- **col="black"** (text, rectangles, lines, points)
- **alpha=1** (text, rectangles, lines, points)
- **fill="transparent"** (lines, points)
- **lty=1** (lines)
- **lwd=1** (lines, points)
- **font=1** (text, points)
- **fontface (text, points)**
- **fontfamily (text, points)**
- **pch=8** (lines, points)
- **adj=0** (text)
- **type="l"** (lines)
- **size=5** (rectangles, lines)
- **height=1** (rectangles)
- **lineheight=1** (text)
- **angle=0** (rectangles, but ignored)
- **density=-1** (rectangles, but ignored)

In addition, the component border can be included inside the "rect" component to control the border color of the rectangles; when specified at the top level, border controls the border of the entire key (see below).

angle and density are unimplemented. size determines the width of columns of rectangles and lines in character widths. type is relevant for lines; "l" denotes a line, "p" denotes a point, and "b" and "o" both denote both together. height gives heights of rectangles as a fraction of the default.

Other possible components of key are:

- **reverse.rows** Logical flag, defaulting to FALSE. If TRUE, all components are reversed after being replicated (the details of which may depend on the value of rep). This is useful in certain situations, e.g., with a grouped barchart with stack = TRUE with the categorical variable on the vertical axis, where the bars in the plot will usually be ordered from bottom to top, but the corresponding legend will have the levels from top to bottom unless reverse.rows = TRUE. Note that in this case, unless all columns have the same number or rows, they will no longer be aligned.
between Numeric vector giving the amount of space (character widths) surrounding each column (split equally on both sides).

title String or expression giving a title for the key.

rep Logical flag, defaults to TRUE. By default, it is assumed that all columns in the key (except the "text"s) will have the same number of rows, and all components are replicated to be as long as the longest. This can be suppressed by specifying rep=FALSE, in which case the length of each column will be determined by components of that column alone.

cex.title Zoom factor for the title.

lines.title The amount of vertical space to be occupied by the title in lines (in multiples of itself). Defaults to 2.

padding.text The amount of space (padding) to be used above and below each row containing text, in multiples of the default, which is currently 0.2 * "lines". This padding is in addition to the normal height of any row that contains text, which is the minimum amount necessary to contain all the text entries.

background Background color for the legend. Defaults to the global background color.

alpha.background An alpha transparency value between 0 and 1 for the background.

border Either a color for the border, or a logical flag. In the latter case, the border color is black if border is TRUE, and no border is drawn if it is FALSE (the default).

transparent=FALSE Logical flag, whether legend should have a transparent background.

just A character or numeric vector of length one or two giving horizontal and vertical justification for the placement of the legend. See grid.layout for more precise details.

columns The number of column-blocks (drawn side by side) the legend is to be divided into.

between.columns Space between column blocks, in addition to between.

divide Number of point symbols to divide each line when type is "b" or "o" in lines.

legend: The legend argument can be useful if one wants to place more than one key. It also allows the use of arbitrary "grob"s (grid objects) as legends. If used, legend must be a list, with an arbitrary number of components. Each component must be named one of "left", "right", "top", "bottom", or "inside". The name "inside" can be repeated, but not the others. This name will be used to determine the location for that component, and is similar to the space component of key. If key (or colorkey for levelplot and wireframe) is specified, their space component must not conflict with the name of any component of legend. Each component of legend must have a component called Fun. This can be a "grob", or a function (or the name of a function) that produces a "grob" when called. If this function expects any arguments, they must be supplied as a list in another component called args. For components named "inside", there can be additional components called x, y and corner, which work in the same way as for key.
page: A function of one argument (page number) to be called after drawing each page. The function must be 'grid-compliant', and is called with the whole display area as the default viewport.

xlab.top, ylab.right: Labels for the x-axis on top, and y-axis on the right. Similar to xlab and ylab, but less commonly used.

main: Typically a character string or expression describing the main title to be placed on top of each page. Defaults to NULL. main (as well as xlab, ylab and sub) is usually a character string or an expression that gets used as the label, but can also be a list that controls further details. Expressions are treated as specification of LaTeX-like markup as described in plotmath. The label can be a vector, in which case the components will be spaced out horizontally (or vertically for ylab). This feature can be used to provide column or row labels rather than a single axis label. When main (etc.) is a list, the actual label should be specified as the label component (which may be unnamed if it is the first component). The label can be missing, in which case the default will be used (xlab and ylab usually have defaults, but main and sub do not). Further named arguments are passed on to textGrob; this can include arguments controlling positioning like just and rot as well as graphical parameters such as col and font (see gpar for a full list).

main, sub, xlab, ylab, xlab.top, and ylab.right can also be arbitrary "grob"s (grid graphical objects).

sub: Character string or expression (or a list or "grob") for a subtitle to be placed at the bottom of each page. See entry for main for finer control options.

par.strip.text: A list of parameters to control the appearance of strip text. Notable components are col, cex, font, and lines. The first three control graphical parameters while the last is a means of altering the height of the strips. This can be useful, for example, if the strip labels (derived from factor levels, say) are double height (i.e., contains "\n"-s) or if the default height seems too small or too large. Additionally, the lineheight component can control the space between multiple lines. The labels can be abbreviated when shown by specifying abbreviate = TRUE, in which case the components minlength and dot (passed along to the abbreviate function) can be specified to control the details of how this is done.

layout: In general, a conditioning plot in Lattice consists of several panels arranged in a rectangular array, possibly spanning multiple pages. layout determines this arrangement.

layout is a numeric vector of length 2 or 3 giving the number of columns, rows, and pages (optional) in a multipanel display. By default, the number of columns is the number of levels of the first conditioning variable and the number of rows is the number of levels of the second conditioning variable. If there is only one conditioning variable, the default layout vector is c(0, n), where n is the number of levels of the given vector. Any time the first value in the layout vector is 0, the second value is used as the desired number of panels per page and the actual layout is computed from this, taking into account the aspect ratio of the panels and the device dimensions (via par("din")). If NA is specified for the number of rows or columns (but not both), that dimension will be filled out according to the number of panels.

The number of pages is by default set to as many as is required to plot all the
panels, and so rarely needs to be specified. However, in certain situations
the default calculation may be incorrect, and in that case the number of
pages needs to be specified explicitly.

skip: A logical vector (default FALSE), replicated to be as long as the number of
panels (spanning all pages). For elements that are TRUE, the corresponding
panel position is skipped; i.e., nothing is plotted in that position. The panel
that was supposed to be drawn there is now drawn in the next available
panel position, and the positions of all the subsequent panels are bumped
up accordingly. This may be useful for arranging plots in an informative
manner.

strip.left: strip.left can be used to draw strips on the left of each panel,
which can be useful for wide short panels, as in time-series (or similar)
plots. See the entry for strip for detailed usage.

xlab.default, ylab.default: Fallback default for xlab and ylab when they
are not specified. If NULL, the defaults are parsed from the Trellis formula.
This is rarely useful for the end-user, but can be helpful when developing
new Lattice functions.

xscale.components, yscale.components: Functions that determine axis an-
notation for the x and y axes respectively. See documentation for
xscale.components.default, the default values of these arguments, to
learn more.

axis: Function responsible for drawing axis annotation. See documentation for
axis.default, the default value of this argument, to learn more.

perm.cond: An integer vector, a permutation of 1:n, where n is the number
of conditioning variables. By default, the order in which panels are drawn
depends on the order of the conditioning variables specified in the formula.
perm.cond can modify this order. If the trellis display is thought of as an n-
dimensional array, then during printing, its dimensions are permuted using
perm.cond as the perm argument does in aperm.

index.cond: Whereas perm.cond permutes the dimensions of the multidimen-
sional array of panels, index.cond can be used to subset (or reorder) mar-
gins of that array. index.cond can be a list or a function, with behavior in
each case described below.

The panel display order within each conditioning variable depends on the
order of their levels. index.cond can be used to choose a 'subset' (in the
R sense) of these levels, which is then used as the display order for that
variable. If index.cond is a list, it has to be as long as the number of
conditioning variables, and the i-th component has to be a valid indexing
vector for levels(g_i), where g_i is the i-th conditioning variable in the
plot (note that these levels may not contain all levels of the original vari-
able, depending on the effects of the subset and drop.unused.levels
arguments). In particular, this indexing may repeat levels, or drop some
altogether. The result of this indexing determines the order of panels within
that conditioning variable. To keep the order of a particular variable un-
changed, the corresponding component must be set to TRUE.

Note that the components of index.cond are interpreted in the order of
the conditioning variables in the original call, and is not affected by perm.cond.
Another possibility is to specify index.cond as a function. In this case,
this function is called once for each panel, potentially with all arguments
that are passed to the panel function for that panel. (More specifically,
if this function has a ... argument, then all panel arguments are passed,
otherwise, only named arguments that match are passed.) If there is only
one conditioning variable, the levels of that variable are then sorted so that these values are in ascending order. For multiple conditioning variables, the order for each variable is determined by first taking the average over all other conditioning variables.

Although they can be supplied in high-level function calls directly, it is more typical to use perm.cond and index.cond to update an existing "trellis" object, thus allowing it to be displayed in a different arrangement without re-calculating the data subsets that go into each panel. In the update.trellis method, both can be set to NULL, which reverts these back to their defaults.

par.settings: A list that could be supplied to trellis.par.set. When the resulting object is plotted, these options are applied temporarily for the duration of the plotting, after which the settings revert back to what they were before. This enables the user to attach some display settings to the trellis object itself rather than change the settings globally. See also the lattice.options argument described above for a similar treatment of non-graphical options.

plot.args: A list containing possible arguments to plot.trellis, which will be used by the plot or print methods when drawing the object, unless overridden explicitly. This enables the user to attach such arguments to the trellis object itself. Partial matching is not performed.

Details

The high-level functions documented here, as well as other high-level Lattice functions, are generic, with the formula method usually doing the most substantial work. The structure of the plot that is produced is mostly controlled by the formula (implicitly in the case of the non-formula methods). For each unique combination of the levels of the conditioning variables g1, g2, ..., a separate “packet” is produced, consisting of the points (x, y) for the subset of the data defined by that combination. The display can be thought of as a three-dimensional array of panels, consisting of one two-dimensional matrix per page. The dimensions of this array are determined by the layout argument. If there are no conditioning variables, the plot produced consists of a single packet. Each packet usually corresponds to one panel, but this is not strictly necessary (see the entry for index.cond above).

The coordinate system used by lattice by default is like a graph, with the origin at the bottom left, with axes increasing to the right and top. In particular, panels are by default drawn starting from the bottom left corner, going right and then up, unless as.table = TRUE, in which case panels are drawn from the top left corner, going right and then down. It is possible to set a global preference for the table-like arrangement by changing the default to as.table=TRUE; this can be done by setting lattice.options(default.args = list(as.table = TRUE)). Default values can be set in this manner for the following arguments: as.table, aspect, between, page, main, sub, par.strip.text, layout, skip and strip. Note that these global defaults are sometimes overridden by individual functions.

The order of the panels depends on the order in which the conditioning variables are specified, with g1 varying fastest, followed by g2, and so on. Within a conditioning variable, the order depends on the order of the levels (which for factors is usually in alphabetical order). Both of these orders can be modified using the index.cond and perm.cond arguments, possibly using the update (and other related) method(s).
Value

The high-level functions documented here, as well as other high-level Lattice functions, return an object of class "trellis". The update method can be used to subsequently update components of the object, and the print method (usually called by default) will plot it on an appropriate plotting device.

Note

Most of the arguments documented here are also applicable for the other high-level functions in the lattice package. These are not described in any detail elsewhere unless relevant, and this should be considered the canonical documentation for such arguments.

Any arguments passed to these functions and not recognized by them will be passed to the panel function. Most predefined panel functions have arguments that customize its output. These arguments are described only in the help pages for these panel functions, but can usually be supplied as arguments to the high-level plot.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References


See Also

Lattice for an overview of the package, as well as barchart.table, print.trellis, shingle, banking, reshape, panel.xyplot, panel.bwplot, panel.barchart, panel.dotplot, panel.stripplot, panel.superpose, panel.loess, panel.average, strip.default, simpleKey trellis.par.set

Examples

```
require(stats)

## Tonga Trench Earthquakes

Depth <- equal.count(quakes$depth, number=8, overlap=.1)
xypplot(lat ~ long | Depth, data = quakes)
update(trellis.last.object(),
      strip = strip.custom(strip.names = TRUE, strip.levels = TRUE),
      par.strip.text = list(cex = 0.75),
      aspect = "iso")

## Extended formula interface

dxypplot(Sepal.Length + Sepal.Width ~ Petal.Length + Petal.Width | Species,
         data = iris, scales = "free", layout = c(2, 2),
         auto.key = list(x = .75, y = .75, corner = c(0.5, 0.5)))

## user defined panel functions

states <- data.frame(state.x77,
```
state.name = dimnames(state.x77)[[1]],
state.region = state.region)
xyplot(Murder ~ Population | state.region, data = states,
       xnames = states$state.name,
       panel = function(x, y, subscripts, xnames) {
         panel.text(x = x, y = y, labels = xnames[subscripts], cex = 1,
                     fontfamily = "HersheySans")
       })

## Stacked bar chart
barchart(yield ~ variety | site, data = barley,
         groups = year, layout = c(1,6), stack = TRUE,
         auto.key = list(space = "right"),
         ylab = "Barley Yield (bushels/acre)",
         scales = list(x = list(rot = 45)))

bwplot(voice.part ~ height, data = singer, xlab = "Height (inches)"

dotplot(variety ~ yield | year * site, data=barley)

## Grouped dot plot showing anomaly at Morris
dotplot(variety ~ yield | site, data = barley, groups = year,
        key = simpleKey(levels(barley$year), space = "right"),
        xlab = "Barley Yield (bushels/acre)",
        aspect=0.5, layout = c(1,6), ylab=NA)

stripplot(voice.part ~ jitter(height), data = singer, aspect = 1,
          jitter.data = TRUE, xlab = "Height (inches)"

## Interaction Plot
xyplot(decrease ~ treatment, OrchardSprays, groups = rowpos,
       type = "a",
       auto.key =
       list(space = "right", points = FALSE, lines = TRUE))

## longer version with no x-ticks
## Not run:
bwplot(decrease ~ treatment, OrchardSprays, groups = rowpos,
       panel = "panel.superpose",
       panel.groups = "panel.linejoin",
       xlab = "treatment",
       key = list(lines = Rows(trellis.par.get("superpose.line"),
                               c(1:7, 1)),
                  text = list(label = as.character(unique(OrchardSprays$rowpos)),
                              columns = 4, title = "Row position"))
## End(Not run)
Description

This function handles time series plotting, including cut-and-stack plots. Examples are given of superposing, juxtaposing and styling different time series.

Usage

```r
## S3 method for class 'ts'
xyplot(x, data = NULL,
       screens = if (superpose) 1 else colnames(x),
       ..., 
       superpose = FALSE,
       cut = FALSE,
       type = "l",
       col = NULL,
       lty = NULL,
       lwd = NULL,
       pch = NULL,
       cex = NULL,
       fill = NULL,
       auto.key = superpose,
       panel = if (superpose) "panel.superpose"
       else "panel.superpose.plain",
       par.settings = list(),
       layout = NULL, as.table = TRUE,
       xlab = "Time", ylab = NULL,
       default.scales = list(y = list(relation =
       if (missing(cut)) "free" else "same")))
```

Arguments

- **x** an object of class `ts`, which may be multi-variate, i.e. have a matrix structure with multiple columns.
- **data** not used, and must be left as NULL.
- **...** additional arguments passed to `xyplot`, which may pass them on to `panel.xyplot`.
- **screens** factor (or coerced to factor) whose levels specify which panel each series is to be plotted in. `screens = c(1, 2, 1)` would plot series 1, 2 and 3 in panels 1, 2 and 1. May also be a named list, see Details below.
- **superpose** overlays all series in one panel (via `screens = 1`) and uses grouped style settings (from `trellis.par.get("superpose.line")`, etc). Note that this is just a convenience argument: its only action is to change the default values of other arguments.
- **cut** defines a cut-and-stack plot. `cut` can be a list of arguments to the function `equal.count`, i.e. number (number of intervals to divide into) and overlap (the fraction of overlap between cuts, default 0.5). If `cut` is numeric this is passed as the number argument.
  - `cut = TRUE` tries to choose an appropriate number of cuts (up to a maximum of 6), using `banking`, and assuming a square plot region. This should have the effect of minimising wasted space when `aspect = "xy"`. 


type, col, lty, lwd, pch, cex, fill

graphical arguments, which are processed and eventually passed to
`panel.xyplot`. These arguments can also be vectors or (named) lists, see De-
tails for more information.

auto.key

a logical, or a list describing how to draw a key. See the auto.key entry in
`xyplot`. The default here is to draw lines, not points, and any specified style
arguments should show up automatically.

panel

the panel function. It is recommended to leave this alone, but one can pass a
`panel.groups` argument which is handled by `panel.superpose` for each series.

par.settings

style settings beyond the standard col, lty, lwd, etc; see `trellis.par.set` and
`simpleTheme`.

layout

numeric vector of length 2 specifying number of columns and rows in the plot.
The default is to fill columns with up to 6 rows.

as.table

to draw panels from top to bottom. The order is determined by the order of
columns in x.

xlab, ylab

X axis and Y axis labels; see `xyplot`. Note in particular that ylab may be a
character vector, in which case the labels are spaced out equally, to correspond
to the panels; but NOTE in this case the vector should be reversed OR the argument
as.table set to FALSE.

default.scales

scales specification. The default is set to have "free" Y axis scales un-
less cut is given. Note, users should pass the scales argument rather than
default.scales.

Details

The handling of several graphical parameters is more flexible for multivariate series. These param-
eters can be vectors of the same length as the number of series plotted or are recycled if shorter.
They can also be (partially) named list, e.g., list(A = c(1,2), c(3,4)) in which c(3, 4) is the
default value and c(1, 2) the value only for series A. The screens argument can be specified in a
similar way.

Some examples are given below.

Value

An object of class "trellis". The `update` method can be used to update components of the object
and the `print` method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Gabor Grothendieck, Achim Zeileis, Deepayan Sarkar and Felix Andrews <felix@nfrac.org>. The
first two authors developed `xyplot.ts` in their `zoo` package, including the screens approach.
The third author developed a different `xyplot.ts` for cut-and-stack plots in the `latticeExtra` pack-
age. The final author fused these together.

References

//lmdvr.r-forge.r-project.org/](http://lmdvr.r-forge.r-project.org/) (cut-and-stack plots)

See Also

`xyplot, panel.xyplot, plot.ts, ts, xyplot.zoo` in the `zoo` package.
**Examples**

```r
xyplot(ts(c(1:10,10:1)))
```

### Figure 14.1 from Sarkar (2008)

```r
xyplot(sunspot.year, aspect = "xy", strip = FALSE, strip.left = TRUE, 
cut = list(number = 4, overlap = 0.05))
```

### A multivariate example; first juxtaposed, then superposed

```r
xyplot(EuStockMarkets, scales = list(y = "same"))
```

```r
xyplot(EuStockMarkets, superpose = TRUE, aspect = "xy", lwd = 2, 
type = c("l","g"), ylim = c(0, max(EuStockMarkets)))
```

### Examples using screens (these two are identical)

```r
xyplot(EuStockMarkets, screens = c(rep("Continental", 3), "UK"))
```

```r
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"))
```

### Automatic group styles

```r
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"), 
superpose = TRUE)
```

```r
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"), 
superpose = TRUE, xlim = extendrange(1996:1998), 
par.settings = standard.theme(color = FALSE))
```

### Specifying styles for series by name

```r
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"), 
col = list(DAX = "red", FTSE = "blue", "black"), auto.key = TRUE)
```

```r
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"), 
col = list(DAX = "red"), lty = list(SMI = 2), lwd = 1:2, 
auto.key = TRUE)
```

### Example with simpler data, few data points

```r
set.seed(1)
z <- ts(cbind(a = 1:5, b = 11:15, c = 21:25) + rnorm(5))
```

```r
xyplot(z, screens = 1)
```

```r
xyplot(z, screens = list(a = "primary (a)", "other (b & c)")
```

```r
xyplot(z, screens = list(a = "primary (a)", "other (b & c)"
```

```r
type = list(a = c("p", "h"), b = c("p", "s"), "o"),
```

```r
pch = list(a = 2, c = 3), auto.key = list(type = "o"))
```

---

**Description**

Contingency tables are often displayed using bar charts and dot plots. These methods operate directly on tables, bypassing the need to convert them to data frames for use with the formula interface. Matrices and arrays are also supported, by coercing them to tables.

**Usage**

```r
## S3 method for class 'table'
barchart(x, data, groups = TRUE,
```
B_02_barchart.table

origin = 0, stack = TRUE, ..., horizontal = TRUE)

## S3 method for class 'array'
barchart(x, data, ...)

## S3 method for class 'matrix'
barchart(x, data, ...)

## S3 method for class 'table'
dotplot(x, data, groups = TRUE, ..., horizontal = TRUE)

## S3 method for class 'array'
dotplot(x, data, ...)

## S3 method for class 'matrix'
dotplot(x, data, ...)

Arguments

x A table, array or matrix object.

data Should not be specified. If specified, will be ignored with a warning.

groups A logical flag, indicating whether to use the last dimension as a grouping variable in the display.

origin, stack Arguments to `panel.barchart`. The defaults for the `table` method are different.

horizontal Logical flag, indicating whether the plot should be horizontal (with the categorical variable on the y-axis) or vertical.

... Other arguments, passed to the underlying formula method.

Details

The first dimension is used as the variable on the categorical axis. The last dimension is optionally used as a grouping variable (to produce stacked barcharts by default). All other dimensions are used as conditioning variables. The order of these variables cannot be altered (except by permuting the original argument beforehand using `t` or `aperm`). For more flexibility, use the formula method after converting the table to a data frame using the relevant `as.data.frame` method.

Value

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`barchart`, `t`, `aperm`, `table`, `panel.barchart`, `Lattice`
Examples

barchart(Titanic, scales = list(x = "free"),
  auto.key = list(title = "Survived"))

Description

Draw Histograms and Kernel Density Plots, possibly conditioned on other variables.

Usage

histogram(x, data, ...)
densityplot(x, data, ...)

## S3 method for class 'formula'
histogram(x, 
  data, 
  allow.multiple, outer = TRUE,
  auto.key = lattice.getOption("default.args")$auto.key,
  aspect = "fill",
  panel = lattice.getOption("panel.histogram"),
  prepanel, scales, strip, groups,
  xlab, xlim, ylab, ylim,
  type = c("percent", "count", "density"),
  nint = if (is.factor(x)) nlevels(x)
  else round(log2(length(x)) + 1),
  endpoints = extend.limits(range(as.numeric(x),
   finite = TRUE), prop = 0.04),
  breaks,
  equal.widths = TRUE,
  drop.unused.levels =
  lattice.getOption("drop.unused.levels"),
  ..., 
  lattice.options = NULL,
  default.scales = list(),
  default.prepanel =
  lattice.getOption("prepanel.default.histogram"),
  subscripts,
  subset)

## S3 method for class 'data.frame'
histogram(x, data = NULL, formula = data, ...)

## S3 method for class 'numeric'
histogram(x, data = NULL, xlab, ...)

## S3 method for class 'factor'
histagram(x, data = NULL, xlab, ...)
## Arguments

**x**  
The object on which method dispatch is carried out.  
For the formula method, `x` can be a formula of the form `~ x | g1 * g2 * ....`, indicating that histograms or kernel density estimates of the `x` variable should be produced conditioned on the levels of the (optional) variables `g1`, `g2`, .... `x` should be numeric (or possibly a factor in the case of histogram), and each of `g1`, `g2`, .... should be either factors or shingles.  
As a special case, the right hand side of the formula can contain more than one term separated by `+` signs (e.g., `~ x1 + x2 | g1 * g2`). What happens in this case is described in the documentation for `xyplot`. Note that in either form, all the terms in the formula must have the same length after evaluation.  
For the numeric and factor methods, `x` is the variable whose histogram or Kernel density estimate is drawn. Conditioning is not allowed in these cases.

**data**  
For the formula method, an optional data source (usually a data frame) in which variables are to be evaluated (see `xyplot` for details). `data` should not be specified for the other methods, and is ignored with a warning if it is.

**formula**  
The formula to be used for the "data.frame" methods. See documentation for argument `x` for details.

**type**  
A character string indicating the type of histogram that is to be drawn. "percent" and "count" give relative frequency and frequency histograms re-
spectively, and can be misleading when breakpoints are not equally spaced. "density" produces a density histogram.

type defaults to "density" when the breakpoints are unequally spaced, and when breaks is NULL or a function, and to "percent" otherwise.

nint An integer specifying the number of histogram bins, applicable only when breaks is unspecified or NULL in the call. Ignored when the variable being plotted is a factor.

eqwidths A logical flag, relevant only when breaks=NULL. If TRUE, equally spaced bins will be selected, otherwise, approximately equal area bins will be selected (typically producing unequally spaced breakpoints).

n Integer, giving the number of points at which the kernel density is to be evaluated. Passed on as an argument to density.

panel A function, called once for each panel, that uses the packet (subset of panel variables) corresponding to the panel to create a display. The default panel functions panel.histogram and panel.densityplot are documented separately, and have arguments that can be used to customize its output in various ways. Such arguments can usually be directly supplied to the high-level function.

allow.multiple, outer
auto.key
aspect
prepanel
scales
See xyplot.
strip See xyplot.
groups See xyplot. Note that the default panel function for histogram does not support grouped displays, whereas the one for densityplot does.

xlab, ylab See xyplot.
xlim, ylim See xyplot.
drop.unused.levels See xyplot.
lattice.options See xyplot.
default.scales See xyplot.
subscripts See xyplot.
subset See xyplot.
default.prepanel Fallback prepanel function. See xyplot.
weights numeric vector of weights for the density calculations, evaluated in the non-standard manner used for groups and terms in the formula, if any. If this is specified, it is subsetted using subscripts inside the panel function to match it to the corresponding x values.
At the time of writing, weights do not work in conjunction with an extended formula specification (this is not too hard to fix, so just bug the maintainer if you need this feature).

bw, adjust, width Arguments controlling bandwidth. Passed on as arguments to density.
kernel, window The choice of kernel. Passed on as arguments to density.
give.Rkern Logical flag, passed on as argument to density. This argument is made available only for ease of implementation, and will produce an error if TRUE.
from, to, cut Controls range over which density is evaluated. Passed on as arguments to density.
na.rm Logical flag specifying whether NA values should be ignored. Passed on as argument to density, but unlike in density, the default is TRUE.

... Further arguments. See corresponding entry in xyplot for non-trivial details.

Details

histogram draws Conditional Histograms, and densityplot draws Conditional Kernel Density Plots. The default panel function uses the density function to compute the density estimate, and all arguments accepted by density can be specified in the call to densityplot to control the output. See documentation of density for details.

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for xyplot, which should be consulted to learn more detailed usage.
do.breaks is an utility function that calculates breakpoints given an interval and the number of pieces to break it into.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.
Note

The form of the arguments accepted by the default panel function panel.histogram is different from that in S-PLUS. Whereas S-PLUS calculates the heights inside histogram and passes only the breakpoints and the heights to the panel function, lattice simply passes along the original variable x along with the breakpoints. This approach is more flexible; see the example below with an estimated density superimposed over the histogram.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References


See Also

`xyplot`, `panel.histogram`, `density`, `panel.densityplot`, `panel.mathdensity`, `Lattice`

Examples

```r
require(stats)
histogram(~ height | voice.part, data = singer, nint = 17,
          endpoints = c(59.5, 76.5), layout = c(2,4), aspect = 1,
          xlab = "Height (inches)")

histogram(~ height | voice.part, data = singer,
          xlab = "Height (inches)", type = "density",
          panel = function(x, ...) {
            panel.histogram(x, ...)
            panel.mathdensity(dmath = dnorm, col = "black",
                              args = list(mean=mean(x),sd=sd(x)))
          })

densityplot(~ height | voice.part, data = singer, layout = c(2, 4),
            xlab = "Height (inches)", bw = 5)
```

---

**Q-Q Plot with Theoretical Distribution**

Description

Draw quantile-Quantile plots of a sample against a theoretical distribution, possibly conditioned on other variables.

Usage

```r
qqmath(x, data, ...)
```

## S3 method for class 'formula'
qqmath(x, 

Arguments

x The object on which method dispatch is carried out. For the "formula" method, x should be a formula of the form ~ x | g1 * g2 * ..., where x should be a numeric variable. For the "numeric" method, x should be a numeric vector.

data For the formula method, an optional data source (usually a data frame) in which variables are to be evaluated (see xyplot for details). data should not be specified for the other methods, and is ignored with a warning if it is.

formula The formula to be used for the "data.frame" methods. See documentation for argument x for details.

distribution A quantile function that takes a vector of probabilities as argument and produces the corresponding quantiles from a theoretical distribution. Possible values are qnorm, qunif, etc. Distributions with other required arguments need to be provided as user-defined functions (see example with qt).

f.value An optional numeric vector of probabilities, quantiles corresponding to which should be plotted. This can also be a function of a single integer (representing sample size) that returns such a numeric vector. A typical value for this argument is the function ppoints, which is also the S-PLUS default. If specified, the probabilities generated by this function are used for the plotted quantiles, through the quantile function for the sample, and the function specified as the distribution argument for the theoretical distribution.

f.value defaults to NULL, which has the effect of using ppoints for the quantiles of the theoretical distribution, but the exact data values for the sample. This is similar to what happens for qnorm, but different from the S-PLUS default of f.value=ppoints.
For large \( x \), this argument can be used to restrict the number of points plotted. See also the tails.n argument in \texttt{panel.qqmath}.

**panel**

A function, called once for each panel, that uses the packet (subset of panel variables) corresponding to the panel to create a display. The default panel function \texttt{panel.qqmath} is documented separately, and has arguments that can be used to customize its output in various ways. Such arguments can usually be directly supplied to the high-level function.

**allow.multiple, outer**

See \texttt{xyplot}.

**auto.key**

See \texttt{xyplot}.

**aspect**

See \texttt{xyplot}.

**prepanel**

See \texttt{xyplot}.

**scales**

See \texttt{xyplot}.

**strip**

See \texttt{xyplot}.

**groups**

See \texttt{xyplot}.

**xlab, ylab**

See \texttt{xyplot}.

**xlim, ylim**

See \texttt{xyplot}.

**drop.unused.levels**

See \texttt{xyplot}.

**lattice.options**

See \texttt{xyplot}.

**default.scales**

See \texttt{xyplot}.

**subscripts**

See \texttt{xyplot}.

**subset**

See \texttt{xyplot}.

**default.prepanel**

Fallback prepanel function. See \texttt{xyplot}.

... Further arguments. See corresponding entry in \texttt{xyplot} for non-trivial details.

**Details**

\texttt{qqmath} produces Q-Q plots of the given sample against a theoretical distribution. The default behaviour of \texttt{qqmath} is different from the corresponding S-PLUS function, but is similar to \texttt{qqnorm}. See the entry for \texttt{f.value} for specifics.

The implementation details are also different from S-PLUS. In particular, all the important calculations are done by the panel (and prepanel function) and not \texttt{qqmath} itself. In fact, both the arguments \texttt{distribution} and \texttt{f.value} are passed unchanged to the panel and prepanel function. This allows, among other things, display of grouped Q-Q plots, which are often useful. See the help page for \texttt{panel.qqmath} for further details.

This and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for \texttt{xyplot}, which should be consulted to learn more detailed usage.

**Value**

An object of class "trellis". The \texttt{update} method can be used to update components of the object and the \texttt{print} method (usually called by default) will plot it on an appropriate plotting device.
Quantile-Quantile Plots of Two Samples

Description

Quantile-Quantile plots for comparing two Distributions

Usage

qq(x, data, ...)

## S3 method for class 'formula'
qq(x, data, aspect = "fill",
panel = lattice.getOption("panel.qq"),
prepanel, scales, strip,
groups, xlab, xline, ylab, ylim, f.value = NULL,
drop.unused.levels = lattice.getOption("drop.unused.levels"),
...,
lattice.options = NULL,
qtype = 7,
default.scales = list(),

Examples

qqmath(~ rnorm(100), distribution = function(p) qt(p, df = 10))
qqmath(~ height | voice.part, aspect = "xy", data = singer,
panel = prepanel.qqmathline,
panel = function(x, ...) {
  panel.qqmathline(x, ...)
  panel.qqmath(x, ...)
})

vp.comb <-
  factor(sapply(strsplit(as.character(singer$voice.part), split = " "),
               "[", 1),
  levels = c("Bass", "Tenor", "Alto", "Soprano")
vp.group <-
  factor(sapply(strsplit(as.character(singer$voice.part), split = " "),
               ",{", 2))
qqmath(~ height | vp.comb, data = singer,
groups = vp.group, auto.key = list(space = "right"),
aspect = "xy",
prepanel = prepanel.qqmathline,
panel = function(x, ...) {
  panel.qqmathline(x, ...)
  panel.qqmath(x, ...)
})
default.prepanel = lattice.getOption("prepanel.default.qq"),
subscripts,
subset)

## S3 method for class 'data.frame'
qq(x, data = NULL, formula = data, ...)

Arguments

\texttt{x} \quad \text{The object on which method dispatch is carried out.}
For the "formula" method, \textit{x} should be a formula of the form \( y \sim x | g1 \ast g2 \ast \ldots \), where \( x \) should be a numeric variable, and \( y \) a factor, shingle, character, or numeric variable, with the restriction that there must be exactly two levels of \( y \), which divide the values of \( x \) into two groups. Quantiles for these groups will be plotted against each other along the two axes.

\texttt{data} \quad \text{For the formula method, an optional data source (usually a data frame) in which variables are to be evaluated (see \texttt{xyplot} for details).}

\texttt{formula} \quad \text{The formula to be used for the "data.frame" method. See documentation for argument \texttt{x} for details.}

\texttt{f.value} \quad \text{An optional numeric vector of probabilities, quantiles corresponding to which should be plotted. This can also be a function of a single integer (representing sample size) that returns such a numeric vector. A typical value for this argument is the function \texttt{ppoints}, which is also the S-PLUS default. If specified, the probabilities generated by this function is used for the plotted quantiles, through the \texttt{quantile} function. \texttt{f.value} defaults to NULL, which is equivalent to}

\[
\texttt{f.value} = \text{function(n) ppoints(n, a = 1)}
\]

This has the effect of including the minimum and maximum data values in the computed quantiles. This is similar to what happens for \texttt{qqplot} but different from the default behaviour of \texttt{qq} in S-PLUS.

For large \( x \), this argument can be used to restrict the number of quantiles plotted.

\texttt{panel} \quad \text{A function, called once for each panel, that uses the packet (subset of panel variables) corresponding to the panel to create a display. The default panel function \texttt{panel.qq} is documented separately, and has arguments that can be used to customize its output in various ways. Such arguments can usually be directly supplied to the high-level function.}

\texttt{qtype} \quad \text{The type argument for \texttt{quantile}.}

\texttt{aspect} \quad \text{See \texttt{xyplot}.}

\texttt{prepanel} \quad \text{See \texttt{xyplot}.}

\texttt{scales} \quad \text{See \texttt{xyplot}.}

\texttt{strip} \quad \text{See \texttt{xyplot}.}

\texttt{groups} \quad \text{See \texttt{xyplot}.}

\texttt{xlab, ylab} \quad \text{See \texttt{xyplot}.}

\texttt{xlim, ylim} \quad \text{See \texttt{xyplot}.}

\texttt{drop.unused.levels} \quad \text{See \texttt{xyplot}.}
lattice.options  
See xyplot.
default.scales  See xyplot.
subscripts  See xyplot.
subset  See xyplot.
default.prepanel  
Fallback prepanel function. See xyplot.
...
Further arguments. See corresponding entry in xyplot for non-trivial details.

Details

qq produces Q-Q plots of two samples. The default behaviour of qq is different from the corresponding S-PLUS function. See the entry for f.value for specifics.

This and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for xyplot, which should be consulted to learn more detailed usage.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot,panel.qq,qqmath,Lattice

Examples

qq(voice.part ~ height, aspect = 1, data = singer,  
subset = (voice.part == "Bass 2" | voice.part == "Tenor 1"))

Description

Draws false color level plots and contour plots.

Usage

levelplot(x, data, ...)
contourplot(x, data, ...)

## S3 method for class 'formula'
levelplot(x,  
data,
allow.multiple = is.null(groups) || outer,
outer = TRUE,
aspect = "fill",
panel = if (useRaster) lattice.getOption("panel.levelplot.raster")
  else lattice.getOption("panel.levelplot"),
prepanel = NULL,
scales = list(),
strip = TRUE,
groups = NULL,
xlab, xlim, ylab, ylim, at,
cuts = 15,
pretty = FALSE,
region = TRUE,
drop.unused.levels =
  lattice.getOption("drop.unused.levels"),
...,
useRaster = FALSE,
lattice.options = NULL,
default.scales = list(),
default.prepanel =
  lattice.getOption("prepanel.default.levelplot"),
colkey = region,
col.regions, alpha.regions,
subset = TRUE)

## S3 method for class 'formula'
contourplot(x,
data,
panel = lattice.getOption("panel.contourplot"),
default.prepanel =
  lattice.getOption("prepanel.default.contourplot"),
cuts = 7,
labels = TRUE,
contour = TRUE,
pretty = TRUE,
region = FALSE,
...)

## S3 method for class 'data.frame'
levelplot(x, data = NULL, formula = data, ...)

## S3 method for class 'data.frame'
contourplot(x, data = NULL, formula = data, ...)

## S3 method for class 'table'
levelplot(x, data = NULL, aspect = "iso", ..., xlim, ylim)

## S3 method for class 'table'
contourplot(x, data = NULL, aspect = "iso", ..., xlim, ylim)

## S3 method for class 'matrix'
levelplot(x, data = NULL, aspect = "iso",
          ..., xlim, ylim,
          row.values = seq_len(nrow(x)),
          column.values = seq_len(ncol(x)))

## S3 method for class 'matrix'
contourplot(x, data = NULL, aspect = "iso",
             ..., xlim, ylim,
             row.values = seq_len(nrow(x)),
             column.values = seq_len(ncol(x)))

## S3 method for class 'array'
levelplot(x, data = NULL, ...)

## S3 method for class 'array'
contourplot(x, data = NULL, ...)

Arguments

x

for the formula method, a formula of the form z ~ x * y | g1 * g2 * ..., where z is a numeric response, and x, y are numeric values evaluated on a rectangular grid. g1, g2, ... are optional conditional variables, and must be either factors or shingles if present.

Calculations are based on the assumption that all x and y values are evaluated on a grid (defined by their unique values). The function will not return an error if this is not true, but the display might not be meaningful. However, the x and y values need not be equally spaced.

Both levelplot and wireframe have methods for matrix, array, and table objects, in which case x provides the z vector described above, while its rows and columns are interpreted as the x and y vectors respectively. This is similar to the form used in filled.contour and image. For higher-dimensional arrays and tables, further dimensions are used as conditioning variables. Note that the dimnames may be duplicated; this is handled by calling make.unique to make the names unique (although the original labels are used for the x- and y-axes).

data

For the formula methods, an optional data frame in which variables in the formula (as well as groups and subset, if any) are to be evaluated. Usually ignored with a warning in other cases.

formula

The formula to be used for the "data.frame" methods. See documentation for argument x for details.

row.values, column.values

Optional vectors of values that define the grid when x is a matrix. row.values and column.values must have the same lengths as nrow(x) and ncol(x) respectively. By default, row and column numbers.

panel

panel function used to create the display, as described in xyplot

aspect

For the matrix methods, the default aspect ratio is chosen to make each cell square. The usual default is aspect="fill", as described in xyplot.
at: A numeric vector giving breakpoints along the range of z. Contours (if any) will be drawn at these heights, and the regions in between would be colored using col.regions. In the latter case, values outside the range of at will not be drawn at all. This serves as a way to limit the range of the data shown, similar to what a zlim argument might have been used for. However, this also means that when supplying at explicitly, one has to be careful to include values outside the range of z to ensure that all the data are shown.

at can have length one only if region=FALSE.

col.regions: color vector to be used if regions is TRUE. The general idea is that this should be a color vector of moderately large length (longer than the number of regions. By default this is 100). It is expected that this vector would be gradually varying in color (so that nearby colors would be similar). When the colors are actually chosen, they are chosen to be equally spaced along this vector. When there are more regions than colors in col.regions, the colors are recycled. The actual color assignment is performed by level.colors, which is documented separately.

alpha.regions: Numeric, specifying alpha transparency (works only on some devices)

colorkey: A logical flag specifying whether a colorkey is to be drawn alongside the plot, or a list describing the colorkey. The list may contain the following components:

space: location of the colorkey, can be one of "left", "right", "top" and "bottom". Defaults to "right".

x, y: location, currently unused

col: A color ramp specification, as in the col.regions argument in level.colors

at: A numeric vector specifying where the colors change. must be of length 1 more than the col vector.

tri.lower, tri.upper: Logical or numeric controlling whether the first and last intervals should be triangular instead of rectangular. With the default value (NA), this happens only if the corresponding extreme at values are -Inf or Inf respectively, and the triangles occupy 5% of the total length of the color key. If numeric and between 0 and 0.25, these give the corresponding fraction, which is again 5% when specified as TRUE.

labels: A character vector for labelling the at values, or more commonly, a list describing characteristics of the labels. This list may include components labels, at, cex, col, rot, font, fontface and fontfamily.

title: Usually a character vector or expression providing a title for the colorkey, or a list controlling the title in further detail, or an arbitrary "grob". For details of how the list form is interpreted, see the entry for main in xyplot; generally speaking, the actual label should be specified as the label component (which may be unnamed if it is the first component), and the remaining arguments are used as appropriate in a call to textGrob. Further control of the placement of the title is possible through the component title.control. In particular, if a rot component is not specified, its default depends on the value of title.control$side (0 for top or bottom, and 90 for left or right).

title defaults to NULL, which means no title is drawn.

title.control: A list providing control over the placement of a title, if specified. Currently two components are honoured: side can take values "top", "bottom", "left", and "right", and specifies the side of the colorkey on which the title is to be placed. Defaults to the value of the "space" component. padding is a multiplier for the default amount of padding between the title and the colorkey.
tick.number: The approximate number of ticks desired.
tck: A (scalar) multiplier for tick lengths.
corner: Interacts with x, y; currently unimplemented
width: The width of the key
height: The length of key as a fraction of the appropriate side of plot.
raster: A logical flag indicating whether the colorkey should be rendered as a
   raster image using grid.raster. See also panel.levelplot.raster.
interpolate: Logical flag, passed to rasterGrob when raster=TRUE.
axis.line: A list giving graphical parameters for the color key boundary and
tick marks. Defaults to trellis.par.get("axis.line").
axis.text: A list giving graphical parameters for the tick mark labels on the
color key. Defaults to trellis.par.get("axis.text").
contour: A logical flag, indicating whether to draw contour lines.
cuts: The number of levels the range of z would be divided into.
labels: Typically a logical indicating whether contour lines should be labelled, but other
   possibilities for more sophisticated control exists. Details are documented in
   the help page for panel.levelplot, to which this argument is passed on un-
   changed. That help page also documents the label.style argument, which
   affects how the labels are rendered.
pretty: A logical flag, indicating whether to use pretty cut locations and labels.
region: A logical flag, indicating whether regions between contour lines should be filled
   as in a level plot.
allow.multiple, outer, prepanel, scales, strip, groups, xlab, xlim, ylab, ylim, drop.unused.levels, la
... Further arguments may be supplied. Some are processed by levelplot or
contourplot, and those that are unrecognized are passed on to the panel func-
ion.
useRaster: A logical flag indicating whether raster representations should be used, both
   for the false color image and the color key (if present). Effectively, setting
   this to TRUE changes the default panel function from panel.levelplot to
   panel.levelplot.raster, and sets the default value of colorkey$raster to
   TRUE.
   Note that panel.levelplot.raster provides only a subset of the features of
   panel.levelplot, but setting useRaster=TRUE will not check whether any of
   the additional features have been requested.
   Not all devices support raster images. For devices that appear to lack support,
   useRaster=TRUE will be ignored with a warning.

Details

These and all other high level Trellis functions have several arguments in common. These are
extensively documented only in the help page for xyplot, which should be consulted to learn more
detailed usage.

Other useful arguments are mentioned in the help page for the default panel function
panel.levelplot (these are formally arguments to the panel function, but can be specified in
the high level calls directly).
Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References


See Also

xyplot, Lattice, panel.levelplot

Examples

```r
x <- seq(pi/4, 5 * pi, length.out = 100)
y <- seq(pi/4, 5 * pi, length.out = 100)
r <- as.vector(sqrt(outer(x^2, y^2, "*")))
grid <- expand.grid(x=x, y=y)
grid$z <- cos(r^2) * exp(-r/(pi^3))
levelplot(z ~ x * y, grid, cuts = 50, scales=list(log="e"), xlab="", ylab="", main="Weird Function", sub="with log scales", colorkey = FALSE, region = TRUE)
## triangular end-points in color key, with a title
levelplot(z ~ x * y, grid, col.regions = hcl.colors(10), at = c(-Inf, seq(-0.8, 0.8, by = 0.2), Inf))
#S-PLUS example
require(stats)
attach(environmental)
ozo.m <- loess((ozone^(1/3)) ~ wind * temperature * radiation, parametric = c("radiation", "wind"), span = 1, degree = 2)
w.marginal <- seq(min(wind), max(wind), length.out = 50)
t.marginal <- seq(min(temperature), max(temperature), length.out = 50)
r.marginal <- seq(min(radiation), max(radiation), length.out = 4)
wtr.marginal <- list(wind = w.marginal, temperature = t.marginal, radiation = r.marginal)
grid <- expand.grid(wtr.marginal)
grid[, "fit"] <- c(predict(ozo.m, grid))
contourplot(fit ~ wind * temperature | radiation, data = grid, cuts = 10, region = TRUE, xlab = "Wind Speed (mph)", ylab = "Temperature (F)", main = "Cube Root Ozone (cube root ppb)")
detach()
```
3d Scatter Plot and Wireframe Surface Plot

Description

Generic functions to draw 3d scatter plots and surfaces. The "formula" methods do most of the actual work.

Usage

cloud(x, data, ...)
wireframe(x, data, ...)

## S3 method for class 'formula'
cloud(x,
data,
    allow.multiple = is.null(groups) || outer,
    outer = FALSE,
    auto.key = lattice.getOption("default.args")$auto.key,
    aspect = c(1,1),
    panel.aspect = 1,
    panel = lattice.getOption("panel.cloud"),
    prepanel = NULL,
    scales = list(),
    strip = TRUE,
    groups = NULL,
    xlab,
    ylab,
    zlab,
    xlim = if (is.factor(x)) levels(x) else range(x, finite = TRUE),
    ylim = if (is.factor(y)) levels(y) else range(y, finite = TRUE),
    zlim = if (is.factor(z)) levels(z) else range(z, finite = TRUE),
    at,
    drape = FALSE,
    pretty = FALSE,
    drop.unused.levels,
    ...,
    lattice.options = NULL,
    default.scales =
        list(distance = c(1, 1, 1),
            arrows = TRUE,
            axs = axs.default),
    default.prepanel = lattice.getOption("prepanel.default.cloud"),
    colorkey,
    col.regions,
    alpha.regions,
    cuts = 70,
    subset = TRUE,
    axs.default = "r")

## S3 method for class 'data.frame'
cloud(x, data = NULL, formula = data, ...)

## S3 method for class 'formula'
wireframe(x,
    data,
    panel = lattice.getOption("panel.wireframe"),
    default.prepanel = lattice.getOption("prepanel.default.wireframe"),
    ...)

## S3 method for class 'data.frame'
wireframe(x, data = NULL, formula = data, ...)

## S3 method for class 'matrix'
cloud(x, data = NULL, type = "h",
    zlab = deparse(substitute(x)), aspect, ...,
    xlim, ylim, row.values, column.values)

## S3 method for class 'table'
cloud(x, data = NULL, groups = FALSE,
    zlab = deparse(substitute(x)),
    type = "h", ...)

## S3 method for class 'matrix'
wireframe(x, data = NULL,
    zlab = deparse(substitute(x)), aspect, ...,
    xlim, ylim, row.values, column.values)

Arguments

x
The object on which method dispatch is carried out.
For the "formula" methods, a formula of the form \( z \sim x \times y \mid g1 \times g2 \times \ldots \),
where \( z \) is a numeric response, and \( x, y \) are numeric values. \( g1, g2, \ldots \) if
present, are conditioning variables used for conditioning, and must be either
factors or shingles. In the case of wireframe, calculations are based on
the assumption that the \( x \) and \( y \) values are evaluated on a rectangular grid defined
by their unique values. The grid points need not be equally spaced.
For wireframe, \( x, y \) and \( z \) may also be matrices (of the same dimension),
in which case they are taken to represent a 3-D surface parametrized on a 2-D grid
e.g., a sphere). Conditioning is not possible with this feature. See details below.
Missing values are allowed, either as NA values in the \( z \) vector, or missing rows
in the data frame (note however that in that case the \( X \) and \( Y \) grids will be
determined only by the available values). For a grouped display (producing
multiple surfaces), missing rows are not allowed, but NA-s in \( z \) are.
Both wireframe and cloud have methods for matrix objects, in which case
\( x \) provides the \( z \) vector described above, while its rows and columns are interpreted as the \( x \) and \( y \) vectors respectively. This is similar to the form used in
persp.

data
For the "formula" methods, an optional data frame in which variables in the
formula (as well as groups and subset, if any) are to be evaluated. data should
not be specified except when using the "formula" method.

formula
The formula to be used for the "data.frame" methods. See documentation for
argument x for details.
row.values, column.values

Optional vectors of values that define the grid when x is a matrix. row.values and column.values must have the same lengths as nrow(x) and ncol(x) respectively. By default, row and column numbers.

allow.multiple, outer, auto.key, prepanel, strip, groups, xlab, xlim, ylab, ylim, drop.unused.levels, These arguments are documented in the help page for xyplot. For the cloud.table method, groups must be a logical indicating whether the last dimension should be used as a grouping variable as opposed to a conditioning variable. This is only relevant if the table has more than 2 dimensions.

type
type of display in cloud (see panel.3dscatter for details). Defaults to "h" for the matrix method.

aspect, panel.aspect

Unlike other high level functions, aspect is taken to be a numeric vector of length 2, giving the relative aspects of the y-size/x-size and z-size/x-size of the enclosing cube. The usual role of the aspect argument in determining the aspect ratio of the panel (see xyplot for details) is played by panel.aspect, except that it can only be a numeric value.

For the matrix methods, the default y/x aspect is ncol(x) / nrow(x) and the z/x aspect is the smaller of the y/x aspect and 1.

panel

panel function used to create the display. See panel.cloud for (non-trivial) details.

default.prepanel

Fallback prepanel function. See xyplot.

scales

a list describing the scales. As with other high level functions (see xyplot for details), this list can contain parameters in name=value form. It can also contain components with the special names x, y and z, which can be similar lists with axis-specific values overriding the ones specified in scales.

The most common use for this argument is to set arrows=FALSE, which causes tick marks and labels to be used instead of arrows being drawn (the default). Both can be suppressed by draw=FALSE. Another special component is distance, which specifies the relative distance of the axis label from the bounding box. If specified as a component of scales (as opposed to one of scales$x etc), this can be (and is recycled if not) a vector of length 3, specifying distances for the x, y and z labels respectively.

Other components that work in the scales argument of xyplot etc. should also work here (as long as they make sense), including explicit specification of tick mark locations and labels. (Not everything is implemented yet, but if you find something that should work but does not, feel free to bug the maintainer.) Note, however, that for these functions scales cannot contain information that is specific to particular panels. If you really need that, consider using the scales.3d argument of panel.cloud.

axs.default

Unlike 2-D display functions, cloud does not expand the bounding box to slightly beyond the range of the data, even though it should. This is primarily because this is the natural behaviour in wireframe, which uses the same code. axs.default is intended to provide a different default for cloud. However, this feature has not yet been implemented.

zlab

Specifies a label describing the z variable in ways similar to xlab and ylab (i.e. “grob”, character string, expression or list) in other high level functions. Additionally, if zlab (and xlab and ylab) is a list, it can contain a component called rot, controlling the rotation for the label.
zlim limits for the z-axis. Similar to xlim and ylim in other high level functions
drape logical, whether the wireframe is to be draped in color. If TRUE, the height of a
facet is used to determine its color in a manner similar to the coloring scheme
used in levelplot. Otherwise, the background color is used to color the facets.
This argument is ignored if shade = TRUE (see panel.3dwire).
at, col.regions, alpha.regions
these arguments are analogous to those in levelplot if drape=TRUE, at gives
the vector of cutpoints where the colors change, and col.regions the vec-
tor of colors to be used in that case. alpha.regions determines the alpha-
transparency on supporting devices. These are passed down to the panel func-
tion, and also used in the colorkey if appropriate. The default for col.regions
and alpha.regions is derived from the Trellis setting "regions"
cuts if at is unspecified, the approximate number of cutpoints if drape=TRUE
pretty whether automatic choice of cutpoints should be prettified
colorkey logical indicating whether a color key should be drawn alongside, or a list de-
scribing such a key. See levelplot for details.
...
Any number of other arguments can be specified, and are passed to the panel
function. In particular, the arguments distance, perspective, screen and
R.mat are very important in determining the 3-D display. The argument shade
can be useful for wireframe calls, and controls shading of the rendered surface.
These arguments are described in detail in the help page for panel.cloud.
Additionally, an argument called zoom may be specified, which should be a nu-
meric scalar to be interpreted as a scale factor by which the projection is magni-
fied. This can be useful to get the variable names into the plot. This argument is
actually only used by the default prepanel function.

Details

These functions produce three dimensional plots in each panel (as long as the default panel functions
are used). The orientation is obtained as follows: the data are scaled to fall within a bounding box
that is contained in the [-0.5, 0.5] cube (even smaller for non-default values of aspect). The viewing
direction is given by a sequence of rotations specified by the screen argument, starting from the
positive Z-axis. The viewing point (camera) is located at a distance of 1/distance from the origin.
If perspective=FALSE, distance is set to 0 (i.e., the viewing point is at an infinite distance).

cloud draws a 3-D Scatter Plot, while wireframe draws a 3-D surface (usually evaluated on a
grid). Multiple surfaces can be drawn by wireframe using the groups argument (although this is
of limited use because the display is incorrect when the surfaces intersect). Specifying groups with
cloud results in a panel.superpose-like effect (via panel.3dscatter).

wireframe can optionally render the surface as being illuminated by a light source (no shadows
though). Details can be found in the help page for panel.3dwire. Note that although arguments
controlling these are actually arguments for the panel function, they can be supplied to cloud and
wireframe directly.

For single panel plots, wireframe can also plot parametrized 3-D surfaces (i.e., functions of the
form f(u,v) = (x(u,v), y(u,v), z(u,v)), where values of (u,v) lie on a rectangle. The simplest example
of this sort of surface is a sphere parametrized by latitude and longitude. This can be achieved by
calling wireframe with a formula x of the form z~x*y, where x, y and z are all matrices of the same
dimension, representing the values of x(u,v), y(u,v) and z(u,v) evaluated on a discrete rectangular
grid (the actual values of (u,v) are irrelevant).

When this feature is used, the heights used to calculate drape colors or shading colors are no longer
the z values, but the distances of (x, y, z) from the origin.
Note that this feature does not work with groups, subscripts, subset, etc. Conditioning variables are also not supported in this case.

The algorithm for identifying which edges of the bounding box are ‘behind’ the points doesn’t work in some extreme situations. Also, panel.cloud tries to figure out the optimal location of the arrows and axis labels automatically, but can fail on occasion (especially when the view is from ‘below’ the data). This can be manually controlled by the scpos argument in panel.cloud.

These and all other high level Trellis functions have several other arguments in common. These are extensively documented only in the help page for xyplot, which should be consulted to learn more detailed usage.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Note

There is a known problem with grouped wireframe displays when the (x, y) coordinates represented in the data do not represent the full evaluation grid. The problem occurs whether the grouping is specified through the groups argument or through the formula interface, and currently causes memory access violations. Depending on the circumstances, this is manifested either as a meaningless plot or a crash. To work around the problem, it should be enough to have a row in the data frame for each grid point, with an NA response (z) in rows that were previously missing.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References


See Also

Lattice for an overview of the package, as well as xyplot, levelplot, panel.cloud.

For interaction, see panel.identify.cloud.

Examples

```r
## volcano ## 87 x 61 matrix
wireframe(volcano, shade = TRUE,
    aspect = c(61/87, 0.4),
    light.source = c(10,0,10))

g <- expand.grid(x = 1:10, y = 5:15, gr = 1:2)
g$z <- log((g$x^g$gr + g$y^2) * g$gr)
wireframe(z ~ x * y, data = g, groups = gr,
    scales = list(arrows = FALSE),
    drape = TRUE, colorkey = TRUE,
    screen = list(z = 30, x = -60))

cloud(Sepal.Length ~ Petal.Length * Petal.Width | Species, data = iris,
    screen = list(x = -90, y = 70), distance = .4, zoom = .6)
```
## cloud.table

```r
cloud(prop.table(Titanic, margin = 1:3),
    type = c("p", "h"), strip = strip.custom(strip.names = TRUE),
    scales = list(arrows = FALSE, distance = 2), panel.aspect = 0.7,
    zlab = "Proportion")[, 1]
```

## transparent axes

```r
par.set <-
    list(axis.line = list(col = "transparent"),
         clip = list(panel = "off"))
print(cloud(Sepal.Length ~ Petal.Length * Petal.Width,
            data = iris, cex = .8,
            groups = Species,
            main = "Stereo",
            screen = list(z = 20, x = -70, y = 3),
            par.settings = par.set,
            scales = list(col = "black"),
            split = c(1,1,2,1, more = TRUE)
print(cloud(Sepal.Length ~ Petal.Length * Petal.Width,
            data = iris, cex = .8,
            groups = Species,
            main = "Stereo",
            screen = list(z = 20, x = -70, y = 0),
            par.settings = par.set,
            scales = list(col = "black"),
            split = c(2,1,2,1))
```

---

**Scatter Plot Matrices**

### Description

Draw Conditional Scatter Plot Matrices and Parallel Coordinate Plots

### Usage

```r
splom(x, data, ...)
parallelplot(x, data, ...)
```

### S3 method for class 'formula'

```r
splom(x,
     data,
     auto.key = lattice.getOption("default.args")$auto.key,
     aspect = 1,
     between = list(x = 0.5, y = 0.5),
     panel = lattice.getOption("panel.splom"),
     prepanel,
     scales,
     strip,
```
groups,
xlab,
xlim,
ylab = NULL,
ylim,
superpanel = lattice.getOption("panel.pairs"),
pscales = 5,
varnames = NULL,
drop.unused.levels,

lattice.options = NULL,
default.scales,
default.prepanel = lattice.getOption("prepanel.default.splom"),
subset = TRUE)
## S3 method for class 'formula'
parallelplot(x,
data,
auto.key = lattice.getOption("default.args")$auto.key,
aspect = "fill",
between = list(x = 0.5, y = 0.5),
panel = lattice.getOption("panel.parallel"),
prepanel,
scales,
strip,
groups,
xlab = NULL,
xlim,
ylab = NULL,
ylim,
varnames = NULL,
horizontal.axis = TRUE,
drop.unused.levels,

lattice.options = NULL,
default.scales,
default.prepanel = lattice.getOption("prepanel.default.parallel"),
subset = TRUE)
## S3 method for class 'data.frame'
splom(x, data = NULL, ..., groups = NULL, subset = TRUE)
## S3 method for class 'matrix'
splom(x, data = NULL, ..., groups = NULL, subset = TRUE)

## S3 method for class 'matrix'
parallelplot(x, data = NULL, ..., groups = NULL, subset = TRUE)
## S3 method for class 'data.frame'
parallelplot(x, data = NULL, ..., groups = NULL, subset = TRUE)

Arguments

**x**

The object on which method dispatch is carried out.

For the "formula" method, a formula describing the structure of the plot, which should be of the form \( \sim x \mid g1 \ast g2 \ast \ldots \), where \( x \) is a data frame or matrix.
Each of $g_1, g_2, \ldots$ must be either factors or shingles. The conditioning variables $g_1, g_2, \ldots$ may be omitted. For the data.frame methods, a data frame.

**data**
For the formula methods, an optional data frame in which variables in the formula (as well as groups and subset, if any) are to be evaluated.

**aspect**
aspect ratio of each panel (and subpanel), square by default for splom.

**between**
to avoid confusion between panels and subpanels, the default is to show the panels of a splom plot with space between them.

**panel**
For parallelplot, this has the usual interpretation, i.e., a function that creates the display within each panel.

For splom, the terminology is slightly complicated. The role played by the panel function in most other high-level functions is played here by the superpanel function, which is responsible for the display for each conditional data subset. panel is simply an argument to the default superpanel function panel.pairs, and is passed on to it unchanged. It is used there to create each pairwise display. See panel.pairs for more useful options.

**superpanel**
function that sets up the splom display, by default as a scatterplot matrix.

**pscales**
a numeric value or a list, meant to be a less functional substitute for the scales argument in xyplot etc. This argument is passed to the superpanel function, and is handled by the default superpanel function panel.pairs. The help page for the latter documents this argument in more detail.

**varnames**
A character or expression vector or giving names to be used for the variables in $x$. By default, the column names of $x$.

**horizontal.axis**
logical indicating whether the parallel axes should be laid out horizontally (TRUE) or vertically (FALSE).

**auto.key, prepanel, scales, strip, groups, xlab, xlim, ylab, ylim, drop.unused.levels, lattice.options, default.scales, subset**
See xyplot for more useful options.

Further arguments. See corresponding entry in xyplot for non-trivial details.

**Details**

splom produces Scatter Plot Matrices. The role usually played by panel is taken over by superpanel, which takes a data frame subset and is responsible for plotting it. It is called with the coordinate system set up to have both $x$- and $y$-limits from $0.5$ to $\text{ncol}(z) + 0.5$. The only built-in option currently available is panel.pairs, which calls a further panel function for each pair $(i, j)$ of variables in $z$ inside a rectangle of unit width and height centered at $c(i, j)$ (see panel.pairs for details).

Many of the finer customizations usually done via arguments to high level function like xyplot are instead done by panel.pairs for splom. These include control of axis limits, tick locations and prepanel calculations. If you are trying to fine-tune your splom plot, definitely look at the panel.pairs help page. The scales argument is usually not very useful in splom, and trying to change it may have undesired effects.

parallelplot draws Parallel Coordinate Plots. (Difficult to describe, see example.)

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for xyplot, which should be consulted to learn more detailed usage.
Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot, Lattice, panel.pairs, panel.parallel.

Examples

```r
super.sym <- trellis.par.get("superpose.symbol")
splom(~iris[1:4], groups = Species, data = iris,
    panel = panel.superpose,
    key = list(title = "Three Varieties of Iris",
               columns = 3,
               points = list(pch = super.sym$pch[1:3],
                             col = super.sym$col[1:3]),
               text = list(c("Setosa", "Versicolor", "Virginica"))))
splom(~iris[1:3]|Species, data = iris,
    layout=c(2,2), pscales = 0,
    varnames = c("Sepal\nLength", "Sepal\nWidth", "Petal\nLength"),
    page = function(...) {
        ltext(x = seq(.6, .8, length.out = 4),
              y = seq(.9, .6, length.out = 4),
              labels = c("Three", "Varieties", "of", "Iris"),
              cex = 2)
    }
parallelplot(~iris[1:4] | Species, iris)
parallelplot(~iris[1:4], iris, groups = Species,
            horizontal.axis = FALSE, scales = list(x = list(rot = 90)))
```

B_09_tmd

Tukey Mean-Difference Plot

Description

tmd Creates Tukey Mean-Difference Plots from a trellis object returned by xyplot, qq or qqmath. The prepanel and panel functions are used as appropriate. The formula and data.frame methods for tmd are provided for convenience, and simply call tmd on the object created by the corresponding xyplot methods.

Usage

tmd(object, ...)

## S3 method for class 'trellis'
tmd(object,
    xlab = "mean",
    ylab = "difference",
    ...)

```r
tmd <- function(object, xlab = "mean", ylab = "difference", ...) {
    #...
panel, prepanel, ...

prepanel.tmd.qqmath(x,
   f.value = NULL,
   distribution = qnorm,
   qtype = 7,
   groups = NULL,
   subscripts, ...)
panel.tmd.qqmath(x,
   f.value = NULL,
   distribution = qnorm,
   qtype = 7,
   groups = NULL,
   subscripts, ..., identifier = "tmd")
panel.tmd.default(x, y, groups = NULL, ...,
   identifier = "tmd")
prepanel.tmd.default(x, y, ...)

Arguments

object An object of class "trellis" returned by xyplot, qq or qqmath.
xlab x label
ylab y label
panel panel function to be used. See details below.
prepanel prepanel function. See details below.
f.value, distribution, qtype see panel.qqmath.
groups, subscripts see xyplot.
x, y data as passed to panel functions in original call.
... other arguments
identifier A character string that is prepended to the names of grobs that are created by
this panel function.

Details

The Tukey Mean-difference plot is produced by modifying the (x,y) values of each panel as follows:
the new coordinates are given by x=(x+y)/2 and y=y-x, which are then plotted. The default panel
function(s) add a reference line at y=0 as well.
tmd acts on the a "trellis" object, not on the actual plot this object would have produced. As such,
it only uses the arguments supplied to the panel function in the original call, and completely ignores
what the original panel function might have done with this data. tmd uses these panel arguments to
set up its own scales (using its prepanel argument) and display (using panel). It is thus important
to provide suitable prepanel and panel functions to tmd depending on the original call.
Such functions currently exist for xyplot, qq (the ones with default in their name) and qqmath, as
listed in the usage section above. These assume the default displays for the corresponding high-level
call. If unspecified, the prepanel and panel arguments default to suitable choices.
tmdd uses the update method for "trellis" objects, which processes all extra arguments supplied to tmd.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

qq, qqmath, xyplot, Lattice

Examples

tmd(qqmath(~height | voice.part, data = singer))

Residual and Fit Spread Plots

Description

Plots fitted values and residuals (via qqmath) on a common scale for any object that has methods for fitted values and residuals.

Usage

rfs(model, layout=c(2, 1), xlab="f-value", ylab=NULL, distribution = qunif, panel, prepanel, strip, ...)

Arguments

model a fitted model object with methods fitted.values and residuals. Can be the value returned by oneway
layout default layout is c(2,1)
xlab defaults to "f.value"
distribution the distribution function to be used for qqmath
ylab, panel, prepanel, strip See xyplot
... other arguments, passed on to qqmath.

Value

An object of class "trellis". The update method can be used to update components of the object and the print method (usually called by default) will plot it on an appropriate plotting device.
Fits a One-way model to univariate data grouped by a factor, the result often being displayed using `rfs`

**Usage**

```r
doneway(formula, data, location=mean, spread=function(x) sqrt(var(x)))
```

**Arguments**

- `formula`: formula of the form `y ~ x` where `y` is the numeric response and `x` is the grouping factor.
- `data`: data frame in which the model is to be evaluated.
- `location`: function or numeric giving the location statistic to be used for centering the observations, e.g. `median`, 0 (to avoid centering).
- `spread`: function or numeric giving the spread statistic to be used for scaling the observations, e.g. `sd`, 1 (to avoid scaling).

**Value**

A list with components

- `location`: vector of locations for each group.
- `spread`: vector of spreads for each group.
- `fitted.values`: vector of locations for each observation.
- `residuals`: residuals (`y - fitted.values`).
- `scaled.residuals`: residuals scaled by `spread` for their group.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

- `rfs`, `Lattice`
Description

Initialization of a display device with appropriate graphical parameters.

Usage

trellis.device(device = getOption("device"),
               color = !(dev.name == "postscript"),
               theme = lattice.getOption("default.theme"),
               new = TRUE,
               retain = FALSE,
               ...)

Arguments

device function (or the name of one as a character string) that starts a device. Admissible values depend on the platform and how R was compiled (see Devices), but usually "pdf", "postscript", "png", "jpeg" and at least one of "X11", "windows" and "quartz" will be available.

color logical, whether the initial settings should be color or black and white. Defaults to FALSE for postscript devices, TRUE otherwise. Note that this only applies to the initial choice of colors, which can be overridden using theme or subsequent calls to trellis.par.set (and by arguments supplied directly in high level calls for some settings).

theme list of components that changes the settings of the device opened, or, a function that when called produces such a list. The function name can be supplied as a quoted string. These settings are only used to modify the default settings (determined by other arguments), and need not contain all possible parameters. A possible use of this argument is to change the default settings by specifying lattice.options(default.theme = "col.whitebg"). For back-compatibility, this is initially (when lattice is loaded) set togetOption(lattice.theme).

If theme is a function, it will not be supplied any arguments, however, it is guaranteed that a device will already be open when it is called, so one may use .Device inside the function to ascertain what device has been opened.

new logical flag indicating whether a new device should be started. If FALSE, the options for the current device are changed to the defaults determined by the other arguments.

retain logical. If TRUE and a setting for this device already exists, then that is used instead of the defaults for this device. By default, pre-existing settings are overwritten (and lost).

name name of the device for which the setting is required, as returned by .Device

... additional parameters to be passed to the device function, most commonly file for non-screen devices, as well as height, width, etc. See the help file for individual devices for admissible arguments.
The `trellis.device` function sets up an R graphics device for use with lattice graphics, by opening the device if necessary, and defining a set of associated graphical parameters (colors, line types, fonts, etc.).

Even if a device is opened without calling `trellis.device`, for example, by calling a device function directly, `trellis.device` is still called automatically when a "trellis" object is plotted. The default graphical settings used in this case can be customized using `lattice.options`. It is therefore rarely necessary for the user to call `trellis.device` explicitly.

None; `trellis.device` is called for the side effect of opening a device and / or setting associated graphical parameters.

Earlier versions of `trellis.device` had a `bg` argument to set the background color, but this is no longer supported. If supplied, the `bg` argument will be passed on to the device function; however, this will have no effect on the Trellis settings. It is rarely meaningful to change the background alone; if you feel the need to change the background, consider using the `theme` argument instead.

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>


See Also

- `Lattice` for an overview of the `lattice` package.
- `Devices` for valid choices of device on your platform.
- `standard.theme` for the default theme and alternatives.

Built-in graphical parameter settings. These mainly differ in their choice of colors.

---

Description

Built-in graphical parameter settings. These mainly differ in their choice of colors.
Usage

standard.theme(name, color = TRUE,
    symbol = palette.colors(palette = "Okabe-Ito")[c(6, 2, 4, 7, 3, 5, 8)],
    fill = NULL,
    region = hcl.colors(14, palette = "YlGnBu", rev = TRUE),
    reference = "gray90",
    bg = "transparent",
    fg = "black",
...
)
canonical.theme(...)
custom_theme(symbol, fill, region,
    reference = "gray90", bg = "transparent", fg = "black",
    strip.bg = rep("gray95", 7), strip.fg = rep("gray70", 7),
...
)
classic.theme(name, color)
col.whitebg()

Arguments

name character string giving the name of the device for which the setting is required, as returned by .Device. This is only used by classic.theme to allow device-specific setting. It is retained in standard.theme for back-compatibility, but its use is not recommended.
color logical, whether the initial settings should be color or black and white.
symbol vector of colors to be used for symbols and lines.
fill vector of colors to be used as fill colors, e.g., in bar charts and histograms. The default of NULL in standard.theme results in lightened versions of the symbol colors to be used.
region vector of colors to be used to create a color ramp, typically used by levelplot
reference color, to be used for reference lines.
fg color, to be used for foreground elements such as axes and labels.
bg color, to be used as background.
strip.bg color, to be used as strip background.
strip.fg color, to be used as strip foreground.
...
additional arguments, passed on to other functions as appropriate. In particular, additional arguments provided to standard.theme will be passed on to custom_theme, and these may include non-color parameters that will be used to modify the resulting theme via simpleTheme.

Details

Trellis Graphics functions obtain the default values of various graphical parameters (colors, line types, fonts, etc.) from a customizable “settings” list (see trellis.par.set for details). This functionality is analogous to par for standard R graphics and, together with lattice.options, mostly supplants it (par settings are mostly ignored by Lattice). Unlike par, Trellis settings can be controlled separately for each different device type (but not concurrently for different instances of the same device).
The functions documented in this page produce such graphical settings (a.k.a. themes), usually to be used with `trellis.device` or `trellis.par.set`.

`classic.theme` and `col.whitebg` produce predefined themes that are not recommended for routine use but are retained for compatibility.

The `classic.theme` function was intended to provide device specific settings (e.g. light colors on a grey background for screen devices, dark colors or black and white for print devices) and was used to obtain defaults prior to R 2.3.0. However, these settings are not always appropriate, due to the variety of platforms and hardware settings on which R is used, as well as the fact that a plot created on a particular device may be subsequently used in many different ways. For this reason, common device-agnostic defaults were used for all devices from R 2.3.0 onwards.

Since R 4.3.0, a new set of defaults given by `standard.theme` is used. The defaults are based on HCL palettes, but customization of the palettes is allowed. Earlier behaviour can be reinstated by setting `classic.theme` as the default theme argument, e.g., by putting `lattice.options(default.theme = classic.theme("pdf"))` in a startup script (see the entry for `theme` in `trellis.device` for details).

`custom.theme` is the workhorse function called by `standard.theme`. `canonical.theme` is an alias for `standard.theme`.

Value

A list of components defining graphical parameter settings for Lattice displays. It is used internally in `trellis.device`, and can also be used as the theme argument to `trellis.par.set`.

`col.whitebg` returns a similar (but smaller) list that is suitable as the theme argument to `trellis.device` and `trellis.par.set`. It contains settings values which provide colors suitable for plotting on a white background. Note that the name `col.whitebg` is somewhat of a misnomer, since it actually sets the background to transparent rather than white.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References

http://lmdvr.r-forge.r-project.org/

See Also

`Lattice` for an overview of the lattice package.
`Devices` for valid choices of device on your platform.

`trellis.par.get` and `trellis.par.set` can be used to query and modify the settings after a device has been initialized. The `par.settings` argument to high level functions, described in `xyplot`, can be used to attach transient settings to a "trellis" object.
Graphical Parameters for Trellis Displays

Description

Functions used to query, display and modify graphical parameters for fine control of Trellis displays. Modifications are made to the settings for the currently active device only.

Usage

```r
trellis.par.set(name, value, ..., theme, warn = TRUE, strict = FALSE)
trellis.par.get(name = NULL)
show.settings(x = NULL)
```

Arguments

- **name**
  - A character string giving the name of a component. If unspecified in `trellis.par.get()`, the return value is a named list containing all the current settings (this can be used to get the valid values for `name`).

- **value**
  - a list giving the desired value of the component. Components that are already defined as part of the current settings but are not mentioned in `value` will remain unchanged.

- **theme**
  - a list describing how to change the settings, similar to what is returned by `trellis.par.get()`. This is purely for convenience, allowing multiple calls to `trellis.par.set` to be condensed into one. The name of each component must be a valid `name` as described above, with the corresponding value a valid `value` as described above.
  - As in `trellis.device`, `theme` can also be a function that produces such a list when called. The function name can be supplied as a quoted string.

- **...**
  - Multiple settings can be specified in `name = value` form. Equivalent to calling with `theme = list(...)`

- **warn**
  - A logical flag, indicating whether a warning should be issued when `trellis.par.get` is called when no graphics device is open.

- **strict**
  - Usually a logical flag, indicating whether the value should be interpreted strictly. Usually, assignment of value to the corresponding named component is fuzzy in the sense that sub-components that are absent from `value` but not currently `NULL` are retained. By specifying `strict = TRUE`, such values will be removed.
  - An even stricter interpretation is allowed by specifying `strict` as a numeric value larger than 1. In that case, top-level components not specified in the call will also be removed. This is primarily for internal use.

- **x**
  - optional list of components that change the settings (any valid value of `theme`). These are used to modify the current settings (obtained by `trellis.par.get`) before they are displayed.
The various graphical parameters (color, line type, background etc) that control the look and feel of Trellis displays are highly customizable. Also, R can produce graphics on a number of devices, and it is expected that a different set of parameters would be more suited to different devices. These parameters are stored internally in a variable named lattice.theme, which is a list whose components define settings for particular devices. The components are identified by the name of the device they represent (as obtained by .Device), and are created as and when new devices are opened for the first time using trellis.device (or Lattice plots are drawn on a device for the first time in that session).

The initial settings for each device defaults to values appropriate for that device. In practice, this boils down to three distinct settings, one for screen devices like x11 and windows, one for black and white plots (mostly useful for postscript) and one for color printers (color postscript, pdf).

Once a device is open, its settings can be modified. When another instance of the same device is opened later using trellis.device, the settings for that device are reset to its defaults, unless otherwise specified in the call to trellis.device. But settings for different devices are treated separately, i.e., opening a postscript device will not alter the x11 settings, which will remain in effect whenever an x11 device is active.

The functions trellis.par.* are meant to be interfaces to the global settings. They always apply on the settings for the currently ACTIVE device.

trellis.par.get, called without any arguments, returns the full list of settings for the active device. With the name argument present, it returns that component only. trellis.par.get sets the value of the name component of the current active device settings to value.

trellis.par.get is usually used inside trellis functions to get graphical parameters before plotting. Modifications by users via trellis.par.set is traditionally done as follows:

```r
add.line <- trellis.par.get("add.line")
add.line$col <- "red"
trellis.par.set("add.line", add.line)
```

More convenient (but not S compatible) ways to do this are

trellis.par.set(list(add.line = list(col = "red")))

and
trellis.par.set(add.line = list(col = "red"))

The actual list of the components in trellis.settings has not been finalized, so I'm not attempting to list them here. The current value can be obtained by print(trellis.par.get()). Most names should be self-explanatory.

show.settings provides a graphical display summarizing some of the values in the current settings.

### Value

trellis.par.get returns a list giving parameters for that component. If name is missing, it returns the full list.

Most of the settings are graphical parameters that control various elements of a lattice plot. For details, see the examples below. The more unusual settings are described here.

grid.pars Grid graphical parameters that are in effect globally unless overridden by specific settings.

fontsize A list of two components (each a numeric scalar), text and points, for text and symbols respectively.
clip A list of two components (each a character string, either "on" or "off"), panel and strip.
axis.components A list with four components (left, top, right, bottom), each a list giving
numeric multipliers named tck, pad1, and pad2 for corresponding grid layout units.
layout.heights A list with numeric multipliers for grid layout heights.
layout.widths A list with numeric multipliers for grid layout widths.

Note
In some ways, trellis.par.get and trellis.par.set together are a replacement for the \texttt{par}
function used in traditional R graphics. In particular, changing \texttt{par} settings has little (if any)
effect on lattice output. Since lattice plots are implemented using Grid graphics, its parameter system
does have an effect unless overridden by a suitable lattice parameter setting. Such parameters can
be specified as part of a lattice theme by including them in the \texttt{grid.pars} component (see \texttt{gpar}
for a list of valid parameter names).

Author(s)
Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also
\texttt{trellis.device, Lattice, gpar}

Examples

\begin{verbatim}
show.settings()

tp <- trellis.par.get()

unusual <- c("grid.pars", "fontsize", "clip", "axis.components",
             "layout.heights", "layout.widths")

for (u in unusual) tp[[u]] <- NULL

names.tp <- lapply(tp, names)
unames <- sort(unique(unlist(names.tp)))
ans <- matrix(0, nrow = length(names.tp), ncol = length(unames))
rownames(ans) <- names(names.tp)
colnames(ans) <- unames
for (i in seq_along(names.tp))
  ans[i, ] <- as.numeric(unames %in% names.tp[[i]])
ans <- ans[, order(-colSums(ans))]
ans[ans == 0] <- NA

levelplot(t(ans), colorkey = FALSE,
          scales = list(x = list(rot = 90)),
          panel = function(x, y, z, ...) {
            panel.abline(v = unique(as.numeric(x)),
                         h = unique(as.numeric(y)),
                         col = "darkgrey")
            panel.xyplot(x, y, pch = 16 * z, ...)
          },
          xlab = "Graphical parameters",
          ylab = "Setting names")
\end{verbatim}
Function to generate a simple theme

Description

Simple interface to generate a list appropriate as a theme, typically used as the `par.settings` argument in a high level call.

Usage

```r
simpleTheme(col, alpha, 
cex, pch, lty, lwd, font, fill, border, 
col.points, col.line, 
alpha.points, alpha.line)
```

Arguments

- `col`, `col.points`, `col.line`
  A color specification. `col` is used for components "plot.symbol", "plot.line", "plot.polygon", "superpose.symbol", "superpose.line", and "superpose.polygon". `col.points` overrides `col`, but is used only for "plot.symbol" and "superpose.symbol". Similarly, `col.line` overrides `col` for "plot.line" and "superpose.line". The arguments can be vectors, but only the first component is used for scalar targets (i.e., the ones without "superpose" in their name).

- `alpha`, `alpha.points`, `alpha.line`
  A numeric alpha transparency specification. The same rules as `col`, etc., apply.

- `cex`, `pch`, `font`
  Parameters for points. Applicable for components `plot.symbol` (for which only the first component is used) and `superpose.symbol` (for which the arguments can be vectors).

- `lty`, `lwd`
  Parameters for lines. Applicable for components `plot.line` (for which only the first component is used) and `superpose.line` (for which the arguments can be vectors).

- `fill`
  Fill color, applicable for components `plot.symbol`, `plot.polygon`, `superpose.symbol`, and `superpose.polygon`.

- `border`
  Border color, applicable for components `plot.polygon` and `superpose.polygon`.

Details

The appearance of a lattice display depends partly on the “theme” active when the display is plotted (see `trellis.device` for details). This theme is used to obtain defaults for various graphical parameters, and in particular, the `auto.key` argument works on the premise that the same source is used for both the actual graphical encoding and the legend. The easiest way to specify custom settings for a particular display is to use the `par.settings` argument, which is usually tedious to construct as it is a nested list. The `simpleTheme` function can be used in such situations as a wrapper that generates a suitable list given parameters in simple name=value form, with the nesting made implicit. This is less flexible, but straightforward and sufficient in most situations.
Value

A list that would work as the theme argument to \texttt{trellis.device} and \texttt{trellis.par.set}, or as the \texttt{par.settings} argument to any high level lattice function such as \texttt{xyplot}.

Author(s)

Deepayan Sarkar \texttt{<Deepayan.Sarkar@R-project.org>}, based on a suggestion from John Maindonald.

See Also

\texttt{trellis.device, xyplot, Lattice}

Examples

\begin{verbatim}
str(simpleTheme(pch = 16))

dotplot(variety ~ yield | site, data = barley, groups = year,
  auto.key = list(space = "right"),
  par.settings = simpleTheme(pch = 16),
  xlab = "Barley Yield (bushels/acre) ",
  aspect=0.5, layout = c(1,6))
\end{verbatim}
Details

These functions are modeled on options and getOption, and behave similarly for the most part. Some of the available components are documented here, but not all. The purpose of the ones not documented are either fairly obvious, or not of interest to the end-user.

panel.error A function, or NULL. If the former, every call to the panel function will be wrapped inside tryCatch with the specified function as an error handler. The default is to use the panel.error function. This prevents the plot from failing due to errors in a single panel, and leaving the grid operations in an unmanageable state. If set to NULL, errors in panel functions will not be caught using tryCatch.

save.object Logical flag indicating whether a "trellis" object should be saved when plotted for subsequent retrieval and further manipulation. Defaults to TRUE.

layout.widths, layout.heights Controls details of the default space allocation in the grid layout created in the course of plotting a "trellis" object. Each named component is a list of arguments to the grid function unit (x, units, and optionally data).

Usually not of interest to the end-user, who should instead use the similarly named component in the graphical settings, modifiable using trellis.par.set.

drop.unused.levels A list of two components named cond and data, both logical flags. The flags indicate whether the unused levels of factors (conditioning variables and primary variables respectively) will be dropped, which is usually relevant when a subsetting operation is performed or an 'interaction' is created. See xyplot for more details. Note that this does not control dropping of levels of the 'groups' argument.

legend.bbox A character string, either "full" or "panel". This determines the interpretation of x and y when space="inside" in key (determining the legend; see xyplot): either the full figure region ("full"), or just the region that bounds the panels and strips ("panel").

default.args A list giving default values for various standard arguments: as.table, auto.key, aspect, between, grid, skip, strip, xscale.components, yscale.components, and axis.

highlight.gpar A list giving arguments to gpar used to highlight a viewport chosen using trellis.focus.

banking The banking function. See banking.

axis.padding List with components named "numeric" and "factor", both scalar numbers. Panel limits are extended by this amount, to provide padding for numeric and factor scales respectively. The value for numeric is multiplicative, whereas factor is additive.

skip.boundary.labels Numeric scalar between 0 and 1. Tick marks that are too close to the limits are not drawn unless explicitly requested. The limits are contracted by this proportion, and anything outside is skipped.

interaction.sep The separator for creating interactions with the extended formula interface (see xyplot).

optimize.grid Logical flag, FALSE by default. Complicated grid unit calculations can be slow. Sometimes these can be optimized at the cost of potential loss of accuracy. This option controls whether such optimization should be applied.

axis.units List determining default units for axis components. Should not be of interest to the end-user.

In addition, there is an option for the default prepanel and panel function for each high-level function; e.g., panel.xyplot and prepanel.default.xyplot for xyplot. The options for the others have similarly patterned names.
Value

lattice.getOption returns the value of a single component, whereas lattice.options always returns a list with one or more named components. When changing the values of components, the old values of the modified components are returned by lattice.options. If called without any arguments, the full list is returned.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

options, trellis.device, trellis.par.get, Lattice

Examples

names(lattice.options())
str(lattice.getOption("layout.widths"), max.level = 2)

## Not run:
## change default settings for subsequent plots
lattice.options(default.args = list(as.table = TRUE,
  grid = TRUE,
  auto.key = TRUE))

## End(Not run)
## S3 method for class 'trellis'
print(x, ...)

## S3 method for class 'trellis'
summary(object, ...)

## S3 method for class 'trellis'
dim(x)

## S3 method for class 'trellis'
dimnames(x)

panel.error(e)

### Arguments

- **x, object**: an object of class "trellis"
- **position**: a vector of 4 numbers, typically c(xmin, ymin, xmax, ymax) that give the lower-left and upper-right corners of a rectangle in which the Trellis plot of x is to be positioned. The coordinate system for this rectangle is [0-1] in both the x and y directions.
- **split**: a vector of 4 integers, c(x,y,nx,ny), that says to position the current plot at the x,y position in a regular array of nx by ny plots. (Note: this has origin at top left)
- **more**: A logical specifying whether more plots will follow on this page.
- **newpage**: A logical specifying whether the plot should be on a new page. This option is specific to lattice, and is useful for including lattice plots in an arbitrary grid viewport (see the details section).
- **packet.panel**: a function that determines which packet (data subset) is plotted in which panel. Panels are always drawn in an order such that columns vary the fastest, then rows and then pages. This function determines, given the column, row and page and other relevant information, the packet (if any) which should be used in that panel. By default, the association is determined by matching panel order with packet order, which is determined by varying the first conditioning variable the fastest, then the second, and so on. This association rule is encoded in the default, namely the function `packet.panel.default`, whose help page details the arguments supplied to whichever function is specified as the `packet.panel` argument.
- **draw.in**: An optional (grid) viewport (used as the name argument in `downViewport`) in which the plot is to be drawn. If specified, the `newpage` argument is ignored. This feature is not well-tested.
- **panel.width**, **panel.height**: lists with 2 components, that should be valid x and units arguments to `unit()` (the data argument cannot be specified currently, but can be considered for addition if needed). The resulting `unit` object will be the width/height of each panel in the Lattice plot. These arguments can be used to explicitly control the dimensions of the panel, rather than letting them expand to maximize available space. Vector widths are allowed, and can specify unequal lengths across rows or columns.

Note that this option should not be used in conjunction with non-default values of the `aspect` argument in the original high level call (no error will be produced, but the resulting behaviour is undefined).
save.object

logical, specifying whether the object being printed is to be saved. The last object thus saved can be subsequently retrieved. This is an experimental feature that should allow access to a panel’s data after the plot is done, making it possible to enhance the plot after the fact. This also allows the user to invoke the update method on the current plot, even if it was not assigned to a variable explicitly. For more details, see trellis.focus.

panel.error

a function, or a character string naming a function, that is to be executed when an error occurs during the execution of the panel function. The error is caught (using tryCatch) and supplied as the only argument to panel.error. The default behaviour (implemented as the panel.error function) is to print the corresponding error message in the panel and continue. To stop execution on error, use panel.error = stop.

Normal error recovery and debugging tools are unhelpful when tryCatch is used. tryCatch can be completely bypassed by setting panel.error to NULL.

prefix

A character string acting as a prefix identifying the plot of a "trellis" object, primarily used in constructing viewport and grob names, to distinguish similar viewports if a page contains multiple plots. The default is based on the serial number of the current plot on the current page (specifically, "plot_01", "plot_02", etc.). If supplied explicitly, this must be a valid R symbol name (briefly, it must start with a letter or a period followed by a letter) and must not contain the grid path separator (currently "::").

e

an error condition caught by tryCatch

...

extra arguments, ignored by the print method. All arguments to the plot method are passed on to the print method.

Details

This is the default print method for objects of class "trellis", produced by calls to functions like xyplot, bwplot etc. It is usually called automatically when a trellis object is produced. It can also be called explicitly to control plot positioning by means of the arguments split and position.

When newpage = FALSE, the current grid viewport is treated as the plotting area, making it possible to embed a Lattice plot inside an arbitrary grid viewport. The draw.in argument provides an alternative mechanism that may be simpler to use.

The print method uses the information in x (the object to be printed) to produce a display using the Grid graphics engine. At the heart of the plot is a grid layout, of which the entries of most interest to the user are the ones containing the display panels.

Unlike in older versions of Lattice (and Grid), the grid display tree is retained after the plot is produced, making it possible to access individual viewport locations and make additions to the plot. For more details and a lattice level interface to these viewports, see trellis.focus.

Note

Unlike S-PLUS, trying to position a multipage display (using position and/or split) will mess things up.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, unit, update.trellis, trellis.focus, packet.panel.default
Examples

```r
p11 <- histogram(~ height | voice.part, data = singer, xlab="Height")
p12 <- densityplot(~ height | voice.part, data = singer, xlab = "Height")
p2 <- histogram(~ height, data = singer, xlab = "Height")

## simple positioning by split
print(p11, split=c(1,1,1,2), more=TRUE)
print(p2, split=c(1,2,1,2))

## Combining split and position:
print(p11, position = c(0,0,.75,.75), split=c(1,1,1,2), more=TRUE)
print(p12, position = c(0,0,.75,.75), split=c(1,2,1,2), more=TRUE)
print(p2, position = c(.5,.75,1,1), more=FALSE)

## Using seekViewport

## repeat same plot, with different polynomial fits in each panel
xyplot(Armed.Forces ~ Year, longley, index.cond = list(rep(1, 6)),
       layout = c(3, 2),
       panel = function(x, y, ...)
       {
         panel.xyplot(x, y, ...)
         fm <- lm(y ~ poly(x, panel.number()))
         llines(x, predict(fm))
       })

## Not run:
grid::seekViewport(trellis.vpname("panel", 1, 1))
cat("Click somewhere inside the first panel:\n")
ltext(grid::grid.locator(), lab = "linear")

## End(Not run)

grid::seekViewport(trellis.vpname("panel", 1, 1))
ggrid::grid.text("linear")

ggrid::seekViewport(trellis.vpname("panel", 2, 1))
ggrid::grid.text("quadratic")

ggrid::seekViewport(trellis.vpname("panel", 3, 1))
ggrid::grid.text("cubic")

ggrid::seekViewport(trellis.vpname("panel", 1, 2))
ggrid::grid.text("degree 4")

ggrid::seekViewport(trellis.vpname("panel", 2, 2))
ggrid::grid.text("degree 5")

ggrid::seekViewport(trellis.vpname("panel", 3, 2))
ggrid::grid.text("degree 6")
```

C_06_update.trellis    Retrieve and Update Trellis Object
Description

Update method for objects of class "trellis", and a way to retrieve the last printed trellis object (that was saved).

Usage

## S3 method for class 'trellis'
update(object,
    panel,
    aspect,
    as.table,
    between,
    key,
    auto.key,
    legend,
    layout,
    main,
    page,
    par.strip.text,
    prepanel,
    scales,
    skip,
    strip,
    strip.left,
    sub,
    xlab,
    ylab,
    xlab.top,
    ylab.right,
    xlim,
    ylim,
    xscale.components,
    yscale.components,
    axis,
    par.settings,
    plot.args,
    lattice.options,
    index.cond,
    perm.cond,
    ...)

## S3 method for class 'trellis'
t(x)

## S3 method for class 'trellis'
x[i, j, ...., drop = FALSE]

trellis.last.object(..., prefix)
Arguments

object, x  The object to be updated, of class "trellis".

i, j  indices to be used. Names are not currently allowed.

drop  logical, whether dimensions with only one level are to be dropped. Currently ignored, behaves as if it were FALSE.

panel, aspect, as.table, between, key, auto.key, legend, layout, main, page, par.strip.text, prepanel arguments that will be used to update object. See details below.

prefix  A character string acting as a prefix identifying the plot of a "trellis" object. Only relevant when a particular page is occupied by more than one plot. Defaults to the value appropriate for the last "trellis" object printed. See trellis.focus.

Details

All high level lattice functions such as xyplot produce an object of (S3) class "trellis", which is usually displayed by its print method. However, the object itself can be manipulated and modified to a large extent using the update method, and then re-displayed as needed.

Most arguments to high level functions can also be supplied to the update method as well, with some exceptions. Generally speaking, anything that would needs to change the data within each panel is a no-no (this includes the formula, data, groups, subscripts and subset). Everything else is technically game, though might not be implemented yet. If you find something missing that you wish to have, feel free to make a request.

Not all arguments accepted by a Lattice function are processed by update, but the ones listed above should work. The purpose of these arguments are described in the help page for xyplot. Any other argument is added to the list of arguments to be passed to the panel function. Because of their somewhat special nature, updates to objects produced by cloud and wireframe do not work very well yet.

The "[" method is a convenient shortcut for updating index.cond. The t method is a convenient shortcut for updating perm.cond in the special (but frequent) case where there are exactly two conditioning variables, when it has the effect of switching ('transposing') their order.

The print method for "trellis" objects optionally saves the object after printing it. If this feature is enabled, trellis.last.object can retrieve it. By default, the last object plotted is retrieved, but if multiple objects are plotted on the current page, then others can be retrieved using the appropriate prefix argument. If trellis.last.object is called with arguments, these are used to update the retrieved object before returning it.

Value

An object of class trellis, by default plotted by print.trellis. trellis.last.object returns NULL is no saved object is available.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

trellis.object, Lattice, xyplot
Examples

```r
spots <- by(sunspots, gl(235, 12, labels = 1749:1983), mean)
old.options <- lattice.options(save.object = TRUE)
xyplot(spots ~ 1749:1983, xlab = "", type = "l",
scales = list(x = list(alternating = 2)),
main = "Average Yearly Sunspots")
update(trellis.last.object(), aspect = "xy")
trellis.last.object(xlab = "Year")
lattice.options(old.options)
```

Description

Functions to handle shingles

Usage

```r
shingle(x, intervals=sort(unique(x)))
equal.count(x, ...)
as.shingle(x)
is.shingle(x)
```

## S3 method for class 'shingle'
```r
plot(x, panel, xlab, ylab, ...)
```

## S3 method for class 'shingle'
```r
print(x, showValues = TRUE, ...)
```

## S3 method for class 'shingleLevel'
```r
as.character(x, ...)
```

## S3 method for class 'shingleLevel'
```r
print(x, ...)
```

## S3 method for class 'shingle'
```r
summary(object, showValues = FALSE, ...)
```

```
# S3 method for class 'shingle'
x[subset, drop = FALSE]
```

as.factorOrShingle(x, subset, drop)

Arguments

- `x` numeric variable or R object, shingle in plot.shingle and x[]. An object (list of intervals) of class "shingleLevel" in print.shingleLevel
- `object` shingle object to be summarized
showValues: logical, whether to print the numeric part. If FALSE, only the intervals are printed.

intervals: numeric vector or matrix with 2 columns

subset: logical vector

drop: whether redundant shingle levels are to be dropped

panel, xlab, ylab: standard Trellis arguments (see `xyplot`

... other arguments, passed down as appropriate. For example, extra arguments to `equal.count` are passed on to `co.intervals`. Graphical parameters can be passed as arguments to the `plot` method.

Details

A shingle is a data structure used in Trellis, and is a generalization of factors to ‘continuous’ variables. It consists of a numeric vector along with some possibly overlapping intervals. These intervals are the ‘levels’ of the shingle. The `levels` and `nlevels` functions, usually applicable to factors, also work on shingles. The implementation of shingles is slightly different from S.

There are print methods for shingles, as well as for printing the result of `levels()` applied to a shingle. For use in labelling, the `as.character` method can be used to convert levels of a shingle to character strings.

`equal.count` converts `x` to a shingle using the equal count algorithm. This is essentially a wrapper around `co.intervals`. All arguments are passed to `co.intervals`.

`shingle` creates a shingle using the given `intervals`. If `intervals` is a vector, these are used to form 0 length intervals.

`as.shingle` returns `shingle(x)` if `x` is not a shingle.

`is.shingle` tests whether `x` is a shingle.

`plot.shingle` displays the ranges of shingles via rectangles. `print.shingle` and `summary.shingle` describe the shingle object.

Value

`x$intervals` for `levels.shingle(x)`, logical for `is.shingle`, an object of class ”trellis” for `plot` (printed by default by `print.trellis`), and an object of class ”shingle” for the others.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`xyplot`, `co.intervals`, `Lattice`

Examples

```
z <- equal.count(rnorm(50))
plot(z)
print(z)
print(levels(z))```
D_draw.colorkey

Produce a colorkey typically for levelplot

Description

Creates (and optionally draws) a grid frame grob representing a color key that can be placed in other grid-based plots. Primarily used by levelplot when a color key is requested.

Usage

draw.colorkey(key, draw = FALSE, vp = NULL)

Arguments

key A list determining the key. See documentation for levelplot, in particular the section describing the colorkey argument, for details.
draw A scalar logical, indicating whether the grob is to be drawn.
vp The viewport in which to draw the grob, if applicable.

Value

A grid frame object (that inherits from "grob")

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot, levelplot

D_draw.key

Produce a Legend or Key

Description

Produces (and possibly draws) a Grid frame grob which is a legend (aka key) that can be placed in other Grid plots.

Usage

draw.key(key, draw=FALSE, vp=NULL, ...)

Arguments

key A list determining the key. See documentation for xyplot, in particular the section describing the key argument, for details.
draw logical, whether the grob is to be drawn.
vp viewport
... ignored
Value

A Grid frame object (that inherits from ‘grob’).

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot

---

D_level.colors  
A function to compute false colors representing a numeric or categorical variable

Description

Calculates false colors from a numeric variable (including factors, using their numeric codes) given a color scheme and breakpoints.

Usage

level.colors(x, at, col.regions, colors = TRUE, ...)

Arguments

x
A numeric or factor variable.

at
A numeric variable of breakpoints defining intervals along the range of x.

col.regions
A specification of the colors to be assigned to each interval defined by at. This could be either a vector of colors, or a function that produces a vector of colors when called with a single argument giving the number of colors. See details below.

colors
logical indicating whether colors should be computed and returned. If FALSE, only the indices representing which interval (among those defined by at) each value in x falls into is returned.

...
Extra arguments, ignored.

Details

If at has length n, then it defines n-1 intervals. Values of x outside the range of at are not assigned to an interval, and the return value is NA for such values.

Colors are chosen by assigning a color to each of the n-1 intervals. If col.regions is a palette function (such as topo.colors, or the result of calling colorRampPalette), it is called with n-1 as an argument to obtain the colors. Otherwise, if there are exactly n-1 colors in col.regions, these get assigned to the intervals. If there are fewer than n-1 colors, col.regions gets recycled. If there are more, a more or less equally spaced (along the length of col.regions) subset is chosen.
**D_make.groups**

**Grouped data from multiple vectors**

**Description**

Combines two or more vectors, possibly of different lengths, producing a data frame with a second column indicating which of these vectors that row came from. This is mostly useful for getting data into a form suitable for use in high level Lattice functions.

**Usage**

```r
make.groups(...)```

**Arguments**

```r
...```

one or more vectors of the same type (coercion is attempted if not), or one or more data frames with similar columns, with possibly differing number of rows.

**Value**

A vector of the same length as `x`. Depending on the `colors` argument, this could be either a vector of colors (in a form usable by R), or a vector of integer indices representing which interval the values of `x` fall in.

**Author(s)**

Deepayan Sarkar <deepayan.sarkar@r-project.org>

**See Also**

`levelplot`, `colorRampPalette`.

**Examples**

```r
depth.col <-
  with(quakes,
    level.colors(depth, at = do.breaks(range(depth), 30),
    col.regions = hcl.colors))

xyplot(lat ~ long | equal.count(stations), quakes,
  strip = strip.custom(var.name = "Stations"),
  colours = depth.col,
  panel = function(x, y, colours, subscripts, ...) {
    panel.xyplot(x, y, pch = 21, col = "transparent",
    fill = colours[subscripts], ...)
  })
```
Value

When all the input arguments are vectors, a data frame with two columns

- **data**: all the vectors supplied, concatenated
- **which**: factor indicating which vector the corresponding data value came from

When all the input arguments are data frames, the result of `rbind` applied to them, along with an additional `which` column as described above.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

- Lattice

Examples

```r
sim.dat <- make.groups(uniform = runif(200),
                        exponential = rexp(175),
                        lognormal = rlnorm(150),
                        normal = rnorm(125))
qqmath(~ data | which, sim.dat, scales = list(y = "free"))
```

D_simpleKey

---

Function to generate a simple key

Description

Simple interface to generate a list appropriate for `draw.key`

Usage

```r
simpleKey(text, points = TRUE,
          rectangles = FALSE,
          lines = FALSE,
          col, cex, alpha, font,
          fontface, fontfamily,
          lineheight, ...)
```

Arguments

- **text**: character or expression vector, to be used as labels for levels of the grouping variable
- **points**: logical
- **rectangles**: logical
- **lines**: logical
- **col, cex, alpha, font, fontface, fontfamily, lineheight**: Used as top-level components of the list produced, to be used for the text labels. Defaults to the values in `trellis.par.get("add.text")`
- **...**: further arguments added to the list, eventually passed to `draw.key`
Details

A lattice plot can include a legend (key) if an appropriate list is specified as the key argument to a high level Lattice function such as `xyplot`. This key can be very flexible, but that flexibility comes at a cost: this list needs to be fairly complicated even in simple situations. `simpleKey` is designed as a useful shortcut in the common case of a key drawn in conjunction with a grouping variable, using the default graphical settings.

The `simpleKey` function produces a suitable key argument using a simpler interface. The resulting list will use the text argument as a text component, along with at most one set each of points, rectangles, and lines. The number of entries (rows) in the key will be the length of the text component. The graphical parameters for the additional components will be derived from the default graphical settings (wherein lies the simplification, as otherwise these would have to be provided explicitly).

Calling `simpleKey` directly is usually unnecessary. It is most commonly invoked (during the plotting of the "trellis" object) when the `auto.key` argument is supplied in a high-level plot with a `groups` argument. In that case, the text argument of `simpleKey` defaults to `levels(groups)`, and the defaults for the other arguments depend on the relevant high-level function. Note that these defaults can be overridden by supplying `auto.key` as a list containing the replacement values.

Value

A list that would work as the key argument to `xyplot`, etc.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`Lattice`, `draw.key`, `trellis.par.get`, and `xyplot`, specifically the entry for `auto.key`.

---

**D_strip.default**

**Default Trellis Strip Function**

**Description**

`strip.default` is the function that draws the strips by default in Trellis plots. Users can write their own strip functions, but most commonly this involves calling `strip.default` with a slightly different arguments. `strip.custom` provides a convenient way to obtain new strip functions that differ from `strip.default` only in the default values of certain arguments.

**Usage**

```r
strip.default(which.given, 
    which.panel, 
    var.name, 
    factor.levels, 
    shingle.intervals, 
    strip.names = c(FALSE, TRUE), 
    strip.levels = c(TRUE, FALSE), 
    sep = " : ", 
    style = 1,
```
horizontal = TRUE,
bg = trellis.par.get("strip.background")$col[which.given],
fg = trellis.par.get("strip.shingle")$col[which.given],
par.strip.text = trellis.par.get("add.text")
strip.custom(...)

**Arguments**

- **which.given** integer index specifying which of the conditioning variables this strip corresponds to.
- **which.panel** vector of integers as long as the number of conditioning variables. The contents are indices specifying the current levels of each of the conditioning variables (thus, this would be unique for each distinct packet). This is identical to the return value of *which.packet*, which is a more accurate name.
- **var.name** vector of character strings or expressions as long as the number of conditioning variables. The contents are interpreted as names for the conditioning variables. Whether they are shown on the strip depends on the values of *strip.names* and *style* (see below). By default, the names are shown for shingles, but not for factors.
- **factor.levels** vector of character strings or expressions giving the levels of the conditioning variable currently being drawn. For more than one conditioning variable, this will vary with *which.given*. Whether these levels are shown on the strip depends on the values of *strip.levels* and *style* (see below). *factor.levels* may be specified for both factors and shingles (despite the name), but by default they are shown only for factors. If shown, the labels may optionally be abbreviated by specifying suitable components in *par.strip.text* (see *xyplot*).
- **shingle.intervals** if the current strip corresponds to a shingle, this should be a 2-column matrix giving the levels of the shingle. (of the form that would be produced by *printing levels(shingle)*). Otherwise, it should be NULL.
- **strip.names** a logical vector of length 2, indicating whether or not the name of the conditioning variable that corresponds to the strip being drawn is to be written on the strip. The two components give the values for factors and shingles respectively. This argument is ignored for a factor when *style* is not one of 1 and 3.
- **strip.levels** a logical vector of length 2, indicating whether or not the level of the conditioning variable that corresponds to the strip being drawn is to be written on the strip. The two components give the values for factors and shingles respectively.
- **sep** character or expression, serving as a separator if the name and level are both to be shown.
- **style** integer, with values 1, 2, 3, 4 and 5 currently supported, controlling how the current level of a factor is encoded. Ignored for shingles (actually, when shingle.intervals is non-null).

The best way to find out what effect the value of *style* has is to try them out. Here is a short description: for a style value of 1, the strip is colored in the background color with the strip text (as determined by other arguments) centered on it. A value of 3 is the same, except that a part of the strip is colored in the foreground color, indicating the current level of the factor. For styles 2 and 4, the part corresponding to the current level remains colored in the foreground color, however, for style = 2, the remaining part is not colored at all, whereas for 4, it is colored with the background color. For both these, the names of all the levels
of the factor are placed on the strip from left to right. Styles 5 and 6 produce
the same effect (they are subtly different in S, this implementation corresponds
to 5), they are similar to style 1, except that the strip text is not centered, it is
instead positioned according to the current level.
Note that unlike S-PLUS, the default value of style is 1. strip.names and
strip.levels have no effect if style is not 1 or 3.
horizontal logical, specifying whether the labels etc should be horizontal.
horizontal=FALSE is useful for strips on the left of panels using
strip.left=TRUE
par.strip.text list with parameters controlling the text on each strip, with components col,
cex, font, etc.
bg strip background color.
fg strip foreground color.
... arguments to be passed on to strip.default, overriding whatever value it
would have normally assumed

Details
default strip function for trellis functions. Useful mostly because of the style argument — non-
default styles are often more informative, especially when the names of the levels of the factor x are
small. Traditional use is as strip = function(...) strip.default(style=2,...), though this
can be simplified by the use of strip.custom.

Value

strip.default is called for its side-effect, which is to draw a strip appropriate for multi-panel
Trellis conditioning plots. strip.custom returns a function that is similar to strip.default, but
with different defaults for the arguments specified in the call.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot, Lattice

Examples

## Traditional use
xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = function(..., style) strip.default(..., style = 4))

## equivalent call using strip.custom
xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = strip.custom(style = 4))

xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = FALSE,
       strip.left = strip.custom(style = 4, horizontal = FALSE))
A Trellis Plot Object

Description

This class of objects is returned by high level lattice functions, and is usually plotted by default by its `print` method.

Details

A trellis object, as returned by high level lattice functions like `xyplot`, is a list with the "class" attribute set to "trellis". Many of the components of this list are simply the arguments to the high level function that produced the object. Among them are: `as.table`, `layout`, `page`, `panel`, `prepanel`, `main`, `sub`, `par.strip.text`, `strip`, `skip`, `xlab ylab`, `par.settings`, `lattice.options` and `plot.args`. Some other typical components are:

- `formula` the Trellis formula used in the call
- `index.cond` list with index for each of the conditioning variables
- `perm.cond` permutation of the order of the conditioning variables
- `aspect.fill` logical, whether aspect is "fill"
- `aspect.ratio` numeric, aspect ratio to be used if `aspect.fill` is FALSE
- `call` call that generated the object.
- `condlevels` list with levels of the conditioning variables
- `legend` list describing the legend(s) to be drawn
- `panel.args` a list as long as the number of panels, each element being a list itself, containing the arguments in named form to be passed to the panel function in that panel.
- `panel.args.common` a list containing the arguments common to all the panel functions in name=value form
- `x.scales` list describing x-scale, can consist of several other lists, paralleling `panel.args`, if x-relation is not "same"
- `y.scales` list describing y-scale, similar to `x.scales`
- `x.between` numeric vector of interpanel x-space
- `y.between` numeric vector of interpanel y-space
- `x.limits` numeric vector of length 2 or list, giving x-axis limits
- `y.limits` similar to `x.limits`
- `packet.sizes` array recording the number of observations in each packet

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot, print.trellis
Description
The classic Trellis paradigm is to plot the whole object at once, without the possibility of interacting with it afterwards. However, by keeping track of the grid viewports where the panels and strips are drawn, it is possible to go back to them afterwards and enhance them one panel at a time. These functions provide convenient interfaces to help in this. Note that these are still experimental and the exact details may change in future.

Usage
panel.identify(x, y = NULL,
    subscripts = seq_along(x),
    labels = subscripts,
    n = length(x), offset = 0.5,
    threshold = 18, ## in points, roughly 0.25 inches
    panel.args = trellis.panelArgs(),
    ...
)

panel.identify.qqmath(x, distribution, groups, subscripts, labels,
    panel.args = trellis.panelArgs(),
    ...
)

panel.identify.cloud(x, y, z, subscripts,
    perspective, distance,
    xlim, ylim, zlim,
    screen, R.mat, aspect, scales.3d,
    ..., panel.3d.identify,
    n = length(subscripts),
    offset = 0.5,
    threshold = 18,
    labels = subscripts,
    panel.args = trellis.panelArgs())

panel.link.splom(threshold = 18, verbose = getOption("verbose"), ...)
panel.brush.splom(threshold = 18, verbose = getOption("verbose"), ...)

trellis.vpname(name = c("position", "split", "split.location", "toplevel",
    "figure", "panel", "strip", "strip.left",
    "legend", "legend.region", "main", "sub",
    "xlab", "ylab", "xlab.top", "ylab.right", "page"),
    column, row,
    side = c("left", "top", "right", "bottom", "inside"),
    clip.off = FALSE, prefix)

trellis.grobname(name,
    type = c("", "panel", "strip", "strip.left",
    "key", "colorkey"),
    group = 0,
    which.given = lattice.getStatus("current.which.given",
    prefix = prefix),
which.panel = lattice.getStatus("current.which.panel",
    prefix = prefix),
column = lattice.getStatus("current.focus.column",
    prefix = prefix),
row = lattice.getStatus("current.focus.row",
    prefix = prefix),
    prefix = lattice.getStatus("current.prefix"))
trellis.focus(name, column, row, side, clip.off,
    highlight = interactive(), ..., prefix,
    guess = TRUE, verbose = getOption("verbose"))
trellis.switchFocus(name, side, clip.off, highlight, ..., prefix)
trellis.unfocus()
trellis.panelArgs(x, packet.number)

Arguments

x, y, z variables defining the contents of the panel. In the case of trellis.panelArgs, a "trellis" object.

n the number of points to identify by default (overridden by a right click)

subscripts an optional vector of integer indices associated with each point. See details below.

labels an optional vector of labels associated with each point. Defaults to subscripts
distribution, groups

typical panel arguments of panel.qqmath. These will usually be obtained from panel.args

offset the labels are printed either below, above, to the left or to the right of the identified point, depending on the relative location of the mouse click. The offset specifies (in "char" units) how far from the identified point the labels should be printed.

threshold threshold in grid’s "points" units. Points further than these from the mouse click position are not considered

panel.args list that contains components names x (and usually y), to be used if x is missing. Typically, when called after trellis.focus, this would appropriately be the arguments passed to that panel.

perspective, distance, xlim, ylim, zlim, screen, R.mat, aspect, scales.3d

arguments as passed to panel.cloud. These are required to recompute the relevant three-dimensional projections in panel.identify.cloud.

panel.3d.identify

the function that is responsible for the actual interaction once the data rescaling and rotation computations have been done. By default, an internal function similar to panel.identify is used.

name A character string indicating which viewport or grob we are looking for. Although these do not necessarily provide access to all viewports and grobs created by a lattice plot, they cover most of the ones that end-users may find interesting. trellis.vpname and trellis.focus deal with viewport names only, and only accept the values explicitly listed above. trellis.grobname is meant to create names for grobs, and can currently accept any value.

If name, as well as column and row is missing in a call to trellis.focus, the user can click inside a panel (or an associated strip) to focus on that panel. Note
however that this assumes equal width and height for each panel, and may not
work when this is not true.
When name is "panel", "strip", or "strip.left", column and row must also
be specified. When name is "legend", side must also be specified.

column, row  
integers, indicating position of the panel or strip that should be assigned focus
in the Trellis layout. Rows are usually calculated from the bottom up, unless the
plot was created with as.table=TRUE

guess  
logical. If TRUE, and the display has only one panel, that panel will be automa-
tically selected by a call to trellis.focus.

side  
character string, relevant only for legends (i.e., when name="legend"), indicat-
ing their position. Partial specification is allowed, as long as it is unambiguous.

clip.off  
logical, whether clipping should be off, relevant when name is "panel" or
"strip". This is necessary if axes are to be drawn outside the panel or strip.
Note that setting clip.off=FALSE does not necessarily mean that clipping is
on; that is determined by conditions in effect during printing.

type  
A character string specifying whether the grob is specific to a particular panel
or strip.
When type is "panel", "strip", or "strip.left", information about the
panel is added to the grob name.

group  
An integer specifying whether the grob is specific to a particular group within
the plot.
When group is greater than zero, information about the group is added to the
grob name.

which.given, which.panel  
integers, indicating which conditional variable is being represented (within a
strip) and the current levels of the conditional variables.
When which.panel has length greater than 1, and the type is "strip" or
"strip.left", information about the conditional variable is added to the grob
name.

prefix  
A character string acting as a prefix identifying the plot of a "trellis" object,
primarily used to distinguish otherwise equivalent viewports in different plots.
This only becomes relevant when a particular page is occupied by more than one
plot. Defaults to the value appropriate for the last "trellis" object printed, as
determined by the prefix argument in print.trellis.
Users should not usually need to supply a value for this argument except to
interact with an existing plot other than the one plotted last.
For switchFocus, ignored except when it does not match the prefix of the cur-
rently active plot, in which case an error occurs.

highlight  
logical, whether the viewport being assigned focus should be high-
lighted. For trellis.focus, the default is TRUE in interactive mode, and
trellis.switchFocus by default preserves the setting currently active.

packet.number  
integer, which panel to get data from. See packet.number for details on how
this is calculated

verbose  
whether details will be printed

...  
For panel.identify.qqmath, extra parameters are passed on to
panel.identify. For panel.identify, extra arguments are treated as
graphical parameters and are used for labelling. For trellis.focus and
trellis.switchFocus, these are used (in combination with
lattice.options) for highlighting the chosen viewport if so requested.
Graphical parameters can be supplied for panel.link.splom.
Details

panel.identify is similar to identify. When called, it waits for the user to identify points (in the panel being drawn) via mouse clicks. Clicks other than left-clicks terminate the procedure. Although it is possible to call it as part of the panel function, it is more typical to use it to identify points after plotting the whole object, in which case a call to trellis.focus first is necessary.

panel.link.splom is meant for use with splom, and requires a panel to be chosen using trellis.focus before it is called. Clicking on a point causes that and the corresponding projections in other pairwise scatter plots to be highlighted. panel.brush.splom is a (misnamed) alias for panel.link.splom, retained for back-compatibility.

panel.identify.qqmath is a specialized wrapper meant for use with the display produced by qqmath. panel.identify.qqmath is a specialized wrapper meant for use with the display produced by cloud. It would be unusual to call them except in a context where default panel function arguments are available through trellis.panelArgs (see below).

One way in which panel.identify etc. are different from identify is in how it uses the subscripts argument. In general, when one identifies points in a panel, one wants to identify the origin in the data frame used to produce the plot, and not within that particular panel. This information is available to the panel function, but only in certain situations. One way to ensure that subscripts is available is to specify subscripts = TRUE in the high level call such as xyplot. If subscripts is not explicitly specified in the call to panel.identify, but is available in panel.args, then those values will be used. Otherwise, they default to seq_along(x). In either case, the final return value will be the subscripts that were marked.

The process of printing (plotting) a Trellis object builds up a grid layout with named viewports which can then be accessed to modify the plot further. While full flexibility can only be obtained by using grid functions directly, a few lattice functions are available for the more common tasks.

trellis.focus can be used to move to a particular panel or strip, identified by its position in the array of panels. It can also be used to focus on the viewport corresponding to one of the labels or a legend, though such usage would be less useful. The exact viewport is determined by the name along with the other arguments, not all of which are relevant for all names. Note that when more than one object is plotted on a page, trellis.focus will always go to the plot that was created last. For more flexibility, use grid functions directly (see note below).

After a successful call to trellis.focus, the desired viewport (typically panel or strip area) will be made the ‘current’ viewport (plotting area), which can then be enhanced by calls to standard lattice panel functions as well as grid functions.

It is quite common to have the layout of panels chosen when a "trellis" object is drawn, and not before then. Information on the layout (specifically, how many rows and columns, and which packet belongs in which position in this layout) is retained for the last "trellis" object plotted, and is available through trellis.currentLayout.

trellis.unfocus unsets the focus, and makes the top level viewport the current viewport.

trellis.switchFocus is a convenience function to switch from one viewport to another, while preserving the current row and column. Although the rows and columns only make sense for panels and strips, they would be preserved even when the user switches to some other viewport (where row/column is irrelevant) and then switches back.

Once a panel or strip is in focus, trellis.panelArgs can be used to retrieve the arguments that were available to the panel function at that position. In this case, it can be called without arguments as

```
trellis.panelArgs()
```
This usage is also allowed when a "trellis" object is being printed, e.g. inside the panel functions or the axis function (but not inside the prepanel function). `trellis.panelArgs` can also retrieve the panel arguments from any "trellis" object. Note that for this usage, one needs to specify the `packet.number` (as described under the panel entry in `xyplot`) and not the position in the layout, because a layout determines the panel only after the object has been printed.

It is usually not necessary to call `trellis.vpname` and `trellis.grobname` directly. However, they can be useful in generating appropriate names in a portable way when using grid functions to interact with the plots directly, as described in the note below.

**Value**

`panel.identify` returns an integer vector containing the subscripts of the identified points (see details above). The equivalent of `identify` with `pos=TRUE` is not yet implemented, but can be considered for addition if requested.

`trellis.panelArgs` returns a named list of arguments that were available to the panel function for the chosen panel.

`trellis.vpname` and `trellis.grobname` return character strings.

`trellis.focus` has a meaningful return value only if it has been used to focus on a panel interactively, in which case the return value is a list with components `col` and `row` giving the column and row positions respectively of the chosen panel, unless the choice was cancelled (by a right click), in which case the return value is `NULL`. If click was outside a panel, both `col` and `row` are set to 0.

**Note**

The viewports created by lattice are accessible to the user through `trellis.focus` as described above. Functions from the grid package can also be used directly. For example, `current.vpTree` can be used to inspect the current viewport tree and `seekViewport` or `downViewport` can be used to navigate to these viewports. For such usage, `trellis.vpname` and `trellis.grobname` provides a portable way to access the appropriate viewports and grobs by name.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>. Felix Andrews provided initial implementations of `panel.identify.qqmath` and support for focusing on panels interactively.

**See Also**

`identify`, `Lattice`, `print.trellis`, `trellis.currentLayout`, `current.vpTree`, `viewports`

**Examples**

```r
## Not run:
xyplot(1:10 ~ 1:10)
trellis.focus("panel", 1, 1)
panel.identify()

## End(Not run)
xyplot(Petal.Length ~ Sepal.Length | Species, iris, layout = c(2, 2))
Sys.sleep()
trellis.focus("panel", 1, 1)
do.call("panel.lmline", trellis.panelArgs())
```
Sys.sleep(0.5)
trellis.unfocus()

trellis.focus("panel", 2, 1)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()

Sys.sleep(0.5)
trellis.focus("panel", 1, 2)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()

## choosing loess smoothing parameter

p <- xyplot(dist ~ speed, cars)

panel.loessresid <-
  function(x = panel.args$x,
y = panel.args$y,
  span,
  panel.args = trellis.panelArgs())
{
  fm <- loess(y ~ x, span = span)
xgrid <- do.breaks(current.panel.limits()$xlim, 50)
ygrid <- predict(fm, newdata = data.frame(x = xgrid))
panel.lines(xgrid, ygrid)
pred <- predict(fm)
## center residuals so that they fall inside panel
resids <- y - pred + mean(y)
fm.resid <- loess.smooth(x, resids, span = span)
##panel.points(x, resids, col = 1, pch = 4)
panel.lines(fm.resid, col = 1)
}

spans <- c(0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8)
update(p, index.cond = list(rep(1, length(spans))))

panel.locs <- trellis.currentLayout()
i <- 1
for (row in 1:nrow(panel.locs))
  for (column in 1:ncol(panel.locs))
    if (panel.locs[row, column] > 0)
      {
        trellis.focus("panel", row = row, column = column,
highlight = FALSE)
        panel.loessresid(span = spans[i])
        grid::grid.text(paste("span = ", spans[i]),
          x = 0.25,
y = 0.75,
default.units = "npc")
        trellis.unfocus()
i <- i + 1
      }
Default Panel Function for barchart

Description

Default panel function for barchart.

Usage

panel.barchart(x, y, box.ratio = 1, box.width,
               horizontal = TRUE,
               origin = NULL, reference = TRUE,
               stack = FALSE,
               groups = NULL,
               col = if (is.null(groups)) plot.polygon$col
                   else superpose.polygon$col,
               border = if (is.null(groups)) plot.polygon$border
                   else superpose.polygon$border,
               lty = if (is.null(groups)) plot.polygon$lty
                   else superpose.polygon$lty,
               lwd = if (is.null(groups)) plot.polygon$lwd
                   else superpose.polygon$lwd,
               ..., identifier = "barchart")

Arguments

x                              Extent of Bars. By default, bars start at left of panel, unless origin is specified, in which case they start there.
y                              Horizontal location of bars. Possibly a factor.
box.ratio                      Ratio of bar width to inter-bar space.
box.width                      Thickness of bars in absolute units; overrides box.ratio. Useful for specifying thickness when the categorical variable is not a factor, as use of box.ratio alone cannot achieve a thickness greater than 1.
horizontal                     Logical flag. If FALSE, the plot is ‘transposed’ in the sense that the behaviours of x and y are switched. x is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of bwplot for a fuller explanation.
origin                         The origin for the bars. For grouped displays with stack = TRUE, this argument is ignored and the origin set to 0. Otherwise, defaults to NULL, in which case bars start at the left (or bottom) end of a panel. This choice is somewhat unfortunate, as it can be misleading, but is the default for historical reasons. For tabular (or similar) data, origin = 0 is usually more appropriate; if not, one should reconsider the use of a bar chart in the first place (dot plots are often a good alternative).
reference                      Logical, whether a reference line is to be drawn at the origin.
stack                          logical, relevant when groups is non-null. If FALSE (the default), bars for different values of the grouping variable are drawn side by side, otherwise they are stacked.
groups Optional grouping variable.

col, border, lty, lwd

Graphical parameters for the bars. By default, the trellis parameter plot.polygon is used if there is no grouping variable, otherwise superpose.polygon is used. col gives the fill color, border the border color, and lty and lwd the line type and width of the borders.

Extra arguments will be accepted but ignored.

identifier A character string that is prepended to the names of grobs that are created by this panel function.

Details

A barchart is drawn in the panel. Note that most arguments controlling the display can be supplied to the high-level barchart call directly.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

barchart

Examples

barchart(yield ~ variety | site, data = barley,
groups = year, layout = c(1,6), origin = 0,
ylab = "Barley Yield (bushels/acre)",
scales = list(x = list(abbreviate = TRUE,
    minlength = 5)))

Description

This is the default panel function for bwplot.

Usage

panel.bwplot(x, y, box.ratio = 1,
box.width = box.ratio / (1 + box.ratio),
horizontal = TRUE,
pch, col, alpha, cex,
font, fontfamily, fontface,
fill, varwidth = FALSE,
notch = FALSE, notch.frac = 0.5,
...,
levels.fos,
stats = boxplot.stats,
F_1_panel.bwplot

coef = 1.5,
do.out = TRUE,
identifier = "bwplot"

Arguments

- **x**, **y**: numeric vector or factor. Boxplots drawn for each unique value of y (x) if horizontal is TRUE (FALSE).
- **box.ratio**: ratio of box thickness to inter box space.
- **box.width**: thickness of box in absolute units; overrides box.ratio. Useful for specifying thickness when the categorical variable is not a factor, as use of box.ratio alone cannot achieve a thickness greater than 1.
- **horizontal**: logical. If FALSE, the plot is ‘transposed’ in the sense that the behaviours of x and y are switched. x is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of bwplot for a fuller explanation.
- **pch**, **col**, **alpha**, **cex**, **font**, **fontfamily**, **fontface**: graphical parameters controlling the dot. pch="|" is treated specially, by replacing the dot with a line (similar to boxplot).
- **fill**: color to fill the boxplot.
- **varwidth**: logical. If TRUE, widths of boxplots are proportional to the number of points used in creating it.
- **notch**: if notch is TRUE, a notch is drawn in each side of the boxes. If the notches of two plots do not overlap this is ‘strong evidence’ that the two medians differ (Chambers et al., 1983, p. 62). See boxplot.stats for the calculations used.
- **notch.frac**: numeric in (0,1). When notch=TRUE, the fraction of the box width that the notches should use.
- **stats**: a function, defaulting to boxplot.stats, that accepts a numeric vector and returns a list similar to the return value of boxplot.stats. The function must accept arguments coef and do.out even if they do not use them (a ... argument is good enough). This function is used to determine the box and whisker plot.
- **coef**, **do.out**: passed to stats.
- **levels.fos**: numeric values corresponding to positions of the factor or shingle variable. For internal use.
- **...**: further arguments, ignored.
- **identifier**: A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates Box and Whisker plot of x for every level of y (or the other way round if horizontal=FALSE). By default, the actual boxplot statistics are calculated using boxplot.stats. Note that most arguments controlling the display can be supplied to the high-level bwplot call directly.

Although the graphical parameters for the dot representing the median can be controlled by optional arguments, many others cannot. These parameters are obtained from the relevant settings parameters ("box.rectangle" for the box, "box.umbrella" for the whiskers and "plot.symbol" for the outliers).
Author(s)
Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also
bwplot, boxplot.stats

Examples

bwplot(voice.part ~ height, data = singer,
   xlab = "Height (inches)",
   panel = function(...) {
      panel.grid(v = -1, h = 0)
      panel.bwplot(...)
   },
   par.settings = list(plot.symbol = list(pch = 4)))

bwplot(voice.part ~ height, data = singer,
   xlab = "Height (inches)",
   notch = TRUE, pch = "|")

Description
Default panel functions controlling cloud and wireframe displays.

Usage

panel.cloud(x, y, subscripts, z,
    groups = NULL,
    perspective = TRUE,
    distance = if (perspective) 0.2 else 0,
    xlim, ylim, zlim,
    panel.3d.cloud = "panel.3dscatter",
    panel.3d.wireframe = "panel.3dwire",
    screen = list(z = 40, x = -60),
    R.mat = diag(4), aspect = c(1, 1),
    par.box = NULL,
    xlab, ylab, zlab,
    xlab.default, ylab.default, zlab.default,
    scales.3d,
    proportion = 0.6,
    wireframe = FALSE,
    scpos,
    ...,
    at,
    identifier = "cloud")

panel.wireframe(...)
Arguments

x, y, z numeric (or possibly factors) vectors representing the data to be displayed. The interpretation depends on the context. For panel.cloud these are essentially the same as the data passed to the high level plot (except if formula was a matrix, the appropriate x and y vectors are generated). By the time they are passed to panel.3dscatter and panel.3dwire, they have been appropriately subsetted (using subscripts) and scaled (to lie inside a bounding box, usually the \([-0.5, 0.5]\) cube).

Further, for panel.3dwire, x and y are shorter than z and represent the sorted locations defining a rectangular grid. Also in this case, z may be a matrix if the display is grouped, with each column representing one surface.

In panel.cloud (called from wireframe) and panel.3wire, x, y and z could also be matrices (of the same dimension) when they represent a 3-D surface parametrized on a 2-D grid.

subscripts index specifying which points to draw. The same x, y and z values (representing the whole data) are passed to panel.cloud for each panel. subscripts specifies the subset of rows to be used for the particular panel.

groups specification of a grouping variable, passed down from the high level functions.

perspective logical, whether to plot a perspective view. Setting this to FALSE is equivalent to setting distance to 0.
distance numeric, between 0 and 1, controls amount of perspective. The distance of
the viewing point from the origin (in the transformed coordinate system) is \(1/distance\). This is described in a little more detail in the documentation for cloud

screen A list determining the sequence of rotations to be applied to the data before being plotted. The initial position starts with the viewing point along the positive z-axis, and the x and y axes in the usual position. Each component of the list should be named one of "x", "y" or "z" (repetitions are allowed), with their values indicating the amount of rotation about that axis in degrees.

R.mat initial rotation matrix in homogeneous coordinates, to be applied to the data before screen rotates the view further.

par.box graphical parameters for box, namely, col, lty and lwd. By default obtained from the parameter box.3d.

xlim, ylim, zlim limits for the respective axes. As with other lattice functions, these could each be a numeric 2-vector or a character vector indicating levels of a factor.

panel.3d.cloud, panel.3d.wireframe functions that draw the data-driven part of the plot (as opposed to the bounding box and scales) in cloud and wireframe. This function is called after the ‘back’ of the bounding box is drawn, but before the ‘front’ is drawn.

Any user-defined custom display would probably want to change these functions. The intention is to pass as much information to this function as might be useful (not all of which are used by the defaults). In particular, these functions can expect arguments called xlim, ylim, zlim which give the bounding box ranges in the original data scale and xlim.scaled, ylim.scaled, zlim.scaled which give the bounding box ranges in the transformed scale. More arguments can be considered on request.

aspect aspect as in cloud

xlab, ylab, zlab Labels, have to be lists. Typically the user will not manipulate these, but instead control this via arguments to cloud directly.

xlab.default for internal use
ylab.default for internal use
zlab.default for internal use

scales.3d list defining the scales

proportion numeric scalar, gives the length of arrows as a proportion of the sides

scpos A list with three components x, y and z (each a scalar integer), describing which of the 12 sides of the cube the scales should be drawn. The defaults should be OK. Valid values are x: 1, 3, 9, 11; y: 8, 5, 7, 6 and z: 4, 2, 10, 12. (See comments in the source code of panel.cloud to see the details of this enumeration.)

wireframe logical, indicating whether this is a wireframe plot

drape logical, whether the facets will be colored by height, in a manner similar to levelplot. This is ignored if shade=TRUE.

at When drape = TRUE in wireframe, the facets defining the surface are colored as a function of (average) height, similar to levelplot. at is a numeric vector giving the breakpoints along the z-axis where colors change.
col.regions    vector of colors to be used in conjunction with at when drape = TRUE.
In makeShadePalette, which can be used to define a shading palette (see below), col.regions is an initial vector defining the base color (as a function of height) that is then adjusted according to irradiance and reflectance.

alpha.regions numeric scalar controlling transparency when drape = TRUE.

rot.mat        4x4 transformation matrix in homogeneous coordinates. This gives the rotation matrix combining the screen and R.mat arguments to `panel.cloud`

type           Character vector, specifying type of cloud plot. Can include one or more of "p", "l", "h" or "b". "p" and "l" mean ‘points’ and ‘lines’ respectively, and "b" means ‘both’. "h" stands for ‘histogram’, and causes a line to be drawn from each point to the X-Y plane (i.e., the plane representing z = 0), or the lower (or upper) bounding box face, whichever is closer.

xlim.scaled, ylim.scaled, zlim.scaled axis limits (after being scaled to the bounding box)

zero.scaled    z-axis location (after being scaled to the bounding box) of the X-Y plane in the original data scale, to which lines will be dropped (if within range) from each point when type = "h"

cross          logical, defaults to TRUE if pch = "+". `panel.3dscatter` can represent each point by a 3d ‘cross’ of sorts (it’s much easier to understand looking at an example than from a description). This is different from the usual pch argument, and reflects the depth of the points and the orientation of the axes. This argument indicates whether this feature will be used.
This is useful for two reasons. It can be set to FALSE to use "+" as the plotting character in the regular sense. It can also be used to force this feature in grouped displays.

shade          logical, indicating whether the surface is to be colored using an illumination model with a single light source

shade.colors.palette
a function (or the name of one) that is supposed to calculate the color of a facet when shading is being used. Three pieces of information are available to the function: first, the cosine of the angle between the incident light ray and the normal to the surface (representing foreshortening); second, the cosine of half the angle between the reflected ray and the viewing direction (useful for non-Lambertian surfaces); and third, the scaled (average) height of that particular facet with respect to the total plot z-axis limits.
All three numbers should be between 0 and 1. The shade.colors.palette function should return a valid color. The default function is obtained from the trellis settings using `makeShadePalette`.

min            numeric, between 0 and 1, giving a minimum saturation in makeShadePalette

pref           numeric, giving a power that is applied to reflectance value before it is used to ‘darken’ the colors.

light.source   a 3-vector representing (in cartesian coordinates) the light source. This is relative to the viewing point being (0, 0, 1/distance) (along the positive z-axis), keeping in mind that all observations are bounded within the [-0.5, 0.5] cube

polynum        quadrilateral faces are drawn in batches of polynum at a time. Drawing too few at a time increases the total number of calls to the underlying grid.polygon function, which affects speed. Trying to draw too many at once may be unnecessarily memory intensive. This argument controls the trade-off.
col.groups colors for different groups

col, col.point, col.line, lty, lwd, cex, pch, fill, alpha

Graphical parameters. Some other arguments (such as lwd for line width) may also be passed through the ... argument.

... other parameters, passed down when appropriate

.scale Logical flag, indicating whether x, y, and z should be assumed to be in the original data scale and hence scaled before being plotted. x, y, and z are usually already scaled. However, setting .scale=TRUE may be helpful for calls to panel.3dscatter and panel.3dwire in user-supplied panel functions.

identifier A character string that is prepended to the names of grobs that are created by this panel function.

Details

These functions together are responsible for the content drawn inside each panel in cloud and wireframe. panel.wireframe is a wrapper to panel.cloud, which does the actual work.

panel.cloud is responsible for drawing the content that does not depend on the data, namely, the bounding box, the arrows/scales, etc. At some point, depending on whether wireframe is TRUE, it calls either panel.3d.wireframe or panel.3d.cloud, which draws the data-driven part of the plot.

The arguments accepted by these two functions are different, since they have essentially different purposes. For cloud, the data is unstructured, and x, y and z are all passed to the panel.3d.cloud function. For wireframe, on the other hand, x and y are increasing vectors with unique values, defining a rectangular grid. z must be a matrix with length(x) * length(y) rows, and as many columns as the number of groups.

panel.3dscatter is the default panel.3d.cloud function. It has a type argument similar to panel.xyplot, and supports grouped displays. It tries to honour depth ordering, i.e., points and lines closer to the camera are drawn later, overplotting more distant ones. (Of course there is no absolute ordering for line segments, so an ad hoc ordering is used. There is no hidden point removal.)

panel.3dwire is the default panel.3d.wireframe function. It calculates polygons corresponding to the facets one by one, but waits till it has collected information about polynum facets, and draws them all at once. This avoids the overhead of drawing grid.polygon repeatedly, speeding up the rendering considerably. If shade = TRUE, these attempt to color the surface as being illuminated from a light source at light.source. palette.shade is a simple function that provides the deafult shading colors.

Multiple surfaces are drawn if groups is non-null in the call to wireframe, however, the algorithm is not sophisticated enough to render intersecting surfaces correctly.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

cloud, utilities.3d
Examples

```r
wireframe(volcano, shade = TRUE,
  shade.colors.palette = makeShadePalette(hcl.colors(10, "Inferno"),
    pref = 0.2))
wireframe(volcano, shade = TRUE,
  shade.colors.palette = makeShadePalette(hcl.colors(10, "Dark Mint"),
    pref = 0.2))
wireframe(volcano, shade = TRUE,
  shade.colors.palette = makeShadePalette(hcl.colors(10, "Harmonic"),
    pref = 0.2))
```

Description

This is the default panel function for `densityplot`.

Usage

```r
panel.densityplot(x, darg, plot.points = "jitter",
  ref = FALSE,
  groups = NULL,
  weights = NULL,
  jitter.amount,
  type, ...,
  grid = lattice.getOption("default.args")$grid,
  identifier = "density")
```

Arguments

- `x` data points for which density is to be estimated
- `darg` list of arguments to be passed to the `density` function. Typically, this should be a list with zero or more of the following components: `bw`, `adjust`, `kernel`, `window`, `width`, `give.Rkern`, `n`, `from`, `to`, `cut`, `na.rm` (see `density` for details)
- `plot.points` logical specifying whether or not the data points should be plotted along with the estimated density. Alternatively, a character string specifying how the points should be plotted. Meaningful values are "rug", in which case `panel.rug` is used to plot a 'rug'. and "jitter", in which case the points are jittered vertically to better distinguish overlapping points.
- `ref` logical, whether to draw x-axis
- `groups` an optional grouping variable. If present, `panel.superpose` will be used instead to display each subgroup
- `weights` numeric vector of weights for the density calculations. If this is specified, the ... part must also include a `subscripts` argument that matches the weights to `x`
- `jitter.amount` when `plot.points="jitter"`, the value to use as the amount argument to `jitter`
type argument used to plot points, if requested. This is not expected to be useful, it is available mostly to protect a type argument, if specified, from affecting the density curve.

... extra graphical parameters. Note that additional arguments to panel.rug cannot be passed on through panel.densityplot.

grid A logical flag, character string, or list specifying whether and how a background grid should be drawn. In its general form, grid can be a list of arguments to be supplied to panel.grid, which is called with those arguments. Three shortcuts are available:

TRUE: roughly equivalent to list(h = -1, v = -1)
"h": roughly equivalent to list(h = -1, v = 0)
"v": roughly equivalent to list(h = 0, v = -1)

No grid is drawn if grid = FALSE.

identifier A character string that is prepended to the names of grobs that are created by this panel function.

Author(s)
Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also
densityplot, jitter

Description
Default panel function for dotplot.

Usage
panel.dotplot(x, y, horizontal = TRUE,
pch, col, lty, lwd, col.line,
levels.fos,
groups = NULL,
...,
grid = lattice.getOption("default.args")$grid,
identifier = "dotplot")

Arguments

x, y variables to be plotted in the panel. Typically y is the ‘factor’

horizontal logical. If FALSE, the plot is ‘transposed’ in the sense that the behaviours of x and y are switched. x is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of bwplot for a fuller explanation.

pch, col, lty, lwd, col.line graphical parameters
This is the default panel function for `histogram`.

Usage

```r
panel.histogram(x, 
    breaks, 
    equal.widths = TRUE, 
    type = "density", 
    nint = round(log2(length(x)) + 1), 
    alpha, col, border, lty, lwd, 
    ..., 
    identifier = "histogram")
```

Arguments

- `x`: The data points for which the histogram is to be drawn
- `breaks`: The breakpoints for the histogram
- `equal.widths`: Logical used when `breaks` is `NULL`
- `type`: Type of histogram, possible values being "percent", "density" and "count"
Number of bins for the histogram

Graphical parameters for bars; defaults are obtained from the `plot.polygon` settings.

Other arguments, passed to `hist` when deemed appropriate

A character string that is prepended to the names of grobs that are created by this panel function.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`histogram`

---

### Description

These are the default panel functions for `levelplot` and `contourplot`. Also documented is an alternative raster-based panel function for use with `levelplot`.

### Usage

```r
code
```

#### panel.levelplot

```r
code
```

```r
panel.levelplot(x, y, z,
    subscripts,
    at = pretty(z),
    shrink,
    labels,
    label.style = c("mixed", "flat", "align"),
    contour = FALSE,
    region = TRUE,
    col = add.line$col,
    lty = add.line$lty,
    lwd = add.line$lwd,
    border = "transparent",
    border.lty = 1,
    border.lwd = 0.1,
    ...
    region.type = c("grid", "contour"),
    col.regions = regions$col,
    alpharegions = regions$alpha,
    identifier = "levelplot")
```n

#### panel.contourplot

```r
code
```

#### panel.levelplot.raster

```r
code
```
col.regions = regions$col,
alpha.regions = regions$alpha,
interpolate = FALSE,
identifier = "levelplot")

Arguments

x, y, z  
Variables defining the plot.

subscripts  
Integer vector indicating what subset of x, y and z to draw.

at  
Numeric vector giving breakpoints along the range of z. See levelplot for details.

shrink  
Either a numeric vector of length 2 (meant to work as both x and y components), or a list with components x and y which are numeric vectors of length 2. This allows the rectangles to be scaled proportional to the z-value. The specification can be made separately for widths (x) and heights (y). The elements of the length 2 numeric vector gives the minimum and maximum proportion of shrinkage (corresponding to min and max of z).

labels  
Either a logical scalar indicating whether the labels are to be drawn, or a character or expression vector giving the labels associated with the at values. Alternatively, labels can be a list with the following components: labels: a character or expression vector giving the labels. This can be omitted, in which case the defaults will be used.

col, cex, alpha: graphical parameters for label texts
fontfamily, fontface, font: font used for the labels

label.style  
Controls how label positions and rotation are determined. A value of "flat" causes the label to be positioned where the contour is flattest, and the label is not rotated. A value of "align" causes the label to be drawn as far from the boundaries as possible, and the label is rotated to align with the contour at that point. The default is to mix these approaches, preferring the flattest location unless it is too close to the boundaries.

contour  
A logical flag, specifying whether contour lines should be drawn.

region  
A logical flag, specifying whether inter-contour regions should be filled with appropriately colored rectangles.

col, lty, lwd  
Graphical parameters for contour lines.

border  
Border color for rectangles used when region=TRUE.

border.lty, border.lwd  
Graphical parameters for the border

...  
Extra parameters.

region.type  
A character string, one of "grid" and "contour". The former (the default) uses a grid of rectangles to display the colors for the level plot; the latter uses a grid of polygons, mimicking the behavior of filled.contour, which gives a smoother appearance at the cost of increased processing time.

The "contour" option requires x and y to be complete, in the sense that it must include all possible combinations in the underlying grid. However, z values are allowed to be missing.

col.regions  
A vector of colors, or a function to produce a vector of colors, to be used if region=TRUE. Each interval defined by at is assigned a color, so the number of colors actually used is one less than the length of at. See level.colors for details on how the color assignment is done.
alpha.regions numeric scalar controlling transparency of facets
interpolate logical, passed to `grid.raster`.
identifier A character string that is prepended to the names of grobs that are created by this panel function.

Details

The same panel function is used for both `levelplot` and `contourplot` (which differ only in default values of some arguments). `panel.contourplot` is a simple wrapper to `panel.levelplot`.

When `contour=TRUE`, the `contourLines` function is used to calculate the contour lines.

`panel.levelplot.raster` is an alternative panel function that uses the raster drawing abilities in R 2.11.0 and higher (through `grid.raster`). It has fewer options (e.g., can only render data on an equispaced grid), but can be more efficient. When using `panel.levelplot.raster`, it may be desirable to render the color key in the same way. This is possible, but must be done separately; see `levelplot` for details.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>.

The functionality of `region.type = "contour"` is based on code borrowed from the `gridGraphics` package, written by Zhijian (Jason) Wen and Paul Murrell and ported to lattice by Johan Larsson.

See Also

`levelplot`, `level.colors`, `contourLines`, `filled.contour`

Examples

```r
require(grid)
levelplot(rnorm(10) ~ 1:10 + sort(runif(10)), panel = panel.levelplot)
suppressWarnings(plot(levelplot(rnorm(10) ~ 1:10 + sort(runif(10)),
panel = panel.levelplot.raster,
interpolate = TRUE)))
levelplot(volcano, panel = panel.levelplot.raster)
levelplot(volcano, panel = panel.levelplot.raster,
col.regions = hcl.colors, cuts = 30, interpolate = TRUE)
```

Description

This is the default superpanel function for `splom`.
Usage

panel.pairs(z,
   panel = lattice.getOption("panel.splom"),
   lower.panel = panel,
   upper.panel = panel,
   diag.panel = "diag.panel.splom",
   as.matrix = FALSE,
   groups = NULL,
   panel.subscripts,
   subscripts,
   pscales = 5,
   prepanel.limits = scale_limits,
   varnames = colnames(z),
   varname.col, varname.cex, varname.font,
   varname.fontfamily, varname.fontface,
   axis.text.col, axis.text.cex, axis.text.font,
   axis.text.fontfamily, axis.text.fontface,
   axis.text.lineheight,
   axis.line.col, axis.line.lty, axis.line.lwd,
   axis.line.alpha, axis.line.tck,
   ...)

diag.panel.splom(x = NULL,
   varname = NULL, limits, at = NULL, labels = NULL,
   draw = TRUE, tick.number = 5,
   varname.col, varname.cex, varname.lineheight, varname.font,
   varname.fontfamily, varname.fontface,
   axis.text.col, axis.text.alpha, axis.text.font,
   axis.text.cex, axis.text.fontfamily, axis.text.fontface,
   axis.text.lineheight,
   axis.line.col, axis.line.lty, axis.line.lwd,
   axis.line.alpha, axis.line.tck,
   ...)

Arguments

z  The data frame used for the plot.
panel, lower.panel, upper.panel  The panel function used to display each pair of variables. If specified, lower.panel and upper.panel are used for panels below and above the diagonal respectively. In addition to extra arguments not recognized by panel.pairs, the list of arguments passed to the panel function also includes arguments named i and j, with values indicating the row and column of the scatterplot matrix being plotted.
diag.panel  The panel function used for the diagonals. See arguments to diag.panel.splom to know what arguments this function is passed when called. Use diag.panel=NULL to suppress plotting on the diagonal panels.
as.matrix  logical. If TRUE, the layout of the panels will have origin on the top left instead of bottom left (similar to pairs). This is in essence the same functionality as provided by as.table for the panel layout
groups

panel.subscripts

logical specifying whether the panel function accepts an argument named subscripts.

subscripts

The indices of the rows of \( z \) that are to be displayed in this (super)panel.

pscales

Controls axis labels, passed down from splom. If pscales is a single number, it indicates the approximate number of equally-spaced ticks that should appear on each axis. If pscales is a list, it should have one component for each column in \( z \), each of which itself a list with the following valid components:

- at: a numeric vector specifying tick locations
- labels: character vector labels to go with at
- limits: numeric 2-vector specifying axis limits (should be made more flexible at some point to handle factors)

These are specifications on a per-variable basis, and used on all four sides in the diagonal cells used for labelling. Factor variables are labelled with the factor names. Use pscales=0 to suppress the axes entirely.

prepanel.limits

A function to calculate suitable axis limits given a single argument \( x \) containing a data vector. The return value of the function should be similar to the xlim or ylim argument documented in xyplot; that is, it should be a numeric or DateTime vector of length 2 defining a range, or a character vector representing levels of a factor.

Most high-level lattice plots (such as xyplot) use the prepanel function for deciding on axis limits from data. This function serves a similar function by calculating the per-variable limits. These limits can be overridden by the corresponding limits component in the pscales list.

x

data vector corresponding to that row / column (which will be the same for diagonal 'panels').

varname

(scalar) character string or expression that is to be written centred within the panel

limits

numeric of length 2, or, vector of characters, specifying the scale for that panel (used to calculate tick locations when missing)

at

locations of tick marks

labels

optional labels for tick marks

draw

A logical flag specifying whether to draw the tick marks and labels. If FALSE, variable names are shown but axis annotation is omitted.

tick.number

A Numeric scalar giving the suggested number of tick marks.

varnames

A character or expression vector or giving names to be used for the variables in \( x \). By default, the column names of \( x \).

varname.col

Color for the variable name in each diagonal panel. See gpar for details on this and the other graphical parameters listed below.

varname.cex

Size multiplier for the variable name in each diagonal panel.

varname.lineheight

Line height for the variable name in each diagonal panel.

varname.font, varname.fontfamily, varname.fontface

Font specification for the variable name in each diagonal panel.

axis.text.col

Color for axis label text.
F_1_panel.parallel

axis.text.cex  Size multiplier for axis label text.
axis.text.font, axis.text.fontfamily, axis.text.fontface  Font specification for axis label text.
axis.text.lineheight  Line height for axis label text.
axis.text.alpha  Alpha-transparency for axis label text.
axis.line.col  Color for the axes.
axis.line.lty  Line type for the axes.
axis.line.lwd  Line width for the axes.
axis.line.alpha  Alpha-transparency for the axes.
axis.line.tck  A numeric multiplier for the length of tick marks in diagonal panels.

Further arguments, passed on to panel, lower.panel, upper.panel, and diag.panel from panel.pairs. Currently ignored by diag.panel.splom.

Details

panel.pairs is the function that is actually used as the panel function in a "trellis" object produced by splom.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

splom

Examples

Cmat <- outer(1:6, 1:6,
  function(i, j) hcl.colors(11)[i+j-1])  ## rainbow(11, start=.12, end=.5)[i+j-1]

splom(~diag(6), as.matrix = TRUE,
  panel = function(x, y, i, j, ...) {
    panel.fill(Cmat[i, j])
    panel.text(.5,.5, paste("(", i, ",", j, ")", sep=""))
  })

---

F_1_panel.parallel  Default Panel Function for parallel

Description

This is the default panel function for parallel.
Usage

panel.parallel(x, y, z, subscripts,
    groups = NULL,
    col, lwd, lty, alpha,
    common.scale = FALSE,
    lower, upper,
    ...
    horizontal.axis = TRUE,
    identifier = "parallel")

Arguments

x, y       dummy variables, ignored.
z       The data frame used for the plot. Each column will be coerced to numeric before
        being plotted, and an error will be issued if this fails.
subscripts       The indices of the rows of z that are to be displayed in this panel.
groups       An optional grouping variable. If specified, different groups are distinguished
        by use of different graphical parameters (i.e., rows of z in the same group share
        parameters).
col, lwd, lty, alpha
        graphical parameters (defaults to the settings for superpose.line). If groups
        is non-null, these parameters used one for each group. Otherwise, they are recy-
        cled and used to distinguish between rows of the data frame z.
common.scale       logical, whether a common scale should be used columns of z. Defaults to
        FALSE, in which case the horizontal range for each column is different (as deter-
        mined by lower and upper).
lower, upper       numeric vectors replicated to be as long as the number of columns in z. De-
        termines the lower and upper bounds to be used for scaling the corresponding
        columns of z after coercing them to numeric. Defaults to the minimum and max-
        imum of each column. Alternatively, these could be functions (to be applied on
        each column) that return a scalar.
...
other arguments (ignored)
horizontal.axis       logical indicating whether the parallel axes should be laid out horizontally
        (TRUE) or vertically (FALSE).
identifier       A character string that is prepended to the names of grobs that are created by
        this panel function.

Details

Produces parallel coordinate plots, which are easier to understand from an example than through a
verbal description. See example for parallel

Author(s)

Deepayan Sarkar <Deepayan. Sarkar@R-project.org>
References


See Also

parallel

Default Panel Function for qqmath

Description

This is the default panel function for qqmath.

Usage

```r
panel.qqmath(x, f.value = NULL,
            distribution = qnorm,
            qtype = 7,
            groups = NULL, ...,
            tails.n = 0,
            identifier = "qqmath")
```

Arguments

- `x`: vector (typically numeric, coerced if not) of data values to be used in the panel.
- `f.value`, `distribution`: Defines how quantiles are calculated. See `qqmath` for details.
- `qtype`: The type argument to be used in `quantile`
- `groups`: An optional grouping variable. Within each panel, one Q-Q plot is produced for every level of this grouping variable, differentiated by different graphical parameters.
- `...`: Further arguments, often graphical parameters, eventually passed on to `panel.xyplot`. Arguments `grid` and `abline` of `panel.xyplot` may be particularly useful.
- `tails.n`: number of data points to represent exactly on each tail of the distribution. This reproduces the effect of `f.value = NULL` for the extreme data values, while approximating the remaining data. It has no effect if `f.value = NULL`. If `tails.n` is given, `qtype` is forced to be `1`.
- `identifier`: A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates a Q-Q plot of the data and the theoretical distribution given by `distribution`. Note that most of the arguments controlling the display can be supplied directly to the high-level `qqmath` call.
Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

qqmath

Examples

set.seed(0)
xx <- rt(10000, df = 10)
qqmath(~ xx, pch = "+", distribution = qnorm,
   grid = TRUE, abline = c(0, 1),
   xlab.top = c("raw", "ppoints(100)", "tails.n = 50"),
   panel = function(..., f.value) {
     switch(panel.number(),
           panel.qqmath(..., f.value = NULL),
           panel.qqmath(..., f.value = ppoints(100)),
           panel.qqmath(..., f.value = ppoints(100), tails.n = 50))
   }, layout = c(3, 1))[c(1, 1, 1)]

Description

This is the default panel function for stripplot. Also see panel.superpose

Usage

panel.stripplot(x, y, jitter.data = FALSE,
    factor = 0.5, amount = NULL,
    horizontal = TRUE, groups = NULL,
    ...,
    grid = lattice.getOption("default.args")$grid,
    identifier = "stripplot")

Arguments

x, y coordinates of points to be plotted
jitter.data whether points should be jittered to avoid overplotting. The actual jittering is
    performed inside panel.xyplot, using its jitter.x or jitter.y argument
    (depending on the value of horizontal).
factor, amount amount of jittering, see jitter
horizontal logical. If FALSE, the plot is ‘transposed’ in the sense that the behaviours of
    x and y are switched. x is now the ‘factor’. Interpretation of other arguments
    change accordingly. See documentation of bwplot for a fuller explanation.
groups optional grouping variable
... additional arguments, passed on to panel.xyplot
grid  A logical flag, character string, or list specifying whether and how a background grid should be drawn. In its general form, grid can be a list of arguments to be supplied to `panel.grid`, which is called with those arguments. Three shortcuts are available:

TRUE: roughly equivalent to `list(h = -1, v = -1)`
"h": roughly equivalent to `list(h = -1, v = 0)`
"v": roughly equivalent to `list(h = 0, v = -1)`

No grid is drawn if `grid = FALSE`.
identifier  A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates stripplot (one dimensional scatterplot) of `x` for each level of `y` (or vice versa, depending on the value of `horizontal`)

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`stripplot`, `jitter`

Description

This is the default panel function for `xyplot`. Also see `panel.superpose`. The default panel functions for `splom` and `qq` are essentially the same function.

Usage

panel.xyplot(x, y, type = "p",
            groups = NULL,
pch, col, col.line, col.symbol,
font, fontfamily, fontface,
lty, cex, fill, lwd,
horizontal = FALSE, ..., 
smooth = NULL,
grid = latticegetOption("default.args")$grid,
abline = NULL,
jitter.x = FALSE, jitter.y = FALSE,
factor = 0.5, amount = NULL,
identifier = "xyplot")
panel.splom(..., identifier = "splom")
panel.qq(..., identifier = "qq")

F_1_panel.xyplot  Default Panel Function for xyplot
Arguments

\texttt{x, y} \quad \text{variables to be plotted in the scatterplot}

\texttt{type} \quad \text{character vector controlling how \textit{x} and \textit{y} are to be plotted. Can consist of one or more of the following: "p", "l", "h", "b", "o", "s", "S", "g", "r", "a", "smooth", and "spline". If \texttt{type} has more than one element, an attempt is made to combine the effect of each of the components.}

The behaviour if any of the first five are included in \texttt{type} is similar to the effect of the corresponding type in \texttt{plot}: "p" and "l" stand for points and lines respectively; "b" and "o" (for ‘overlay’) plot both; "h" draws vertical (or horizontal if \texttt{horizontal = TRUE}) line segments from the points to the origin. Types "s" and "S" are like "l" in the sense that they join consecutive points, but instead of being joined by a straight line, points are connected by a vertical and a horizontal segment forming a ‘step’, with the vertical segment coming first for "s", and the horizontal segment coming first for "S". Types "s" and "S" sort the values along one of the axes (depending on \texttt{horizontal}); this is unlike the behavior in \texttt{plot}. For the latter behavior, use \texttt{type = "s"} with \texttt{panel = panel.points}.

Type "g" adds a reference grid using \texttt{panel.grid} in the background, but using the grid argument is now the preferred way to do so.

The remaining values of \texttt{type} lead to various types of smoothing. This can also be achieved using the \texttt{smooth} argument, or by calling the relevant panel functions directly. The panel functions provide finer control over graphical and other parameters, but using \texttt{smooth} or \texttt{type} is convenient for simple usage. Using \texttt{smooth} is recommended, but \texttt{type} is also supported for backwards compatibility.

Type "r" adds a linear regression line, "smooth" adds a loess fit, "spline" adds a cubic smoothing spline fit, and "a" draws line segments joining the average \textit{y} value for each distinct \textit{x} value. See \texttt{smooth} for details.

See \texttt{example(xyplot)} and \texttt{demo(lattice)} for examples.

\texttt{groups} \quad \text{an optional grouping variable. If present, \texttt{panel.superpose} will be used instead to display each subgroup}

\texttt{col, col.line, col.symbol} \quad \text{default colours are obtained from \texttt{plot.symbol} and \texttt{plot.line} using \texttt{trellis.par.get}}

\texttt{font, fontface, fontfamily} \quad \text{font used when \texttt{pch} is a character}

\texttt{pch, lty, cex, lwd, fill} \quad \text{other graphical parameters. \texttt{fill} serves the purpose of \texttt{bg} in \texttt{points} for certain values of \texttt{pch}}

\texttt{horizontal} \quad \text{A logical flag controlling the orientation for certain \texttt{type}'s, e.g., "h", "s", ans "S" and the result of smoothing.}

\texttt{...} \quad \text{Extra arguments, if any, for \texttt{panel.xyplot}. Usually passed on as graphical parameters to low level plotting functions, or to the panel functions performing smoothing, if applicable.}

\texttt{smooth} \quad \text{If specified, indicates the type of smooth to be added. Can be a character vector containing one or more values from "lm", "loess", "spline", and "average". Can also be a logical flag: \texttt{TRUE} is interpreted as "loess". Each of these result in calling a corresponding panel function as described below; the \texttt{smooth} argument simply provides a convenient shortcut.
"lm" adds a linear regression line (same as panel.lmline, except for default graphical parameters). "loess" adds a loess fit (same as panel.loess). "spline" adds a cubic smoothing spline fit (same as panel.spline). "average" has the effect of calling panel.average, which in conjunction with a groups argument can be useful for creating interaction plots.

Normally, smoothing is performed with the y variable as the response and the x variable as the predictor. However, the roles of x and y are reversed if horizontal = TRUE.

grid

A logical flag, character string, or list specifying whether and how a background grid should be drawn. This provides the same functionality as type="g", but is the preferred alternative as the effect type="g" is conceptually different from that of other type values (which are all data-dependent). Using the grid argument also allows more flexibility.

Most generally, grid can be a list of arguments to be supplied to panel.grid, which is called with those arguments. Three shortcuts are available:

- TRUE: roughly equivalent to list(h = -1, v = -1)
- "h": roughly equivalent to list(h = -1, v = 0)
- "v": roughly equivalent to list(h = 0, v = -1)

No grid is drawn if grid = FALSE.

abline

A numeric vector or more generally a list containing arguments that are used to call panel.abline. If specified as a numeric vector, abline is used as the first unnamed argument to panel.abline. This allows arguments of the form abline = c(0, 1), which adds the diagonal line, or abline = coef(fm) to fit the regression line from a fitted mode. Use the list form for finer control; e.g., abline = list(h = 0, v = 0, col = "grey").

For more flexibility, use panel.abline directly.

jitter.x, jitter.y

logical, whether the data should be jittered before being plotted.

factor, amount

controls amount of jittering.

identifier

A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates scatterplot of x and y, with various modifications possible via the type argument. panel.qq draws a 45 degree line before calling panel.xyplot.

Note that most of the arguments controlling the display can be supplied directly to the high-level (e.g. xyplot) call.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

panel.superpose, xyplot, splom
Examples

types.plain <- c("p", "l", "o", "r", "g", "s", "S", "h", "a", "smooth")
types.horiz <- c("s", "S", "h", "a", "smooth")
horiz <- rep(c(FALSE, TRUE), c(length(types.plain), length(types.horiz)))

types <- c(types.plain, types.horiz)
x <- sample(seq(-10, 10, length.out = 15), 30, TRUE)
y <- x + 0.25 * (x + 1)^2 + rnorm(length(x), sd = 5)

xyplot(y ~ x | gl(1, length(types)),
       xlab = "type",
       ylab = list(c("horizontal=TRUE", "horizontal=FALSE"), y = c(1/6, 4/6)),
       as.table = TRUE, layout = c(5, 3),
       between = list(y = c(0, 1)),
       strip = function(...) {
         panel.fill(trellis.par.get("strip.background")$col[1])
         type <- types[panel.number()]
         grid::grid.text(label = sprintf("%s", type),
                         x = 0.5, y = 0.5)
         grid::grid.rect()
       },
       scales = list(alternating = c(0, 2), tck = c(0, 0.7), draw = FALSE),
       par.settings = list(layout.widths = list(strip.left = c(1, 0, 0, 0, 0))),
       panel = function(...) {
         type <- types[panel.number()]
         horizontal <- horiz[panel.number()]
         panel.xyplot(...,
                     type = type,
                     horizontal = horizontal)
       })[rep(1, length(types))]

F_2_llines

Replacements of traditional graphics functions

Description

These functions are intended to replace common low level traditional graphics functions, primarily for use in panel functions. The originals can not be used (at least not easily) because lattice panel functions need to use grid graphics. Low level drawing functions in grid can be used directly as well, and is often more flexible. These functions are provided for convenience and portability.

Usage

lplot.xy(xy, type, pch, lty, col, cex, lwd,
        font, fontfamily, fontface,
        col.line, col.symbol, alpha, fill,
        origin = 0, ..., identifier, name.type)
larrows(...)
llines(x, ...)

lpoints(x, ...)  
lpolygon(x, ...)  
lpolypath(x, ...)  
lrect(...)  
lsegments(...)  
ltext(x, ...)  

## Default S3 method:  
larrows(x0 = NULL, y0 = NULL, x1, y1, x2 = NULL, y2 = NULL,  
angle = 30, code = 2, length = 0.25, unit = "inches",  
ends = switch(code, "first", "last", "both"),  
type = "open",  
col = add.line$col,  
alpha = add.line$alpha,  
lty = add.line$lty,  
lwd = add.line$lwd,  
fill = NULL,  
font, fontface,  
..., identifier, name.type)  

## Default S3 method:  
llines(x, y = NULL, type = "l",  
col, alpha, lty, lwd, ..., identifier, name.type)  

## Default S3 method:  
lpoints(x, y = NULL, type = "p", col, pch, alpha, fill,  
font, fontfamily, fontface, cex, ..., identifier, name.type)  

## Default S3 method:  
lpolygon(x, y = NULL,  
border = "black", col = "transparent", fill = NULL,  
font, fontface,  
..., rule = c("none", "winding", "evenodd"),  
exterior, name.type)  

## Default S3 method:  
lpolypath(x, y = NULL,  
border = "black", col = "transparent", fill = NULL,  
font, fontface,  
..., rule = c("winding", "evenodd"),  
exterior, name.type)  

## Default S3 method:  
ltext(x, y = NULL, labels = seq_along(x),  
col, alpha, cex, srt = 0,  
lineheight, font, fontfamily, fontface,  
adj = c(0.5, 0.5), pos = NULL, offset = 0.5, ..., identifier, name.type)  

## Default S3 method:  
lrect(xleft, ybottom, xright, ytop,  
x = (xleft + xright) / 2,  
y = (ybottom + ytop) / 2,  
width = xright - xleft,  
height = ytop - ybottom,  
col = "transparent",  
border = "black",
lty = 1, lwd = 1, alpha = 1,
just = "center",
hjust = NULL, vjust = NULL,
font, fontface,
..., identifier, name.type)

## Default S3 method:
segments(x0, y0, x1, y1, x2, y2,
col, alpha, lty, lwd,
font, fontface, ..., identifier, name.type)

panel.arrows(...)  
panel.lines(...)  
panel.points(...)  
panel.polygon(...)  
panel.rect(...)  
panel.segments(...)  
panel.text(...)

Arguments

x, y, x0, y0, x1, y1, x2, y2, xy

locations. x2 and y2 are available for S compatibility.

length, unit
determines extent of arrow head. length specifies the length in terms of unit,
which can be any valid grid unit as long as it doesn’t need a data argument. unit
defaults to inches, which is the only option in the base version of the function,

arrows.

angle, code, type, labels, srt, adj, pos, offset

arguments controlling behaviour. See respective base functions for details. For
l arrows and panel.larrows, type is either "open" or "closed", indicating
the type of arrowhead.

e nds
serves the same function as code, using descriptive names rather than integer
codes. If specified, this overrides code

col, alpha, lty, lwd, fill, pch, cex, lineheight, font, fontfamily, fontface, col.line, col.symbol, border

graphical parameters. fill applies to points when pch is in 21:25 and specifies
the fill color, similar to the bg argument in the base graphics function points.
For devices that support alpha-transparency, a numeric argument alpha between
0 and 1 can controls transparency. Be careful with this, since for devices that
do not support alpha-transparency, nothing will be drawn at all if this is set to
anything other than 0.

fill, font and fontface are included in lrect, l arrows, lpolygon, and
lsegments only to ensure that they are not passed down (as gpar does not like
them).

origin

for type=“h” or type=“H”, the value to which lines drop down.

xleft, ybottom, xright, ytop

see rect

width, height, just, hjust, vjust

finer control over rectangles, see grid.rect

... extra arguments, passed on to lower level functions as appropriate.

rule

character string specifying how NA values are interpreted for polygons and paths.
This is mainly intended for paths (via grid.path), but can also be specified for
polygons for convenience.
For polygons, the default rule is "none", which treats NA-separated segments as separate polygons. This value is only valid for polygons. For the other rules ("winding" or "evenodd") these segments are interpreted as subpaths, possibly representing holes, of a single path, and are rendered using grid.path. Support and rendering speed may depend on the device being used.

**identifier**  
A character string that is prepended to the name of the grob that is created.

**name.type**  
A character value indicating whether the name of the grob should have panel or strip information added to it. Typically either "panel", "strip", "strip.left", or "" (for no extra information).

**Details**

These functions are meant to be grid replacements of the corresponding base R graphics functions, to allow existing Trellis code to be used with minimal modification. The functions panel.* are essentially identical to the l* versions, are recommended for use in new code (as opposed to ported code) as they have more readable names.

See the documentation of the base functions for usage. Not all arguments are always supported. All these correspond to the default methods only.

**Note**

There is a new type="H" option wherever appropriate, which is similar to type="h", but with horizontal lines.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

points, lines, rect, text, segments, arrows, Lattice

**Examples**

```r
SD <- 0.1
t <- seq(0, 2*pi, length.out = 50) + rnorm(50, sd = SD)
d <- list(x = c(cos(t), NA, rev(0.5 * cos(t))) + rnorm(101, sd = SD),
y = c(sin(t), NA, rev(0.5 * sin(t))) + rnorm(101, sd = SD))

## rectangles
xyplot(y ~ x, d, panel = panel.rect, col = 4, alpha = 0.5, width = 0.1, height = 0.1)

## points and lines
xyplot(y ~ x, d, panel = panel.lines, col = 4, alpha = 0.5,
type = "o", pch = 16)

## polygons and paths (with holes)
xyplot(y ~ x, d, panel = panel.polygon, col = 4, alpha = 0.5, rule = "evenodd")

## Example adapted from https://journal.r-project.org/articles/RJ-2012-017/
x <- c(.1, .5, .9, NA, .4, .5, .6, NA, .4, .6, .5)
y <- c(.1, .8, .1, NA, .5, .4, .5, NA, .3, .3, .2)
d <- data.frame(x = x, y = y)
```
F_2_panel.functions

Useful Panel Function Components

Description

These are predefined panel functions available in lattice for use in constructing new panel functions (often on-the-fly).

Usage

```r
panel.abline(a = NULL, b = 0,
             h = NULL, v = NULL,
             reg = NULL, coef = NULL,
             col, col.line, lty, lwd, alpha, type,
             ..., reference = FALSE,
             identifier = "abline")
```

```r
panel.refline(...)
```

```r
panel.curve(expr, from, to, n = 101,
            curve.type = "l",
            col, lty, lwd, type,
            ..., identifier = "curve")
```

```r
panel.rug(x = NULL, y = NULL,
          regular = TRUE,
          start = if (regular) 0 else 0.97,
          end = if (regular) 0.03 else 1,
          x.units = rep("npc", 2),
          y.units = rep("npc", 2),
          col, col.line, lty, lwd, alpha,
          ..., identifier = "rug")
```

```r
panel.average(x, y, fun = mean, horizontal = TRUE,
               lwd, lty, col, col.line, type,
               ..., identifier = "linejoin")
```

```r
panel.linejoin(x, y, fun = mean, horizontal = TRUE,
               lwd, lty, col, col.line, type,
               ..., identifier = "linejoin")
```
panel.fill(col, border, ..., identifier = "fill")
panel.grid(h=3, v=3, col, col.line, lty, lwd, x, y, ..., identifier = "grid")
panel.lmline(x, y, ..., identifier = "lmline")
panel.mathdensity(dmath = dnorm, args = list(mean=0, sd=1), n = 50, col, col.line, lwd, lty, type, ..., identifier = "mathdensity")

Arguments

x, y Variables defining the contents of the panel. In panel.grid these are optional and are used only to choose an appropriate method of pretty.

a, b Coefficients of the line to be added by panel.abline. a can be a vector of length 2, representing the coefficients of the line to be added, in which case b should be missing. a can also be an appropriate ‘regression’ object, i.e., an object which has a coef method that returns a length 2 numeric vector. The corresponding line will be plotted. The reg argument overrides a if specified.

c coef Coefficients of the line to be added as a vector of length 2.

reg A (linear) regression object, with a coef method that gives the coefficients of the corresponding regression line.

h, v For panel.abline, these are numeric vectors giving locations respectively of horizontal and vertical lines to be added to the plot, in native coordinates. For panel.grid, these usually specify the number of horizontal and vertical reference lines to be added to the plot. Alternatively, they can be negative numbers. h=-1 and v=-1 are intended to make the grids aligned with the axis labels. This doesn’t always work; all that actually happens is that the locations are chosen using pretty, which is also how the label positions are chosen in the most common cases (but not for factor variables, for instance). h and v can be negative numbers other than -1, in which case -h and -v (as appropriate) is supplied as the n argument to pretty.

If x and/or y are specified in panel.grid, they will be used to select an appropriate method for pretty. This is particularly useful while plotting date-time objects.

reference A logical flag determining whether the default graphical parameters for panel.abline should be taken from the “reference.line” parameter settings. The default is to take them from the “add.line” settings. The panel.refline function is a wrapper around panel.abline that calls it with reference = TRUE.

expr An expression considered as a function of x, or a function, to be plotted as a curve.

n The number of points to use for drawing the curve.

from, to optional lower and upper x-limits of curve. If missing, limits of current panel are used

curve.type Type of curve ("p" for points, etc), passed to lines

regular A logical flag indicating whether the ‘rug’ is to be drawn on the ‘regular’ side (left / bottom) or not (right / top).

start, end endpoints of rug segments, in normalized parent coordinates (between 0 and 1). Defaults depend on value of regular, and cover 3% of the panel width and height.
x.units, y.units

Character vectors, replicated to be of length two. Specifies the (grid) units associated with start and end above. x.units and y.units are for the rug on the x-axis and y-axis respectively (and thus are associated with start and end values on the y and x scales respectively).

col, col.line, lty, lwd, alpha, border

Graphical parameters.

type

Usually ignored by the panel functions documented here; the argument is present only to make sure an explicitly specified type argument (perhaps meant for another function) does not affect the display.

fun

The function that will be applied to the subset of x values (or y if horizontal is FALSE) determined by the unique values of y (x).

horizontal

A logical flag. If FALSE, the plot is ‘transposed’ in the sense that the roles of x and y are switched; x is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of bwplot for a fuller explanation.

dmath

A vectorized function that produces density values given a numeric vector named x, e.g., dnorm.

args

A list giving additional arguments to be passed to dmath.

...

Further arguments, typically graphical parameters, passed on to other low-level functions as appropriate. Color can usually be specified by col, col.line, and col.symbol, the last two overriding the first for lines and points respectively.

identifier

A character string that is prepended to the names of grobs that are created by this panel function.

Details

panel.abline adds a line of the form y = a + b * x, or vertical and/or horizontal lines. Graphical parameters are obtained from the “add.line” settings by default. panel.refline is similar, but uses the “reference.line” settings for the defaults.

panel.grid draws a reference grid.

panel.curve adds a curve, similar to what curve does with add = TRUE. Graphical parameters for the curve are obtained from the “add.line” setting.

panel.average treats one of x and y as a factor (according to the value of horizontal), calculates fun applied to the subsets of the other variable determined by each unique value of the factor, and joins them by a line. Can be used in conjunction with panel.xyplot, and more commonly with panel.superpose to produce interaction plots.

panel.linejoin is an alias for panel.average. It is retained for back-compatibility, and may go away in future.

panel.mathdensity plots a (usually theoretical) probability density function. This can be useful in conjunction with histogram and densityplot to visually assess goodness of fit (note, however, that qqmath is more suitable for this).

panel.rug adds a rug representation of the (marginal) data to the panel, much like rug.

panel.lmline(x, y) is equivalent to panel.abline(lm(y ~ x)).

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>
**F_2_panel.loess**  

Panel Function to Add a LOESS Smooth

### Description

A predefined panel function that can be used to add a LOESS smooth based on the provided data.

### Usage

```r
panel.loess(x, y, span = 2/3, degree = 1,
            family = c("symmetric", "gaussian"),
            evaluation = 50,
            lwd, lty, col, col.line, type,
            horizontal = FALSE,
            ..., identifier = "loess")
```

### Arguments

- **x, y**  
  Variables defining the data to be used.
- **lwd, lty, col, col.line**  
  Graphical parameters for the added line. `col.line` overrides `col`.

### Examples

#### Interaction Plot

```r
bwplot(yield ~ site, barley, groups = year,
       panel = function(x, y, groups, subscripts, ...) {
         panel.grid(h = -1, v = 0)
         panel.stripplot(x, y, ..., jitter.data = TRUE, grid = FALSE,
                         groups = groups, subscripts = subscripts)
         panel.superpose(x, y, ..., panel.groups = panel.average, grid = FALSE,
                         groups = groups, subscripts = subscripts)
       },
       auto.key = list(points = FALSE, lines = TRUE, columns = 2))
```

#### Superposing a fitted normal density on a Histogram

```r
histogram(~ height | voice.part, data = singer, layout = c(2, 4),
          type = "density", border = "transparent", col.line = "grey60",
          xlab = "Height (inches)",
          ylab = "Density Histogram\n with Normal Fit",
          panel = function(x, ...) {
            panel.histogram(x, ...)
            panel.mathdensity(dmath = dnorm,
                              args = list(mean = mean(x), sd = sd(x)), ...)
          })
```
type

Ignored. The argument is present only to make sure that an explicitly specified type argument (perhaps meant for another function) does not affect the display.

span, degree, family, evaluation

Arguments to `loess.smooth`, for which `panel.loess` is essentially a wrapper.

horizontal

A logical flag controlling which variable is to be treated as the predictor (by default `x`) and which as the response (by default `y`). If TRUE, the plot is ‘transposed’ in the sense that `y` becomes the predictor and `x` the response. (The name ‘horizontal’ may seem an odd choice for this argument, and originates from similar usage in `bwplot`).

... Extra arguments, passed on to `panel.lines`.

identifier

A character string that is prepended to the names of grobs that are created by this panel function.

Value

The object returned by `loess.smooth`.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`Lattice`, `loess.smooth`, `prepanel.loess`

**Description**

Useful panel function with qqmath. Draws a line passing through the points (usually) determined by the .25 and .75 quantiles of the sample and the theoretical distribution.

**Usage**

```r
panel.qqmathline(x, y = x, 
distribution = qnorm, 
probs = c(0.25, 0.75), 
qtype = 7, 
groups = NULL, 
..., 
identifier = "qqmathline")
```

**Arguments**

- `x` The original sample, possibly reduced to a fewer number of quantiles, as determined by the `f.value` argument to `qqmath`
- `y` an alias for `x` for backwards compatibility
- `distribution` quantile function for reference theoretical distribution.
F_2_panel.smoothScatter

F_2_panel.smoothScatter

Lattice panel function analogous to smoothScatter

Description

This function allows the user to place smoothScatter plots in lattice graphics.

Usage

panel.smoothScatter(x, y = NULL,
    nbin = 64, cuts = 255,
    bandwidth,
    col.regions,
    colramp,
    nrpoints = 100,
    transformation = function(x) x^0.25,
    pch = ".",
    cex = 1, col="black",
    range.x,
    ...,
    raster = FALSE,
    subscripts,
    identifier = "smoothScatter")

Arguments

x
    Numeric vector containing x-values or n by 2 matrix containing x and y values.

y
    Numeric vector containing y-values (optional). The length of x must be the same as that of y.

nbin
    Numeric vector of length 1 (for both directions) or 2 (for x and y separately) containing the number of equally spaced grid points for the density estimation.

cuts
    number of cuts defining the color gradient

probs
    numeric vector of length two, representing probabilities. Corresponding quantile pairs define the line drawn.

qtype
    the type of quantile computation used in quantile

groups
    optional grouping variable. If non-null, a line will be drawn for each group.

... other arguments.

identifier
    A character string that is prepended to the names of grobs that are created by this panel function.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

prepanel.qqmathline, qqmath, quantile
bandwidth  Numeric vector: the smoothing bandwidth. If missing, these functions come up with a more or less useful guess. This parameter then gets passed on to the function `bkde2D`.

col.regions  character vector of colors, or a function producing such a vector. Defaults to the col component of the regions setting of the current theme.

colramp  Function accepting an integer n as an argument and returning n colors. If missing, the default is derived from col.regions with the following modification: if col.regions is a vector of colors, it is prepended by "white" before being converted into a function using `colorRampPalette`.

nrpoints  Numeric vector of length 1 giving number of points to be superimposed on the density image. The first nrpoints points from those areas of lowest regional densities will be plotted. Adding points to the plot allows for the identification of outliers. If all points are to be plotted, choose nrpoints = Inf.

transformation  Function that maps the density scale to the color scale.

pch, cex  graphical parameters for the nrpoints “outlying” points shown in the display range.x  see `bkde2D` for details.

col  points color parameter

...  Further arguments that are passed on to `panel.levelplot`.

raster  logical; if TRUE, `panel.levelplot.raster` is used, making potentially smaller output files.

subscripts  ignored, but necessary for handling of ... in certain situations. Likely to be removed in future.

identifier  A character string that is prepended to the names of grobs that are created by this panel function.

Details

This replicates the display part of the `smoothScatter` function by replacing standard graphics calls by grid-compatible ones.

Value

The function is called for its side effects, namely the production of the appropriate plots on a graphics device.

Author(s)

Deepayan Sarkar <deepayan.sarkar@r-project.org>

Examples

ddf <- as.data.frame(matrix(rnorm(40000), ncol = 4) + 1.5 * rnorm(10000))
ddf[, c(2,4)] <- (-ddf[, c(2,4)])
xyplot(V1 ~ V2 + V3, ddf, outer = TRUE, panel = panel.smoothScatter, aspect = "iso")
## argument to panel.levelplot
xyplot(V1 ~ V2, ddf, panel = panel.smoothScatter, cuts = 10, region.type = "contour")
splom(ddf, panel = panel.smoothScatter, nbin = 64, raster = TRUE)
Panel Function to Add a Spline Smooth

Description

A predefined panel function that can be used to add a spline smooth based on the provided data.

Usage

panel.spline(x, y, npoints = 101,
             lwd = plot.line$lwd,
             lty = plot.line$lty,
             col, col.line = plot.line$col,
             type, horizontal = FALSE, ..., 
             keep.data = FALSE,
             identifier = "spline")

Arguments

x, y Variables defining the data to be used.
npoints The number of equally spaced points within the range of the predictor at which
the fitted model is evaluated for plotting.
lwd, lty, col, col.line Graphical parameters for the added line. col.line overrides col.
type Ignored. The argument is present only to make sure that an explicitly specified
type argument (perhaps meant for another function) does not affect the display.
horizontal A logical flag controlling which variable is to be treated as the predictor (by de-
default x) and which as the response (by default y). If TRUE, the plot is ‘transposed’
in the sense that y becomes the predictor and x the response. (The name ‘horizon-
tal’ may seem an odd choice for this argument, and originates from similar
usage in bwplot).
keep.data Passed on to smooth.spline. The default here (FALSE) is different, and results
in the original data not being retained in the fitted spline model. It may be useful
to set this to TRUE if the return value of panel.spline, which is the fitted model
as returned by smooth.spline, is to be used for subsequent computations.
... Extra arguments, passed on to smooth.spline and panel.lines as appropri-
ate.
identifier A character string that is prepended to the names of grobs that are created by
this panel function.

Value

The fitted model as returned by smooth.spline.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>
See Also

Lattice, smooth.spline, prepanel.spline

panel.superpose  Panel Function for Display Marked by groups

Description

These are panel functions for Trellis displays useful when a grouping variable is specified for use within panels. The x (and y where appropriate) variables are plotted with different graphical parameters for each distinct value of the grouping variable.

Usage

panel.superpose(x, y = NULL, subscripts, groups, panel.groups = "panel.xyplot",
    ..., col, col.line, col.symbol,
    pch, cex, fill, font,
    fontface, fontfamily,
    lty, lwd, alpha,
    type = "p",
    grid = lattice.getOption("default.args")$grid,
    distribute.type = FALSE)

panel.superpose.2(..., distribute.type = TRUE)

panel.superpose.plain(...,
    col, col.line, col.symbol,
    pch, cex, fill, font,
    fontface, fontfamily,
    lty, lwd, alpha)

Arguments

x, y  Coordinates of the points to be displayed. Usually numeric.

panel.groups  The panel function to be used for each subgroup of points. Defaults to panel.xyplot.

To be able to distinguish between different levels of the originating group inside panel.groups, it will be supplied two special arguments called group.number and group.value which will hold the numeric code and factor level corresponding to the current level of groups. No special care needs to be taken when writing a panel.groups function if this feature is not used.

subscripts  An integer vector of subscripts giving indices of the x and y values in the original data source. See the corresponding entry in xyplot for details.

groups  A grouping variable. Different graphical parameters will be used to plot the subsets of observations given by each distinct value of groups. The default graphical parameters are obtained from the "superpose.symbol" and "superpose.line" settings using trellis.par.get wherever appropriate.
Usually a character vector specifying how each group should be drawn. Formally, it is passed on to the panel.groups function, which must know what to do with it. By default, panel.groups is panel.xyplot, whose help page describes the admissible values.

The functions panel.superpose and panel.superpose.2 differ only in the default value of distribute.type, which controls the way the type argument is interpreted. If distribute.type = FALSE, then the interpretation is the same as for panel.xyplot for each of the unique groups. In other words, if type is a vector, all the individual components are honoured concurrently. If distribute.type = TRUE, type is replicated to be as long as the number of unique values in groups, and one component used for the points corresponding to each different group. Even in this case, it is possible to request multiple types per group, specifying type as a list, each component being the desired type vector for the corresponding group.

If distribute.type = FALSE, any occurrence of "g" in type causes a grid to be drawn, and all such occurrences are removed before type is passed on to panel.groups.

grid Logical flag specifying whether a background reference grid should be drawn. See panel.xyplot for details.

col A vector color specification. See Details.

col.line A vector color specification. See Details.

col.symbol A vector color specification. See Details.

pch A vector plotting character specification. See Details.

cex A vector size factor specification. See Details.

fill A vector fill color specification. See Details.

font, fontface, fontfamily A vector color specification. See Details.

lty A vector color specification. See Details.

lwd A vector color specification. See Details.

alpha A vector alpha-transparency specification. See Details.

... Extra arguments. Passed down to panel.superpose from panel.superpose.2, and to panel.groups from panel.superpose.

distribute.type logical controlling interpretation of the type argument.

Details

panel.superpose divides up the x (and optionally y) variable(s) by the unique values of groups[subscripts], and plots each subset with different graphical parameters. The graphical parameters (col.symbol, pch, etc.) are usually supplied as suitable atomic vectors, but can also be lists. When panel.groups is called for the i-th level of groups, the corresponding element of each graphical parameter is passed to it. In the list form, the individual components can themselves be vectors.

The actual plot for each subgroup is created by the panel.groups function. With the default panel.groups, the col argument is overridden by col.line and col.symbol for lines and points respectively, which default to the "superpose.line" and "superpose.symbol" settings. However, col will still be supplied as an argument to panel.groups functions that make use of it, with a default of "black". The defaults of other graphical parameters are also taken from the
"superpose.line" and "superpose.symbol" settings as appropriate. The alpha parameter takes it default from the "superpose.line" setting.

panel.superpose and panel.superpose.2 differ essentially in how type is interpreted by default. The default behaviour in panel.superpose is the opposite of that in S, which is the same as that of panel.superpose.2.

panel.superpose.plain is the same as panel.superpose, except that the default settings for the style arguments are the same for all groups and are taken from the default plot style. It is used in xyplot.ts.

Author(s)
Deepayan Sarkar <Deepayan.Sarkar@R-project.org> (panel.superpose.2 originally contributed by Neil Klepeis)

See Also
Different functions when used as panel.groups gives different types of plots, for example panel.xyplot, panel.dotplot and panel.average (This can be used to produce interaction plots).

See Lattice for an overview of the package, and xyplot for common arguments (in particular, the discussion of the extended formula interface and the groups argument).

---

Panel Function to create Violin Plots

Description
This is a panel function that can create a violin plot. It is typically used in a high-level call to bwplot.

Usage

```r
panel.violin(x, y, box.ratio = 1, box.width,
horizontal = TRUE,
alpha, border, lty, lwd, col,
varwidth = FALSE,
bw, adjust, kernel, window,
width, n = 50, from, to, cut,
na.rm, ..., 
identifier = "violin")
```

Arguments

- **x, y** numeric vector or factor. Violin plots are drawn for each unique value of y (x) if horizontal is TRUE (FALSE)
- **box.ratio** ratio of the thickness of each violin and inter violin space
- **box.width** thickness of the violins in absolute units; overrides box.ratio. Useful for specifying thickness when the categorical variable is not a factor, as use of box.ratio alone cannot achieve a thickness greater than 1.
horizontal logical. If FALSE, the plot is 'transposed' in the sense that the behaviours of \( x \) and \( y \) are switched. \( x \) is now the 'factor'. See documentation of \texttt{bwplot} for a fuller explanation.

alpha, border, lty, lwd, col

graphical parameters controlling the violin. Defaults are taken from the "plot.polygon" settings.

varwidth logical. If FALSE, the densities are scaled separately for each group, so that the maximum value of the density reaches the limit of the allocated space for each violin (as determined by box.ratio). If TRUE, densities across violins will have comparable scale.

bw, adjust, kernel, window, width, n, from, to, cut, na.rm

arguments to \texttt{density}, passed on as appropriate

... arguments passed on to \texttt{density}.

identifier A character string that is prepended to the names of grobs that are created by this panel function.

Details

Creates Violin plot of \( x \) for every level of \( y \). Note that most arguments controlling the display can be supplied to the high-level (typically \texttt{bwplot}) call directly.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

\texttt{bwplot}, \texttt{density}

Examples

```r
bwplot(voice.part ~ height, singer,
panel = function(..., box.ratio) {
  panel.violin(..., col = "transparent",
    varwidth = FALSE, box.ratio = box.ratio)
  panel.bwplot(..., fill = NULL, box.ratio = .1)
})
```

Default Prepanel Functions

These prepanel functions are used as fallback defaults in various high level plot functions in Lattice. These are rarely useful to normal users but may be helpful in developing new displays.
Usage

prepanel.default.bwplot(x, y, horizontal, nlevels, origin, stack, ...)
prepanel.default.histogram(x, breaks, equal.widths, type, nint, ...)
prepanel.default.qq(x, y, ...)
prepanel.default.xyplot(x, y, type, subscripts, groups, ...)
prepanel.default.cloud(perspective, distance,
  xlim, ylim, zlim,
  screen = list(z = 40, x = -60),
  R.mat = diag(4),
  aspect = c(1, 1), panel.aspect = 1,
  ..., zoom = 0.8)
prepanel.default.levelplot(x, y, subscripts, ...)
prepanel.default.qqmath(x, f.value, distribution, qtype,
  groups, subscripts, ..., tails.n = 0)
prepanel.default.densityplot(x, darg, groups, weights, subscripts, ...)
prepanel.default.parallel(x, y, z, ..., horizontal.axis)
prepanel.default.splom(z, ...)

Arguments

x, y x and y values, numeric or factor
horizontal logical, applicable when one of the variables is to be treated as categorical (factor or shingle).
horizontal.axis logical indicating whether the parallel axes should be laid out horizontally (TRUE) or vertically (FALSE).
nlevels number of levels of such a categorical variable.
origin, stack for barcharts or the type="h" plot type
breaks, equal.widths, type, nint details of histogram calculations. type has a different meaning in prepanel.default.xyplot (see panel.xyplot)
groups, subscripts See xyplot. Whenever appropriate, calculations are done separately for each group and then combined.
weights numeric vector of weights for the density calculations. If this is specified, it is subsetted by subscripts to match it to x.
perspective, distance, xlim, ylim, zlim, screen, R.mat, aspect, panel.aspect, zoom see panel.cloud
f.value, distribution, tails.n see panel.qqmath
darg list of arguments passed to density
z see panel.parallel and panel.pairs
qtype type of quantile
... other arguments, usually ignored

Value

A list with components xlim, ylim, dx and dy, and possibly xat and yat, the first two being used to calculate panel axes limits, the last two for banking computations. The form of these components are described in the help page for xyplot.
Useful Prepanel Function for Lattice

These are predefined prepanel functions available in Lattice.

Usage

prepanel.lmline(x, y, ...)
prepanel.qqmathline(x, y = x, distribution = qnorm,
probs = c(0.25, 0.75), qtype = 7,
groups, subscripts,
...)
prepanel.loess(x, y, span, degree, family, evaluation,
horizontal = FALSE, ...)
prepanel.spline(x, y, npoints = 101,
horizontal = FALSE, ..., keep.data = FALSE)

Arguments

x, y  
x and y values, numeric or factor

distribution  
quantile function for theoretical distribution. This is automatically passed in
when this is used as a prepanel function in qqmath.

qtype  
type of quantile

probs  
numeric vector of length two, representing probabilities. If used with
aspect="xy", the aspect ratio will be chosen to make the line passing through
the corresponding quantile pairs as close to 45 degrees as possible.

span, degree, family, evaluation  
Arguments controlling the underlying loess smooth.

horizontal, npoints  
Arguments for corresponding panel function.

keep.data  
Ignored. Present to capture argument of the same name in smooth.spline.

groups, subscripts  
See xyplot. Whenever appropriate, calculations are done separately for each
group and then combined.

...  
Other arguments. These are passed on to other functions if appropriate (in par-
ticular, smooth.spline), and ignored otherwise.
Details

All these prepanel functions compute the limits to be large enough to contain all points as well as the relevant smooth.

In addition, prepanel.lmline computes the dx and dy such that it reflects the slope of the linear regression line; for prepanel.qqmathline, this is the slope of the line passing through the quantile pairs specified by probs. For prepanel.loess and prepanel.spline, dx and dy reflect the piecewise slopes of the nonlinear smooth.

Value

usually a list with components xlim, ylim, dx and dy, the first two being used to calculate panel axes limits, the last two for banking computations. The form of these components are described under xyplot. There are also several prepanel functions that serve as the default for high level functions, see prepanel.default.xyplot

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot, banking, panel.loess, panel.spline.
Arguments

lim the range of the data in that packet (data subset corresponding to a combination of levels of the conditioning variable). The range is not necessarily numeric; e.g. for factors, they could be character vectors representing levels, and for the various date-time representations, they could be vectors of length 2 with the corresponding class.

packet.number which packet (counted according to the packet order, described in print.trellis) is being processed. In cases where all panels have the same limits, this function is called only once (rather than once for each packet), in which case this argument will have the value 0.

packet.list list, as long as the number of packets, giving all the actual packets. Specifically, each component is the list of arguments given to the panel function when and if that packet is drawn in a panel. (This has not yet been implemented.)

top, right the value of the top and right components of the result, as appropriate. See below for interpretation.

side on which side the axis is to be drawn. The usual partial matching rules apply.

scales the appropriate component of the scales argument supplied to the high level function, suitably standardized.

components list, similar to those produced by xscale.components.default and yscale.components.default.

as.table the as.table argument in the high level function.

labels whether labels are to be drawn. By default, the rules determined by scales are used.

ticks whether labels are to be drawn. By default, the rules determined by scales are used.

... many other arguments may be supplied, and are passed on to other internal functions.

prefix A character string identifying the plot being drawn (see print.trellis). Used to retrieve location of current panel in the overall layout, so that axes can be drawn appropriately.

Details

These functions are part of a new API introduced in lattice 0.14 to provide the user more control over how axis annotation is done. While the API has been designed in anticipation of use that was previously unsupported, the implementation has initially focused on reproducing existing capabilities, rather than test new features. At the time of writing, several features are unimplemented. If you require them, please contact the maintainer.

Value

xscale.components.default and yscale.components.default return a list of the form suitable as the components argument of axis.default. Valid components in the return value of xscale.components.default are:

num.limit A numeric limit for the box.
bottom A list with two elements, ticks and labels. ticks must be a list with components at and tck which give the location and lengths of tick marks. tck can be a vector, and will be recycled to be as long as at. labels must be a list with components at, labels, and check overlap. at and labels give the location and labels of the tick labels; this is usually the same as the location of the ticks, but is not required to be so. check overlap is a logical flag indicating whether overlapping of labels should be avoided by omitting some of the labels while rendering.

top This can be a logical flag; if TRUE, top is treated as being the same as bottom; if FALSE, axis annotation for the top axis is omitted. Alternatively, top can be a list like bottom.

Valid components in the return value of yscale.components.default are left and right. Their interpretations are analogous to (respectively) the bottom and top components described above.

Author(s)
Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also
Lattice, xyplot, print.trellis

Examples
str(xscale.components.default(c(0, 1)))

set.seed(36872)
rln <- rlnorm(100)
densityplot(rln, scales = list(x = list(log = 2), alternating = 3),
  xlab = "Simulated lognormal variates",
  xscale.components = function(...) {
    ans <- xscale.components.default(...)   
    ans$top <- ans$bottom
    ans$bottom$labels$labels <- parse(text = ans$bottom$labels$labels)
    ans$top$labels$labels <-
      if (require(MASS))
        fractions(2^(ans$top$labels$at))
      else
        2^(ans$top$labels$at)
    ans
  })

## Direct use of axis to show two temperature scales (Celcius and
## Fahrenheit). This does not work for multi-row plots, and doesn't
## do automatic allocation of space

F2C <- function(f) 5 * (f - 32) / 9
C2F <- function(c) 32 + 9 * c / 5

axis.CF <-
  function(side, ...)
{   
  ylim <- current.panel.limits()$ylim
  }
switch(side, 
  left = {
    prettyF <- pretty(ylim) 
    labF <- parse(text = sprintf("%s ~ degree * F", prettyF)) 
    panel.axis(side = side, outside = TRUE, 
               at = prettyF, labels = labF) 
  }, 
  right = {
    prettyC <- pretty(F2C(ylim)) 
    labC <- parse(text = sprintf("%s ~ degree * C", prettyC)) 
    panel.axis(side = side, outside = TRUE, 
               at = C2F(prettyC), labels = labC) 
  }, 
  axis.default(side = side, ...)) 

xyplot(nhtemp ~ time(nhtemp), aspect = "xy", type = "o", 
       scales = list(y = list(alternating = 3)), 
       axis = axis.CF, xlab = "Year", ylab = "Temperature", 
       main = "Yearly temperature in New Haven, CT") 

## version using yscale.components 

yscale.components.CF <- 
  function(...) 
  { 
    ans <- yscale.components.default(...) 
    ans$right <- ans$left 
    ans$left$labels$labels <- 
      parse(text = sprintf("%s ~ degree * F", ans$left$labels$at)) 
    prettyC <- pretty(F2C(ans$num.limit)) 
    ans$right$ticks$at <- C2F(prettyC) 
    ans$right$labels$at <- C2F(prettyC) 
    ans$right$labels$labels <- 
      parse(text = sprintf("%s ~ degree * C", prettyC)) 
    ans 
  } 

xyplot(nhtemp ~ time(nhtemp), aspect = "xy", type = "o", 
       scales = list(y = list(alternating = 3)), 
       yscale.components = yscale.components.CF, 
       xlab = "Year", ylab = "Temperature", 
       main = "Yearly temperature in New Haven, CT") 

---

**G_banking**  

**Banking**

**Description**

Calculates banking slope
Usage

banking(dx, dy)

Arguments

dx, dy    vector of consecutive x, y differences.

Details

banking is the banking function used when aspect = "xy" in high level Trellis functions. It is usually not very meaningful except with xyplot. It considers the absolute slopes (based on dx and dy) and returns a value which when adjusted by the panel scale limits will make the median of the above absolute slopes correspond to a 45 degree line.

This function was inspired by the discussion of banking in the documentation for Trellis Graphics available at Bell Labs’ website (see Lattice), but is most likely identical to an algorithm described by Cleveland et al (see below). It is not clear (to the author) whether this is the algorithm used in S-PLUS. Alternative banking rules, implemented as a similar function, can be used as a drop-in replacement by suitably modifying lattice.options("banking").

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

References


See Also

Lattice, xyplot

Examples

## with and without banking

plot <- xyplot(sunspot.year ~ 1700:1988, xlab = "", type = "l", scales = list(x = list(alternating = 2)), main = "Yearly Sunspots")
print(plot, position = c(0, .3, 1, .9), more = TRUE)
print(update(plot, aspect = "xy", main = "", xlab = "Year"),
  position = c(0, 0, 1, .3))

## cut-and-stack plot (see also xyplot.ts)

xyplot(sunspot.year ~ time(sunspot.year) | equal.count(time(sunspot.year)), xlab = "", type = "l", aspect = "xy", strip = FALSE,
  scales = list(x = list(alternating = 2, relation = "sliced")), as.table = TRUE, main = "Yearly Sunspots")
Description

this function is used by high level Lattice functions like `xyplot` to parse the formula argument and evaluate various components of the data.

Usage

```r
latticeParseFormula(model, data, dimension = 2, 
subset = TRUE, groups = NULL, 
multiple, outer, 
subscripts, 
drop)
```

Arguments

- `model`: the model/formula to be parsed. This can be in either of two possible forms, one for 2d and one for 3d formulas, determined by the `dimension` argument. The 2d formulas are of the form `y ~ x| g1*...*gn`, and the 3d formulas are of the form `z ~ x * y | g1*...*gn`. In the first form, `y` may be omitted. The conditioning variables `g1, ..., gn` can be omitted in either case.
- `data`: the environment/dataset where the variables in the formula are evaluated.
- `dimension`: dimension of the model, see above
- `subset`: index for choosing a subset of the data frame
- `groups`: the grouping variable, if present
- `multiple, outer`: logicals, determining how a `+` in the `y` and `x` components of the formula are processed. See `xyplot` for details
- `subscripts`: logical, whether subscripts are to be calculated
- `drop`: logical or list, similar to the `drop.unused.levels` argument in `xyplot`, indicating whether unused levels of conditioning factors and data variables that are factors are to be dropped.

Value

returns a list with several components, including `left`, `right`, `left.name`, `right.name`, `condition` for 2-D, and `left`, `right.x`, `right.y`, `left.name`, `right.x.name`, `right.y.name`, `condition` for 3-D. Other possible components are `groups`, `subscr`

Author(s)

Saikat DebRoy, Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

`xyplot`, `Lattice`
Associating Packets with Panels

Description

When a "trellis" object is plotted, panels are always drawn in an order such that columns vary the fastest, then rows and then pages. An optional function can be specified that determines, given the column, row and page and other relevant information, the packet (if any) which should be used in that panel. The function documented here implements the default behaviour, which is to match panel order with packet order, determined by varying the first conditioning variable the fastest, then the second, and so on. This matching is performed after any reordering and/or permutation of the conditioning variables.

Usage

packet.panel.default(layout, condlevels, page, row, column,
  skip, all.pages.skip = TRUE)

Arguments

layout the layout argument in high level functions, suitably standardized.
condlevels a list of levels of conditioning variables, after relevant permutations and/or reordering of levels
page, row, column the location of the panel in the coordinate system of pages, rows and columns.
skip the skip argument in high level functions
all.pages.skip whether skip should be replicated over all pages. If FALSE, skip will be replicated to be only as long as the number of positions on a page, and that template will be used for all pages.

Value

A suitable combination of levels of the conditioning variables in the form of a numeric vector as long as the number of conditioning variables, with each element an integer indexing the levels of the corresponding variable. Specifically, if the return value is p, then the i-th conditioning variable will have level condlevels[[i]][p[i]].

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot
Examples

```r
data(mtcars)
HP <- equal.count(mtcars$hp, 6)

# Define a function to print page number
packet.panel.page <- function(n)
{
  ## returns a function that when used as the 'packet.panel'
  ## argument in print.trellis plots page number 'n' only
  function(layout, page, ...) {
    stopifnot(layout[3] == 1)
    packet.panel.default(layout = layout, page = n, ...)
  }
}

p <- xyplot(mpg ~ disp | HP * factor(cyl),
            mtcars, layout = c(0, 6, 1))

print(p, packet.panel = packet.panel.page(1))  # Print page 1
print(p, packet.panel = packet.panel.page(2))  # Print page 2
```

G_panel.axis

Panel Function for Drawing Axis Ticks and Labels

Description

panel.axis is the function used by lattice to draw axes. It is typically not used by users, except those wishing to create advanced annotation. Keep in mind issues of clipping when trying to use it as part of the panel function. current.panel.limits can be used to retrieve a panel’s x and y limits.

Usage

```r
panel.axis(side = c("bottom", "left", "top", "right"),
at, labels = TRUE,
draw.labels = TRUE,
check.overlap = FALSE,
outside = FALSE,
ticks = TRUE,
half = !outside,
which.half,
tck = as.numeric(ticks),
rot = if (is.logical(labels)) 0 else c(90, 0),
text.col, text.alpha, text.cex, text.font, 
text.fontfamily, text.fontface, text.lineheight, 
line.col, line.lty, line.lwd, line.alpha)
```

current.panel.limits(unit = "native")
Arguments

- **side**: A character string indicating which side axes are to be drawn on. Partial specification is allowed.
- **at**: Numeric vector giving location of labels. Can be missing, in which case they are computed from the native coordinates of the active viewport.
- **labels**: The labels to go along with at, as a character vector or a vector of expressions. This only makes sense provided at is explicitly specified, as otherwise the provided labels may not match the computed at values. Alternatively, labels can be a logical flag: If TRUE, the labels are derived from at, otherwise, labels are empty.
- **draw.labels**: A logical indicating whether labels are to be drawn.
- **check.overlap**: A logical, whether to check for overlapping of labels. This also has the effect of removing at values that are ‘too close’ to the limits.
- **outside**: A logical flag, indicating whether to draw the labels outside the panel or inside. Note that outside=TRUE will only have a visible effect if clipping is disabled for the viewport (panel).
- **ticks**: Logical flag, whether to draw the tickmarks.
- **half**: Logical flag, indicating whether only around half the scales will be drawn for each side. This is primarily used for axis labeling in splom.
- **which.half**: Character string, either "lower" or "upper", indicating which half is to be used for tick locations if half = TRUE. Defaults to whichever is suitable for splom.
- **tck**: A numeric scalar multiplier for tick length. Can be negative, in which case the ticks point inwards.
- **rot**: Rotation angle(s) for labels in degrees. Can be a vector of length 2 for x- and y-axes.
- **text.col**: Color for the axis label text. See gpar for more details on this and the other graphical parameters listed below.
- **text.alpha**: Alpha-transparency value for the axis label text.
- **text.cex**: Size multiplier for the axis label text.
- **text.font, text.fontfamily, text.fontface**: Font for the axis label text.
- **text.lineheight**: Line height for the axis label text.
- **line.col**: Color for the axis label text.
- **line.lty**: Color for the axis.
- **line.lwd**: Color for the axis.
- **line.alpha**: Alpha-transparency value for the axis.
- **unit**: Which grid unit the values should be in.

Details

Panel.axis can draw axis tick marks inside or outside a panel (more precisely, a grid viewport). It honours the (native) axis scales. Used in panel.pairs for splom, as well as for all the usual axis drawing by the print method for "trellis" objects. It can also be used to enhance plots 'after the fact' by adding axes.
Value

current.panel.limits returns a list with components xlim and ylim, which are both numeric vectors of length 2, giving the scales of the current panel (viewport). The values correspond to the unit system specified by unit, by default "native".

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot, trellis.focus, unit

G_panel.number

Accessing Auxiliary Information During Plotting

Description

Control over lattice plots are provided through a collection of user specifiable functions that perform various tasks during the plotting. Not all information is available to all functions. The functions documented here attempt to provide a consistent interface to access relevant information from within these user specified functions, namely those specified as the panel, strip and axis functions. Note that this information is not available to the prepanel function, which is executed prior to the actual plotting.

Usage

current.row(prefix)
current.column(prefix)
panel.number(prefix)
packet.number(prefix)
which.packet(prefix)
trellis.currentLayout(which = c("packet", "panel"), prefix)

Arguments

which whether return value (a matrix) should contain panel numbers or packet numbers, which are usually, but not necessarily, the same (see below for details).

prefix A character string acting as a prefix identifying the plot of a "trellis" object. Only relevant when a particular page is occupied by more than one plot. Defaults to the value appropriate for the last "trellis" object printed. See trellis.focus.
Value

trellis.currentLayout returns a matrix with as many rows and columns as in the layout of panels in the current plot. Entries in the matrix are integer indices indicating which packet (or panel; see below) occupies that position, with 0 indicating the absence of a panel. current.row and current.column return integer indices specifying which row and column in the layout are currently active. panel.number returns an integer counting which panel is being drawn (starting from 1 for the first panel, a.k.a. the panel order). packet.number gives the packet number according to the packet order, which is determined by varying the first conditioning variable the fastest, then the second, and so on. which.packet returns the combination of levels of the conditioning variables in the form of a numeric vector as long as the number of conditioning variables, with each element an integer indexing the levels of the corresponding variable.

Note

The availability of these functions make redundant some features available in earlier versions of lattice, namely optional arguments called panel.number and packet.number that were made available to panel and strip. If you have written such functions, it should be enough to replace instances of panel.number and packet.number by the corresponding function calls. You should also remove panel.number and packet.number from the argument list of your function to avoid a warning.

If these accessor functions are not enough for your needs, feel free to contact the maintainer and ask for more.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

Lattice, xyplot

---

G_Rows

Extract rows from a list

Description

Convenience function to extract subset of a list. Usually used in creating keys.

Usage

Rows(x, which)

Arguments

x          list with each member a vector of the same length
which      index for members of x

Value

A list similar to x, with each x[[i]] replaced by x[[i]][which]
Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

See Also

xyplot, Lattice

---

**G_utilities.3d**

**Utility functions for 3-D plots**

**Description**

These are (related to) the default panel functions for cloud and wireframe.

**Usage**

```r
ltransform3dMatrix(screen, R.mat)
ltransform3dto3d(x, R.mat, dist)
```

**Arguments**

- `x`: `x` can be a numeric matrix with 3 rows for `ltransform3dto3d`
- `screen`: list, as described in `panel.cloud`
- `R.mat`: 4x4 transformation matrix in homogeneous coordinates
- `dist`: controls transformation to account for perspective viewing

**Details**

`ltransform3dMatrix` and `ltransform3dto3d` are utility functions to help in computation of projections. These functions are used inside the panel functions for cloud and wireframe. They may be useful in user-defined panel functions as well.

The first function takes a list of the form of the `screen` argument in cloud and wireframe and a `R.mat`, a 4x4 transformation matrix in homogeneous coordinates, to return a new 4x4 transformation matrix that is the result of applying `R.mat` followed by the rotations in `screen`. The second function applies a 4x4 transformation matrix in homogeneous coordinates to a 3xn matrix representing points in 3-D space, and optionally does some perspective computations. (There has been no testing with non-trivial transformation matrices, and my knowledge of the homogeneous coordinate system is very limited, so there may be bugs here.)

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

cloud, panel.cloud
Yield data from a Minnesota barley trial

Description

Total yield in bushels per acre for 10 varieties at 6 sites in each of two years.

Usage

barley

Format

A data frame with 120 observations on the following 4 variables.

- **yield**: Yield (averaged across three blocks) in bushels/acre.
- **year**: Factor with levels 1932, 1931
- **site**: Factor with 6 levels: "Grand Rapids", "Duluth", "University Farm", "Morris", "Crookston", "Waseca"

Details

These data are yields in bushels per acre, of 10 varieties of barley grown in 1/40 acre plots at University Farm, St. Paul, and at the five branch experiment stations located at Waseca, Morris, Crookston, Grand Rapids, and Duluth (all in Minnesota). The varieties were grown in three randomized blocks at each of the six stations during 1931 and 1932, different land being used each year of the test.

Immer et al. (1934) present the data for each Year*Site*Variety*Block. The data here is the average yield across the three blocks.

Immer et al. (1934) refer (once) to the experiment as being conducted in 1930 and 1931, then later refer to it (repeatedly) as being conducted in 1931 and 1932. Later authors have continued the confusion.

Cleveland (1993) suggests that the data for the Morris site may have had the years switched.

Author(s)

Documentation contributed by Kevin Wright.

Source


References


**H_environmental**

**See Also**

`immer` in the MASS package for data from the same experiment (expressed as total yield for 3 blocks) for a subset of varieties.

**Examples**

```r
# Graphic suggesting the Morris data switched the years 1931 and 1932
# Figure 1.1 from Cleveland
dotplot(variety ~ yield | site, data = barley, groups = year,
    key = simpleKey(levels(barley$year), space = "right"),
    xlab = "Barley Yield (bushels/acre) ",
    aspect=0.5, layout = c(1,6), ylab=NULL)
```

---

**Description**


**Usage**

`environmental`

**Format**

A data frame with 111 observations on the following 4 variables.

- **ozone** Average ozone concentration (of hourly measurements) of in parts per billion.
- **radiation** Solar radiation (from 08:00 to 12:00) in langleys.
- **temperature** Maximum daily emperature in degrees Fahrenheit.
- **wind** Average wind speed (at 07:00 and 10:00) in miles per hour.

**Author(s)**

Documentation contributed by Kevin Wright.

**Source**


**References**

Examples

# Scatter plot matrix with loess lines
splom(~environmental,
    panel=function(x,y){
    panel.xyplot(x,y)
    panel.loess(x,y)
    }
)

# Conditioned plot similar to figure 5.3 from Cleveland
attach(environmental)
Temperature <- equal.count(temperature, 4, 1/2)
Wind <- equal.count(wind, 4, 1/2)
xyplot((ozone^(1/3)) ~ radiation | Temperature * Wind, aspect=1,
    prepanel = function(x, y)
    prepanel.loess(x, y, span = 1),
    panel = function(x, y)(
    panel.grid(h = 2, v = 2)
    panel.xyplot(x, y, cex = .5)
    panel.loess(x, y, span = 1)
    ),
    xlab = "Solar radiation (langleys)",
    ylab = "Ozone (cube root ppb)"
    detach()

    # Similar display using the coplot function
with(environmental,{
    coplot((ozone^.33) ~ radiation | temperature * wind, number=c(4,4),
    panel = function(x, y, ...) panel.smooth(x, y, span = .8, ...),
    xlab="Solar radiation (langleys)",
    ylab="Ozone (cube root ppb)"
})

H_ethanol

Engine exhaust fumes from burning ethanol

Description

Ethanol fuel was burned in a single-cylinder engine. For various settings of the engine compression and equivalence ratio, the emissions of nitrogen oxides were recorded.

Usage

ethanol

Format

A data frame with 88 observations on the following 3 variables.

NOx  Concentration of nitrogen oxides (NO and NO2) in micrograms/J.
C    Compression ratio of the engine.
E    Equivalence ratio--a measure of the richness of the air and ethanol fuel mixture.
Author(s)

Documentation contributed by Kevin Wright.

Source


References


Examples

```r
## Constructing panel functions on the fly
EE <- equal.count(ethanol$E, number=9, overlap=1/4)
xyplot(NOx ~ C | EE, data = ethanol,
     prepanel = function(x, y) prepanel.loess(x, y, span = 1),
     xlab = "Compression ratio", ylab = "NOx (micrograms/J)",
     panel = function(x, y) {
       panel.grid(h=-1, v= 2)
       panel.xyplot(x, y, grid = FALSE)
       panel.loess(x, y, span = 1)
     },
     aspect = "xy")

# Wireframe loess surface fit. See Figure 4.61 from Cleveland.
require(stats)
with(ethanol, {
  eth.lo <- loess(NOx ~ C * E, span = 1/3, parametric = "C",
                  drop.square = "C", family="symmetric")
  eth.marginal <- list(C = seq(min(C), max(C), length.out = 25),
                        E = seq(min(E), max(E), length.out = 25))
  eth.grid <- expand.grid(eth.marginal)
  eth.fit <- predict(eth.lo, eth.grid)
  wireframe(eth.fit ~ eth.grid$C * eth.grid$E,
            shade=TRUE,
            screen = list(z = 40, x = -60, y=0),
            distance = .1,
            xlab = "C", ylab = "E", zlab = "NOx")
})
```

---

**H_melanoma**

*Melanoma skin cancer incidence*

Description

These data from the Connecticut Tumor Registry present age-adjusted numbers of melanoma skin-cancer incidences per 100,000 people in Connecticut for the years from 1936 to 1972.

Usage

melanoma
### Format

A data frame with 37 observations on the following 2 variables.

- **year**  Years 1936 to 1972.
- **incidence** Rate of melanoma cancer per 100,000 population.

### Note

This dataset is not related to the `melanoma` dataset in the `boot` package with the same name. The S-PLUS 6.2 help for the melanoma data says that the incidence rate is per million, but this is not consistent with data found at the National Cancer Institute (https://www.cancer.gov/).

### Author(s)

Documentation contributed by Kevin Wright.

### Source


### References


### Examples

```r
# Time-series plot. Figure 3.64 from Cleveland.
xyplot(incidence ~ year,
data = melanoma,
aspect = "xy",
panel = function(x, y)
panel.xyplot(x, y, type="o", pch = 16),
ylim = c(0, 6),
xlab = "Year",
ylab = "Incidence")
```

---

### H_singer

*Heights of New York Choral Society singers*

### Description

Heights in inches of the singers in the New York Choral Society in 1979. The data are grouped according to voice part. The vocal range for each voice part increases in pitch according to the following order: Bass 2, Bass 1, Tenor 2, Tenor 1, Alto 2, Alto 1, Soprano 2, Soprano 1.

### Usage

`singer`
Format

A data frame with 235 observations on the following 2 variables.

**height** Height in inches of the singers.

**voice.part** (Unordered) factor with levels "Bass 2", "Bass 1", "Tenor 2", "Tenor 1", "Alto 2", "Alto 1", "Soprano 2", "Soprano 1".

Author(s)

Documentation contributed by Kevin Wright.

Source


References


Examples

```r
# Separate histogram for each voice part (Figure 1.2 from Cleveland)
histogram(~ height | voice.part,
data = singer,
aspect = 1,
layout = c(2, 4),
nint = 15,
xlab = "Height (inches)"
)

# Quantile-Quantile plot (Figure 2.11 from Cleveland)
qqmath(~ height | voice.part,
data = singer,
aspect = 1,
layout = c(2,4),
prepanel = prepanel.qqmathline,
panel = function(x, ...) {
  panel.grid()
  panel.qqmathline(x, ...)
  panel.qqmath(x, ..., grid = FALSE)
},
xlab = "Unit Normal Quantile",
ylab="Height (inches)"
)
```

H_USMortality  

**Mortality Rates in US by Cause and Gender**

Description

These datasets record mortality rates across all ages in the USA by cause of death, sex, and rural/urban status, 2011–2013. The two datasets represent the national aggregate rates and the region-wise rates for each administrative region under the Department of Health and Human Services (HHS).
Usage

USMortality
USRegionalMortality

Format

USRegionalMortality is a data frame with 400 observations on the following 6 variables.

Region  A factor specifying HHS Region. See details.
Status  A factor with levels Rural and Urban
Sex    A factor with levels Female and Male
Cause  Cause of death. A factor with levels Alzheimers, Cancer, Cerebrovascular diseases, Diabetes, Flu and pneumonia, Heart disease, Lower respiratory, Nephritis, Suicide, and Unintentional injuries
Rate   Age-adjusted death rate per 100,000 population
SE     Standard error for the rate

USMortality is a data frame with 40 observations, containing the same variables with the exception of Region.

Details

The region-wise data give estimated rates separately for each of 10 HHS regions. The location of the regional offices and their coverage area, available from https://www.hhs.gov/about/agencies/iea/regional-offices/index.html, is given below.

HHS Region 01 - Boston:  Connecticut, Maine, Massachusetts, New Hampshire, Rhode Island, and Vermont
HHS Region 02 - New York:  New Jersey, New York, Puerto Rico, and the Virgin Islands
HHS Region 03 - Philadelphia:  Delaware, District of Columbia, Maryland, Pennsylvania, Virginia, and West Virginia
HHS Region 04 - Atlanta:  Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, and Tennessee
HHS Region 05 - Chicago:  Illinois, Indiana, Michigan, Minnesota, Ohio, and Wisconsin
HHS Region 06 - Dallas:  Arkansas, Louisiana, New Mexico, Oklahoma, and Texas
HHS Region 07 - Kansas City:  Iowa, Kansas, Missouri, and Nebraska
HHS Region 08 - Denver:  Colorado, Montana, North Dakota, South Dakota, Utah, and Wyoming
HHS Region 09 - San Francisco:  Arizona, California, Hawaii, Nevada, American Samoa, Commonwealth of the Northern Mariana Islands, Federated States of Micronesia, Guam, Marshall Islands, and Republic of Palau
HHS Region 10 - Seattle:  Alaska, Idaho, Oregon, and Washington

References

Examples

```r
dotplot(reorder(Cause, Rate) ~ Rate | Status,
    data = USMortality, groups = Sex, grid = FALSE,
    par.settings = simpleTheme(pch = 16), auto.key = list(columns = 2),
    scales = list(x = list(log = TRUE, equispaced.log = FALSE)))
dotplot(reorder(Cause, Rate):Sex ~ Rate | Status,
    data = USRegionalMortality, groups = Sex, auto.key = FALSE,
    scales = list(x = list(log = TRUE, equispaced.log = FALSE)))
```

Description

A (hopefully) simpler alternative to `trellis.par.get/set`. This is deprecated, and the same functionality is now available with `trellis.par.set`

Usage

```r
lset(theme = col.whitebg())
```

Arguments

- **theme**
  
  A list describing how to change the settings of the current active device. Valid components are those in the list returned by `trellis.par.get()`. Each component must itself be a list, with one or more of the appropriate components (need not have all components). Changes are made to the settings for the currently active device only.

Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>
Chapter 24

The mgcv package

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**anova.gam**

*Approximate hypothesis tests related to GAM fits*

**Description**

Performs hypothesis tests relating to one or more fitted gam objects. For a single fitted gam object, Wald tests of the significance of each parametric and smooth term are performed, so interpretation is analogous to `drop1` rather than `anova.lm` (i.e. it’s like type III ANOVA, rather than a sequential type I ANOVA). Otherwise the fitted models are compared using an analysis of deviance table or GLRT test: this latter approach should not be used to test the significance of terms which can be penalized to zero. Models to be compared should be fitted to the same data using the same smoothing parameter selection method.

**Usage**

```r
## S3 method for class 'gam'
anova(object, ..., dispersion = NULL, test = NULL,
      freq = FALSE)
## S3 method for class 'anova.gam'
print(x, digits = max(3, getOption("digits") - 3),...)
```

**Arguments**

- `object,...`  
  fitted model objects of class gam as produced by `gam()`.
- `x`  
  an anova.gam object produced by a single model call to `anova.gam()`.
- `dispersion`  
  a value for the dispersion parameter: not normally used.
- `test`  
  what sort of test to perform for a multi-model call. One of "Chisq", "F" or "Cp". Reset to "Chisq" for extended and general families unless NULL.
- `freq`  
  whether to use frequentist or Bayesian approximations for parametric term p-values. See `summary.gam` for details.
- `digits`  
  number of digits to use when printing output.

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Details

If more than one fitted model is provided than `anova.glm` is used, with the difference in model degrees of freedom being taken as the difference in effective degrees of freedom (when possible this is a smoothing parameter uncertainty corrected version). For extended and general families this is set so that a GLRT test is used. The p-values resulting from the multi-model case are only approximate, and must be used with care. The approximation is most accurate when the comparison relates to unpenalized terms, or smoothers with a null space of dimension greater than zero. (Basically we require that the difference terms could be well approximated by unpenalized terms with degrees of freedom approximately the effective degrees of freedom). In simulations the p-values are usually slightly too low. For terms with a zero-dimensional null space (i.e. those which can be penalized to zero) the approximation is often very poor, and significance can be greatly overstated: i.e. p-values are often substantially too low. This case applies to random effect terms.

Note also that in the multi-model call to `anova.gam`, it is quite possible for a model with more terms to end up with lower effective degrees of freedom, but better fit, than the notionally null model with fewer terms. In such cases it is very rare that it makes sense to perform any sort of test, since there is then no basis on which to accept the notionl null model.

If only one model is provided then the significance of each model term is assessed using Wald like tests, conditional on the smoothing parameter estimates: see `summary.gam` and Wood (2013a,b) for details. The p-values provided here are better justified than in the multi model case, and have close to the correct distribution under the null, unless smoothing parameters are poorly identified. ML or REML smoothing parameter selection leads to the best results in simulations as they tend to avoid occasional severe undersmoothing. In replication of the full simulation study of Scheipl et al. (2008) the tests give almost indistinguishable power to the method recommended there, but slightly too low p-values under the null in their section 3.1.8 test for a smooth interaction (the Scheipl et al. recommendation is not used directly, because it only applies in the Gaussian case, and requires model refits, but it is available in package `RLRsim`).

In the single model case `print.anova.gam` is used as the printing method.

By default the p-values for parametric model terms are also based on Wald tests using the Bayesian covariance matrix for the coefficients. This is appropriate when there are "re" terms present, and is otherwise rather similar to the results using the frequentist covariance matrix (`freq=TRUE`), since the parametric terms themselves are usually unpenalized. Default P-values for parametric terms that are penalized using the `paraPen` argument will not be good.

Value

In the multi-model case `anova.gam` produces output identical to `anova.glm`, which it in fact uses.

In the single model case an object of class `anova.gam` is produced, which is in fact an object returned from `summary.gam`.

`print.anova.gam` simply produces tabulated output.

WARNING

If models 'a' and 'b' differ only in terms with no un-penalized components (such as random effects) then p values from `anova(a,b)` are unreliable, and usually much too low.

Default P-values will usually be wrong for parametric terms penalized using ‘paraPen’: use `freq=TRUE` to obtain better p-values when the penalties are full rank and represent conventional random effects.

For a single model, interpretation is similar to `drop1`, not `anova.lm`.
**Author(s)**

Simon N. Wood <simon.wood@r-project.org> with substantial improvements by Henric Nilsson.

**References**


**See Also**

gam, predict.gam, gam.check, summary.gam

**Examples**

```r
library(mgcv)
set.seed(0)
dat <- gamSim(5,n=200,scale=2)

b<-gam(y ~ x0 + s(x1) + s(x2) + s(x3),data=dat)
anova(b)

b1<-gam(y ~ x0 + s(x1) + s(x2),data=dat)
anova(b,b1,test="F")
```

**bam**

*Generalized additive models for very large datasets*

**Description**

Fits a generalized additive model (GAM) to a very large data set, the term ‘GAM’ being taken to include any quadratically penalized GLM (the extended families listed in `family.mgcv` can also be used). The degree of smoothness of model terms is estimated as part of fitting. In use the function is much like `gam`, except that the numerical methods are designed for datasets containing upwards of several tens of thousands of data (see Wood, Goude and Shaw, 2015). The advantage of `bam` is much lower memory footprint than `gam`, but it can also be much faster, for large datasets. `bam` can also compute on a cluster set up by the `parallel` package.

An alternative fitting approach (Wood et al. 2017, Li and Wood, 2019) is provided by the `discrete=TRUE` method. In this case a method based on discretization of covariate values and C code level parallelization (controlled by the `nthreads` argument instead of the `cluster` argument) is used. This extends both the data set and model size that are practical.
Usage

```
bam(formula, family=gaussian(), data=list(), weights=NULL, subset=NULL, na.action=na.omit, offset=NULL, method="fREML", control=list(), select=FALSE, scale=0, gamma=1, knots=NULL, sp=NULL, min.sp=NULL, paraPen=NULL, chunk.size=10000, rho=0, AR.start=NULL, discrete=FALSE, cluster=NULL, nthreads=1, gc.level=0, use.chol=FALSE, samfrac=1, coef=NULL, drop.unused.levels=TRUE, G=NULL, fit=TRUE, drop.intercept=NULL, in.out=NULL, ...)```

Arguments

- **formula**: A GAM formula (see `formula.gam` and also `gam.models`). This is exactly like the formula for a GLM except that smooth terms, s and te can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).

- **family**: This is a family object specifying the distribution and link to use in fitting etc. See `glm` and `family` for more details. The extended families listed in `family.mgcv` can also be used.

- **data**: A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from `environment(formula)`: typically the environment from which `gam` is called.

- **weights**: prior weights on the contribution of the data to the log likelihood. Note that a weight of 2, for example, is equivalent to having made exactly the same observation twice. If you want to reweight the contributions of each datum without changing the overall magnitude of the log likelihood, then you should normalize the weights (e.g. `weights <- weights/mean(weights)`).

- **subset**: an optional vector specifying a subset of observations to be used in the fitting process.

- **na.action**: a function which indicates what should happen when the data contain ‘NA’s. The default is set by the ‘na.action’ setting of ‘options’, and is ‘na.fail’ if that is unset. The “factory-fresh” default is ‘na.omit’.

- **offset**: Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in `formula` (this used to conform to the behaviour of `lm` and `glm`).

- **method**: The smoothing parameter estimation method. “GCV.Cp” to use GCV for unknown scale parameter and Mallows’ Cp/UBRE/AIC for known scale. “GACV.Cp” is equivalent, but using GACV in place of GCV. ”REML" for REML estimation, including of unknown scale, ”P-REML" for REML estimation, but using a Pearson estimate of the scale. ”ML" and ”P-ML” are similar, but using maximum likelihood in place of REML. Default “fREML” uses fast REML computation.

- **control**: A list of fit control parameters to replace defaults returned by `gam.control`. Any control parameters not supplied stay at their default values.

- **select**: Should selection penalties be added to the smooth effects, so that they can in principle be penalized out of the model? See `gamma` to increase penalization. Has the side effect that smooths no longer have a fixed effect component (improper prior from a Bayesian perspective) allowing REML comparison of models with the same fixed effect structure.
scale  If this is positive then it is taken as the known scale parameter. Negative signals that the scale parameter is unknown. 0 signals that the scale parameter is 1 for Poisson and binomial and unknown otherwise. Note that (RE)ML methods can only work with scale parameter 1 for the Poisson and binomial cases.

gamma Increase above 1 to force smoother fits. gamma is used to multiply the effective degrees of freedom in the GCV/UBRE/AIC score (so \(\log(n)/2\) is BIC like). \(n/gamma\) can be viewed as an effective sample size, which allows it to play a similar role for RE/ML smoothing parameter estimation.

knots  this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the k value supplied (note that the number of knots is not always just k). See tprs for what happens in the "tp"/"ts" case. Different terms can use different numbers of knots, unless they share a covariate.

sp  A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then \(\text{length}(\text{sp})\) must correspond to the number of underlying smoothing parameters. Note that \(\text{discrete}=\text{TRUE}\) may result in re-ordering of variables in tensor product smooths for improved efficiency, and \(\text{sp}\) must be supplied in re-ordered order.

min.sp  Lower bounds can be supplied for the smoothing parameters. Note that if this option is used then the smoothing parameters \(\text{full.sp}\), in the returned object, will need to be added to what is supplied here to get the smoothing parameters actually multiplying the penalties. \(\text{length}(<\text{min.sp}\>)\) should always be the same as the total number of penalties (so it may be longer than \(\text{sp}\), if smooths share smoothing parameters).

paraPen  optional list specifying any penalties to be applied to parametric model terms. \(\text{gam.models}\) explains more.

chunk.size  The model matrix is created in chunks of this size, rather than ever being formed whole. Reset to \(4*p\) if \(\text{chunk.size} < 4*p\) where \(p\) is the number of coefficients.

rho  An AR1 error model can be used for the residuals (based on dataframe order), of Gaussian-identity link models. This is the AR1 correlation parameter. Standardized residuals (approximately uncorrelated under correct model) returned in \(\text{std.rsd}\) if non zero. Also usable with other models when \(\text{discrete}=\text{TRUE}\), in which case the AR model is applied to the working residuals and corresponds to a GEE approximation.

AR.start  logical variable of same length as data, \(\text{TRUE}\) at first observation of an independent section of AR1 correlation. Very first observation in data frame does not need this. If \(\text{NULL}\) then there are no breaks in AR1 correlation.

discrete  with method="FREML" it is possible to discretize covariates for storage and efficiency reasons. If \(\text{discrete}\) is \(\text{TRUE}\), a number or a vector of numbers for each smoother term, then discretization happens. If numbers are supplied they give the number of discretization bins. Parametric terms use the maximum number specified.

cluster  \(\text{bam}\) can compute the computationally dominant QR decomposition in parallel using \(\text{parLapply}\) from the \(\text{parallel}\) package, if it is supplied with a cluster on which to do this (a cluster here can be some cores of a single machine). See details and example code.
nthreads  Number of threads to use for non-cluster computation (e.g. combining results from cluster nodes). If NA set to max(1,length(cluster)). See details.

gc.level  to keep the memory footprint down, it can help to call the garbage collector often, but this takes a substantial amount of time. Setting this to zero means that garbage collection only happens when R decides it should. Setting to 2 gives frequent garbage collection. 1 is in between. Not as much of a problem as it used to be.

use.chol  By default bam uses a very stable QR update approach to obtaining the QR decomposition of the model matrix. For well conditioned models an alternative accumulates the crossproduct of the model matrix and then finds its Choleski decomposition, at the end. This is somewhat more efficient, computationally.

samfrac  For very large sample size Generalized additive models the number of iterations needed for the model fit can be reduced by first fitting a model to a random sample of the data, and using the results to supply starting values. This initial fit is run with sloppy convergence tolerances, so is typically very low cost. samfrac is the sampling fraction to use. 0.1 is often reasonable.

coeff  initial values for model coefficients

drop.unused.levels  by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.

G  if not NULL then this should be the object returned by a previous call to bam with fit=FALSE. Causes all other arguments to be ignored except sp, chunk.size, gamma, nthreads, cluster, rho, gc.level, samfrac, use.chol, method and scale (if >0).

fit  if FALSE then the model is set up for fitting but not estimated, and an object is returned, suitable for passing as the G argument to bam.

drop.intercept  Set to TRUE to force the model to really not have the a constant in the parametric model part, even with factor variables present.

in.out  If supplied then this is a two item list of initial values. sp is initial smoothing parameter estimates and scale the initial scale parameter estimate (set to 1 if family does not have one).

...  further arguments for passing on e.g. to gam.fit (such as mustart).

Details

When discrete=FALSE, bam operates by first setting up the basis characteristics for the smooths, using a representative subsample of the data. Then the model matrix is constructed in blocks using predict.gam. For each block the factor R, from the QR decomposition of the whole model matrix is updated, along with Q'y. and the sum of squares of y. At the end of block processing, fitting takes place, without the need to ever form the whole model matrix.

In the generalized case, the same trick is used with the weighted model matrix and weighted pseudodata, at each step of the PIRLS. Smoothness selection is performed on the working model at each stage (performance oriented iteration), to maintain the small memory footprint. This is trivial to justify in the case of GCV or Cp/UBRE/AIC based model selection, and for REML/ML is justified via the asymptotic multivariate normality of Q'z where z is the IRLS pseudodata.

For full method details see Wood, Goude and Shaw (2015).

Note that POI is not as stable as the default nested iteration used with gam, but that for very large, information rich, datasets, this is unlikely to matter much.
Note also that it is possible to spend most of the computational time on basis evaluation, if an expensive basis is used. In practice this means that the default "tp" basis should be avoided: almost any other basis (e.g. "cr" or "ps") can be used in the 1D case, and tensor product smooths (te) are typically much less costly in the multi-dimensional case.

If cluster is provided as a cluster set up using `makeCluster` (or `makeForkCluster`) from the `parallel` package, then the rate limiting QR decomposition of the model matrix is performed in parallel using this cluster. Note that the speed ups are often not that great. On a multi-core machine it is usually best to set the cluster size to the number of physical cores, which is often less than what is reported by `detectCores`. Using more than the number of physical cores can result in no speed up at all (or even a slow down). Note that a highly parallel BLAS may negate all advantage from using a cluster of cores. Computing in parallel of course requires more memory than computing in series. See examples.

When `discrete=TRUE` the covariate data are first discretized. Discretization takes place on a smooth by smooth basis, or in the case of tensor product smooths (or any smooth that can be represented as such, such as random effects), separately for each marginal smooth. The required spline bases are then evaluated at the discrete values, and stored, along with index vectors indicating which original observation they relate to. Fitting is by a version of performance oriented iteration/PQL using REML smoothing parameter selection on each iterative working model (as for the default method). The iteration is based on the derivatives of the REML score, without computing the score itself, allowing the expensive computations to be reduced to one parallel block Cholesky decomposition per iteration (plus two basic operations of equal cost, but easily parallelized). Unlike standard PQL/PQL, only one step of the smoothing parameter update for the working model is taken at each step (rather than iterating to the optimal set of smoothing parameters for each working model). At each step a weighted model matrix crossproduct of the model matrix is required - this is efficiently computed from the pre-computed basis functions evaluated at the discretized covariate values. Efficient computation with tensor product terms means that some terms within a tensor product may be re-ordered for maximum efficiency. See Wood et al (2017) and Li and Wood (2019) for full details.

When `discrete=TRUE` parallel computation is controlled using the `nthreads` argument. For this method no cluster computation is used, and the `parallel` package is not required. Note that actual speed up from parallelization depends on the BLAS installed and your hardware. With the (R default) reference BLAS using several threads can make a substantial difference, but with a single threaded tuned BLAS, such as openblas, the effect is less marked (since cache use is typically optimized for one thread, and is then sub optimal for several). However the tuned BLAS is usually much faster than using the reference BLAS, however many threads you use. If you have a multi-threaded BLAS installed then you should leave `nthreads` at 1, since calling a multi-threaded BLAS from multiple threads usually slows things down: the only exception to this is that you might choose to form discrete matrix cross products (the main cost in the fitting routine) in a multi-threaded way, but use single threaded code for other computations: this can be achieved by e.g. `nthreads=c(2,1)`, which would use 2 threads for discrete inner products, and 1 for most code calling BLAS. Not that the basic reason that multi-threaded performance is often disappointing is that most computers are heavily memory bandwidth limited, not flop rate limited. It is hard to get data to one core fast enough, let alone trying to get data simultaneously to several cores.

discrete=TRUE will often produce identical results to the methods without discretization, since covariates often only take a modest number of discrete values anyway, so no approximation at all is involved in the discretization process. Even when some approximation is involved, the differences are often very small as the algorithms discretize marginally whenever possible. For example each margin of a tensor product smooth is discretized separately, rather than discretizing onto a grid of covariate values (for an equivalent isotropic smooth we would have to discretize onto a grid). The marginal approach allows quite fine scale discretization and hence very low approximation error. Note that when using the smooth id mechanism to link smoothing parameters, the discrete method
cannot force the linked bases to be identical, so some differences to the none discrete methods will be noticeable.

The extended families given in `family.mgcv` can also be used. The extra parameters of these are estimated by maximizing the penalized likelihood, rather than the restricted marginal likelihood as in `gam`. So estimates may differ slightly from those returned by `gam`. Estimation is accomplished by a Newton iteration to find the extra parameters (e.g. the theta parameter of the negative binomial or the degrees of freedom and scale of the scaled t) maximizing the log likelihood given the model coefficients at each iteration of the fitting procedure.

**Value**

An object of class "gam" as described in `gamObject`.

**WARNINGS**

The routine may be slower than optimal if the default "tp" basis is used.

This routine is less stable than ‘gam’ for the same dataset.

With `discrete=TRUE`, te terms are efficiently computed, but t2 are not.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**See Also**

`mgcv.parallel`, `mgcv-package`, `gamObject`, `gam.models`, `smooth.terms`, `linear.functional.terms`, `s`, `te` `predict.gam`, `plot.gam`, `summary.gam`, `gam.side`, `gam.selection`, `gam.control`, `gam.check`, `linear.functional.terms`, `negbin`, `magic`, `vis.gam`

**Examples**

```R
library(mgcv)
## See help("mgcv-package") for using bam in parallel

## Sample sizes are small for fast run times.

set.seed(3)
dat <- gamSim(1,n=25000,dist="normal",scale=20)
bs <- "cr"; k <- 12
b <- bam(y ~ s(x0,bs=bs)+s(x1,bs=bs)+s(x2,bs=bs,k=k)+
        s(x3,bs=bs),data=dat)
summary(b)
plot(b,pages=1,rug=FALSE) ## plot smooths, but not rug
```
bam.update

Update a strictly additive bam model for new data.

Description

Gaussian with identity link models fitted by bam can be efficiently updated as new data becomes available, by simply updating the QR decomposition on which estimation is based, and re-optimizing the smoothing parameters, starting from the previous estimates. This routine implements this.

Usage

bam.update(b, data, chunk.size=10000)

Arguments

b A gam object fitted by bam and representing a strictly additive model (i.e. gaussian errors, identity link).

data Extra data to augment the original data used to obtain b. Must include a weights column if the original fit was weighted and a AR.start column if AR.start was non NULL in original fit.

chunk.size size of subsets of data to process in one go when getting fitted values.
Details

`bam.update` updates the QR decomposition of the (weighted) model matrix of the GAM represented by `b` to take account of the new data. The orthogonal factor multiplied by the response vector is also updated. Given these updates the model and smoothing parameters can be re-estimated, as if the whole dataset (original and the new data) had been fitted in one go. The function will use the same AR1 model for the residuals as that employed in the original model fit (see `rho` parameter of `bam`).

Note that there may be small numerical differences in fit between fitting the data all at once, and fitting in stages by updating, if the smoothing bases used have any of their details set with reference to the data (e.g. default knot locations).

Value

An object of class "gam" as described in `gamObject`.

WARNINGS

AIC computation does not currently take account of AR model, if used.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

See Also

`mgcv-package`, `bam`

Examples

```r
library(mgcv)
## following is not *very* large, for obvious reasons...
set.seed(8)
n <- 5000
data <- gamSim(1,n=n,dist="normal",scale=5)
data[,c(50,13,3000,3005,3100),]<- NA
data1 <- data[n-999:n,]
data0 <- data[1:(n-1000),]
bs <- "ps"; k <- 20
method <- "GCV.Cp"
b <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
        s(x3,bs=bs,k=k),data=data0,method=method)
b1 <- bam.update(b,dat1)
b2 <- bam.update(bam.update(b,dat1[1:500,]),dat1[501:1000,])
b3 <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
        s(x3,bs=bs,k=k),data=data,method=method)
b1;b2;b3
## example with AR1 errors...
```
e <- rnorm(n)
for (i in 2:n) e[i] <- e[i-1]*.7 + e[i]
dat$y <- dat$f + e*3
dat[c(50,13,3000,3005,3100),]<- NA
dat1 <- dat[(n-999):n]
dat0 <- dat[1:(n-1000),]

b <- bam(y ~ s(x0,bs=bs,k=k)+s(x1,bs=bs,k=k)+s(x2,bs=bs,k=k)+
         s(x3,bs=bs,k=k),data=dat0,rho=0.7)
b1 <- bam.update(b,dat1)

summary(b1);summary(b2);summary(b3)

bandchol

Choleski decomposition of a band diagonal matrix

Description

Computes Choleski decomposition of a (symmetric positive definite) band-diagonal matrix, A.

Usage

bandchol(B)

Arguments

B

An n by k matrix containing the diagonals of the matrix A to be decomposed. First row is leading diagonal, next is first sub-diagonal, etc. sub-diagonals are zero padded at the end. Alternatively gives A directly, i.e. a square matrix with 2k-1 non zero diagonals (those from the lower triangle are not accessed).

Details

Calls dpbtrf from LAPACK. The point of this is that it has $O(k^2n)$ computational cost, rather than the $O(n^3)$ required by dense matrix methods.

Value

Let R be the factor such that t(R)%*%R = A. R is upper triangular and if the rows of B contained the diagonals of A on entry, then what is returned is an n by k matrix containing the diagonals of R, packed as B was packed on entry. If B was square on entry, then R is returned directly. See examples.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Examples

```r
require(mgcv)
## simulate a banded diagonal matrix
n <- 7; set.seed(8)
A <- matrix(0, n, n)
sdiag(A) <- runif(n); sdiag(A, 1) <- runif(n - 1)
sdiag(A, 2) <- runif(n - 2)
A <- crossprod(A)

## full matrix form...
bandexchol(A)
chol(A) ## for comparison

## compact storage form...
B <- matrix(0, 3, n)
B[1, ] <- sdiag(A); B[2, 1:(n-1)] <- sdiag(A, 1)
B[3, 1:(n-2)] <- sdiag(A, 2)
bandchol(B)
```

**betar**

*GAM beta regression family*

**Description**

Family for use with `gam` or `bam`, implementing regression for beta distributed data on (0,1). A linear predictor controls the mean, $\mu$ of the beta distribution, while the variance is then $\mu(1-\mu)/(1+\phi)$, with parameter $\phi$ being estimated during fitting, alongside the smoothing parameters.

**Usage**

```r
betar(theta = NULL, link = "logit", eps = .Machine$double.eps*100)
```

**Arguments**

- `theta` the extra parameter ($\phi$ above).
- `link` The link function: one of "logit", "probit", "cloglog" and "cauchit".
- `eps` the response variable will be truncated to the interval [eps, 1-eps] if there are values outside this range. This truncation is not entirely benign, but too small a value of eps will cause stability problems if there are zeroes or ones in the response.

**Details**

These models are useful for proportions data which can not be modelled as binomial. Note the assumption that data are in (0,1), despite the fact that for some parameter values 0 and 1 are perfectly legitimate observations. The restriction is needed to keep the log likelihood bounded for all parameter values. Any data exactly at 0 or 1 are reset to be just above 0 or just below 1 using the eps argument (in fact any observation <eps is reset to eps and any observation >1-eps is reset to 1-eps). Note the effect of this resetting. If $\mu\phi > 1$ then impossible 0s are replaced with highly improbable eps values. If the inequality is reversed then 0s with infinite probability density are replaced with eps values having high finite probability density. The equivalent condition for 1s is
(1 − μ)ϕ > 1. Clearly all types of resetting are somewhat unsatisfactory, and care is needed if data contain 0s or 1s (often it makes sense to manually reset the 0s and 1s in a manner that somehow reflects the sampling setup).

Value

An object of class extended.family.

WARNINGS

Do read the details section if your data contain 0s and or 1s.

Author(s)

Natalya Pya (nat.pya@gmail.com) and Simon Wood (s.wood@r-project.org)

Examples

```r
library(mgcv)
## Simulate some beta data...
set.seed(3);n=400
dat <- gamSim(1,n=n)
mu <- binomial()$linkinv(dat$f/4-2)
phi <- .5
a <- mu*phi;b <- phi - a;
dat$y <- rbeta(n,a,b)

bm <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=betar(link="logit"),data=dat)

bm
plot(bm,pages=1)
```

blas.thread.test  BLAS thread safety

Description

Most BLAS implementations are thread safe, but some versions of OpenBLAS, for example, are not. This routine is a diagnostic helper function, which you will never need if you don’t set nthreads>1, and even then are unlikely to need.

Usage

```
bblas.thread.test(n=1000,nt=4)
```

Arguments

- **n**  Number of iterations to run of parallel BLAS calling code.
- **nt**  Number of parallel threads to use
Details

While single threaded OpenBLAS 0.2.20 was thread safe, versions 0.3.0-0.3.6 are not, and from version 0.3.7 thread safety of the single threaded OpenBLAS requires making it with the option USE_LOCKING=1. The reference BLAS is thread safe, as are MKL and ATLAS. This routine repeatedly calls the BLAS from multi-threaded code and is sufficient to detect the problem in single threaded OpenBLAS 0.3.x.

A multi-threaded BLAS is often no faster than a single-threaded BLAS, while judicious use of threading in the code calling the BLAS can still deliver a modest speed improvement. For this reason it is often better to use a single threaded BLAS and the codethreads options to bam or gam. For bam(...,discrete=TRUE) using several threads can be a substantial benefit, especially with the reference BLAS.

The MKL BLAS is multithreaded by default. Under linux setting environment variable MKL_NUM_THREADS=1 before starting R gives single threaded operation.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Description

mgcv works largely because many people have reported bugs over the years. If you find something that looks like a bug, please report it, so that the package can be improved. mgcv does not have a large development budget, so it is a big help if bug reports follow the following guidelines.

The ideal report consists of an email to <simon.wood@r-project.org> with a subject line including mgcv somewhere, containing

1. The results of running sessionInfo in the R session where the problem occurs. This provides platform details, R and package version numbers, etc.
3. Short cut and paste-able code that produces the problem, including the code for loading/generating the data (using standard R functions like load, read.table etc).
4. Any required data files. If you send real data it will only be used for the purposes of debugging.

Of course if you have dug deeper and have an idea of what is causing the problem, that is also helpful to know, as is any suggested code fix. (Don’t send a fixed package .tar.gz file, however - I can’t use this).

Author(s)

Simon N. Wood <simon.wood@r-project.org>
**choldrop**  
*Deletion and rank one Cholesky factor update*

**Description**

Given a Cholesky factor, $R$, of a matrix, $A$, choldrop finds the Cholesky factor of $A[-k, -k]$, where $k$ is an integer. cholup finds the factor of $A + uu^T$ (update) or $A - uu^T$ (downdate).

**Usage**

```r
choldrop(R, k)
cholup(R, u, up)
```

**Arguments**

- `R`  
  Cholesky factor of a matrix, $A$.
- `k`  
  row and column of $A$ to drop.
- `u`  
  vector defining rank one update.
- `up`  
  if TRUE compute update, otherwise downdate.

**Details**

First consider choldrop. If $R$ is upper triangular then $t(R[-k]) \times R[-k] == A[-k, -k]$, but $R[-k]$ has elements on the first sub-diagonal, from its kth column onwards. To get from this to a triangular Cholesky factor of $A[-k, -k]$ we can apply a sequence of Givens rotations from the left to eliminate the sub-diagonal elements. The routine does this. If $R$ is a lower triangular factor then Givens rotations from the right are needed to remove the extra elements. If $n$ is the dimension of $R$ then the update has $O(n^2)$ computational cost.

cholup (which assumes $R$ is upper triangular) updates based on the observation that $R^T R + uu^T = [u, R^T]^T u, [u, R^T]^T = [u, R^T] Q^T Q [u, R^T]^T$, and therefore we can construct $Q$ so that $Q[u, R^T]^T = [0, R_1^T]^T$, where $R_1$ is the modified factor. $Q$ is constructed from a sequence of Givens rotations in order to zero the elements of $u$. Downdating is similar except that hyperbolic rotations have to be used in place of Givens rotations — see Golub and van Loan (2013, section 6.5.4) for details. Downdating only works if $A - uu^T$ is positive definite. Again the computational cost is $O(n^2)$.

Note that the updates are vector oriented, and are hence not susceptible to speed up by use of an optimized BLAS. The updates are set up to be relatively Cache friendly, in that in the upper triangular case successive Givens rotations are stored for sequential application column-wise, rather than being applied row-wise as soon as they are computed. Even so, the upper triangular update is slightly slower than the lower triangular update.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Examples

```r
require(mgcv)
set.seed(0)
n <- 6
A <- crossprod(matrix(runif(n*n),n,n))
R0 <- chol(A)
k <- 3
Rd <- choldrop(R0,k)
range(Rd-chol(A[-k,-k]))
Rd;chol(A[-k,-k])

## same but using lower triangular factor A = LL'
L <- t(R0)
Ld <- choldrop(L,k)
range(Ld-t(chol(A[-k,-k])))
Ld;t(chol(A[-k,-k]))

## Rank one update example
u <- runif(n)
R <- cholup(R0,u,TRUE)
Ru <- chol(A+u %*% t(u)) ## direct for comparison
R;Ru
range(R-Ru)

## Downdate - just going back from R to R0
Rd <- cholup(R,u,FALSE)
R0;Rd
range(R0-Rd)
```

choose.k  

Basis dimension choice for smooths

Description

Choosing the basis dimension, and checking the choice, when using penalized regression smoothers.

Penalized regression smoothers gain computational efficiency by virtue of being defined using a basis of relatively modest size, k. When setting up models in the mgcv package, using s or te terms in a model formula, k must be chosen: the defaults are essentially arbitrary.

In practice k\textasciitilde{}1 (or k) sets the upper limit on the degrees of freedom associated with an s smooth (1 degree of freedom is usually lost to the identifiability constraint on the smooth). For te smooths the upper limit of the degrees of freedom is given by the product of the k values provided for each marginal smooth less one, for the constraint. However the actual effective degrees of freedom are controlled by the degree of penalization selected during fitting, by GCV, AIC, REML or whatever is specified. The exception to this is if a smooth is specified using the fx=TRUE option, in which case it is unpenalized.

So, exact choice of k is not generally critical: it should be chosen to be large enough that you are reasonably sure of having enough degrees of freedom to represent the underlying truth reasonably well, but small enough to maintain reasonable computational efficiency. Clearly ‘large’ and ‘small’ are dependent on the particular problem being addressed.
As with all model assumptions, it is useful to be able to check the choice of \( k \) informally. If the effective degrees of freedom for a model term are estimated to be much less than \( k-1 \) then this is unlikely to be very worthwhile, but as the EDF approach \( k-1 \), checking can be important. A useful general purpose approach goes as follows: (i) fit your model and extract the deviance residuals; (ii) for each smooth term in your model, fit an equivalent, single, smooth to the residuals, using a substantially increased \( k \) to see if there is pattern in the residuals that could potentially be explained by increasing \( k \). Examples are provided below.

The obvious, but more costly, alternative is simply to increase the suspect \( k \) and refit the original model. If there are no statistically important changes as a result of doing this, then \( k \) was large enough. (Change in the smoothness selection criterion, and/or the effective degrees of freedom, when \( k \) is increased, provide the obvious numerical measures for whether the fit has changed substantially.)

\texttt{gam.check} runs a simple simulation based check on the basis dimensions, which can help to flag up terms for which \( k \) is too low. Grossly too small \( k \) will also be visible from partial residuals available with \texttt{plot.gam}.

One scenario that can cause confusion is this: a model is fitted with \( k=10 \) for a smooth term, and the EDF for the term is estimated as 7.6, some way below the maximum of 9. The model is then refitted with \( k=20 \) and the EDF increases to 8.7 - what is happening - how come the EDF was not 8.7 the first time around? The explanation is that the function space with \( k=20 \) contains a larger subspace of functions with EDF 8.7 than did the function space with \( k=10 \): one of the functions in this larger subspace fits the data a little better than did any function in the smaller subspace. These subtleties seldom have much impact on the statistical conclusions to be drawn from a model fit, however.

\textbf{Author(s)}

Simon N. Wood <simon.wood@r-project.org>

\textbf{References}


https://www.maths.ed.ac.uk/~swood34/

\textbf{Examples}

```r
## Simulate some data ....
library(mgcv)
set.seed(1)
dat <- gamSim(1,n=400, scale=2)

## fit a GAM with quite low 'k'
b<-gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=6)+s(x3,k=6),data=dat)
plot(b,pages=1,residuals=TRUE) ## hint of a problem in s(x2)

## Another approach (see below for more obvious method)....
## check for residual pattern, removeable by increasing 'k'
## typically 'k', below, should be substantially larger than
## the original, 'k' but certainly less than n/2.
## Note use of cheap "cs" shrinkage smoothers, and gamma=1.4
## to reduce chance of overfitting...
```
rsd <- residuals(b)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x2,k=40,bs="cs"),gamma=1.4,data=dat) ## 'k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

## refit...
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=20)+s(x3,k=6),data=dat)
gam.check(b) ## better

## similar example with multi-dimensional smooth
b1 <- gam(y~s(x0)+s(x1,x2,k=15)+s(x3),data=dat)
rsd <- residuals(b1)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,x2,k=100,bs="ts"),gamma=1.4,data=dat) ## 'k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam.check(b1) ## shows same problem

## and a 'te' example
b2 <- gam(y~s(x0)+te(x1,x2,k=4)+s(x3),data=dat)
rsd <- residuals(b2)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~te(x1,x2,k=10,bs="cs"),gamma=1.4,data=dat) ## 'k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam.check(b2) ## shows same problem

## same approach works with other families in the original model
dat <- gamSim(1,n=400,scale=.25,dist="poisson")
bp<-gam(y~s(x0,k=5)+s(x1,k=5)+s(x2,k=5)+s(x3,k=5),
family=poisson,data=dat,method="ML")
gam.check(bp)

rsd <- residuals(bp)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x2,k=40,bs="cs"),gamma=1.4,data=dat) ## 'k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
rm(dat)

## More obvious, but more expensive tactic... Just increase
## suspicious k until fit is stable.

set.seed(0)
dat <- gamSim(1,n=400,scale=2)
## fit a GAM with quite low 'k'
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=6)+s(x3,k=6),
data=dat,method="REML")
b
## edf for 3rd smooth is highest as proportion of k -- increase k
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=12)+s(x3,k=6),
data=dat,method="REML")
b
## edf substantially up, -ve REML substantially down
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=24)+s(x3,k=6),
data=dat,method="REML")
b
## slight edf increase and -ve REML change
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=40)+s(x3,k=6),
data=dat,method="REML")
b
## definitely stabilized (but really k around 20 would have been fine)

---

**cnorm**

**GAM censored normal family for log-normal AFT and Tobit models**

**Description**

Family for use with `gam` or `bam`, implementing regression for censored normal data. If \( y \) is the response with mean \( \mu \) and standard deviation \( w^{-1/2} \exp(\theta) \), then \( w^{1/2}(y - \mu) \exp(-\theta) \) follows an \( N(0,1) \) distribution. That is

\[
y \sim N(\mu, e^{2\theta} w^{-1}).
\]

\( \theta \) is a single scalar for all observations. Observations may be left, interval or right censored or uncensored.

Useful for log-normal accelerated failure time (AFT) models, Tobit regression, and crudely rounded data, for example.

**Usage**

```r
cnorm(theta=NULL,link="identity")
```

**Arguments**

- `theta` log standard deviation parameter. If supplied and positive then taken as a fixed value of standard deviation (not its log). If supplied and negative taken as negative of initial value for standard deviation (not its log).
- `link` The link function: "identity", "log" or "sqrt".

**Details**

If the family is used with a vector response, then it is assumed that there is no censoring, and a regular Gaussian regression results. If there is censoring then the response should be supplied as a two column matrix. The first column is always numeric. Entries in the second column are as follows.

- If an entry is identical to the corresponding first column entry, then it is an uncensored observation.
- If an entry is numeric and different to the first column entry then there is interval censoring. The first column entry is the lower interval limit and the second column entry is the upper interval limit. \( y \) is only known to be between these limits.
- If the second column entry is \(-\infty\) then the observation is left censored at the value of the entry in the first column. It is only known that \( y \) is less than or equal to the first column value.
• If the second column entry is Inf then the observation is right censored at the value of the entry in the first column. It is only known that $y$ is greater than or equal to the first column value.

Any mixture of censored and uncensored data is allowed, but be aware that data consisting only of right and/or left censored data contain very little information.

**Value**

An object of class `extended.family`.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**Examples**

```r
library(mgcv)

#######################################################
## AFT model example for colon cancer survival data...
#######################################################

library(survival) ## for data
col1 <- colon[colon$etype==1,] ## concentrate on single event
col1$differ <- as.factor(col1$differ)
col1$sex <- as.factor(col1$sex)

## set up the AFT response...
logt <- cbind(log(col1$time),log(col1$time))
logt[col1$status==0,2] <- Inf ## right censoring
col1$logt <- -logt ## -ve conventional for AFT versus Cox PH comparison

## fit the model...
b <- gam(logt~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct+adhere,
   family=cnorm(),data=col1)
plot(b,pages=1)
## ... compare this to ?cox.ph

#######################################################
## A Tobit regression example...
#######################################################

set.seed(3);n<-400
dat <- gamSim(1,n=n)
y <- dat$y - 5 ## shift data down

## truncate at zero, and set up response indicating this has happened...
y <- cbind(y,ys)
y[ys<0,2] <- -Inf
y[ys<0,1] <- 0
```
dat$yt <- y
b <- gam(yt~s(x0)+s(x1)+s(x2)+s(x3),family=cnorm,data=dat)
plot(b,pages=1)

# A model for rounded data...

dat <- gamSim(1,n=n)
y <- round(dat$y)
y <- cbind(y-.5,y+.5) ## set up to indicate interval censoring
dat$yi <- y
b <- gam(yi~s(x0)+s(x1)+s(x2)+s(x3),family=cnorm,data=dat)
plot(b,pages=1)

columb

Reduced version of Columbus OH crime data

Description
By district crime data from Columbus OH, together with polygons describing district shape. Useful for illustrating use of simple Markov Random Field smoothers.

Usage
data(columb)
data(columb.polys)

Format
columb is a 49 row data frame with the following columns

area land area of district
home.value housing value in 1000USD.
income household income in 1000USD.
crime residential burglaries and auto theifs per 1000 households.
open.space measure of open space in district.
district code identifying district, and matching names(columb.polys).
columb.polys contains the polygons defining the areas in the format described below.

Details
The data frame columb relates to the districts whose boundaries are coded in columb.polys. columb.polys[[i]] is a 2 column matrix, containing the vertices of the polygons defining the boundary of the ith district. columb.polys[[2]] has an artificial hole inserted to illustrate how holes in districts can be specified. Different polygons defining the boundary of a district are separated by NA rows in columb.polys[[1]], and a polygon enclosed within another is treated as a hole in that region (a hole should never come first). names(columb.polys) matches columb$district (order unimportant).
concurvity

Source

The data are adapted from the columbus example in the spdep package, where the original source is given as:


Examples

## see ?mrf help files

<table>
<thead>
<tr>
<th>concurvity</th>
<th>GAM concurvity measures</th>
</tr>
</thead>
</table>

Description

Produces summary measures of concurvity between gam components.

Usage

concurvity(b,full=TRUE)

Arguments

b An object inheriting from class "gam".
full If TRUE then concurvity of each term with the whole of the rest of the model is considered. If FALSE then pairwise concurvity measures between each smooth term (as well as the parametric component) are considered.

Details

Concurvity occurs when some smooth term in a model could be approximated by one or more of the other smooth terms in the model. This is often the case when a smooth of space is included in a model, along with smooths of other covariates that also vary more or less smoothly in space. Similarly it tends to be an issue in models including a smooth of time, along with smooths of other time varying covariates.

Concurvity can be viewed as a generalization of co-linearity, and causes similar problems of interpretation. It can also make estimates somewhat unstable (so that they become sensitive to apparently innocuous modelling details, for example).

This routine computes three related indices of concurvity, all bounded between 0 and 1, with 0 indicating no problem, and 1 indicating total lack of identifiability. The three indices are all based on the idea that a smooth term, f, in the model can be decomposed into a part, g, that lies entirely in the space of one or more other terms in the model, and a remainder part that is completely within the term’s own space. If g makes up a large part of f then there is a concurvity problem. The indices used are all based on the square of ||g||/||f||, that is the ratio of the squared Euclidean norms of the vectors of f and g evaluated at the observed covariate values.

The three measures are as follows

worst This is the largest value that the square of ||g||/||f|| could take for any coefficient vector. This is a fairly pessimistic measure, as it looks at the worst case irrespective of data. This is the only measure that is symmetric.
observed  This just returns the value of the square of \( \|g\|/\|f\| \) according to the estimated coefficients. This could be a bit over-optimistic about the potential for a problem in some cases.

estimate  This is the squared F-norm of the basis for \( g \) divided by the F-norm of the basis for \( f \). It is a measure of the extent to which the \( f \) basis can be explained by the \( g \) basis. It does not suffer from the pessimism or potential for over-optimism of the previous two measures, but is less easy to understand.

Value

If `full=TRUE` a matrix with one column for each term and one row for each of the 3 concurvity measures detailed below. If `full=FALSE` a list of 3 matrices, one for each of the three concurvity measures detailed below. Each row of the matrix relates to how the model terms depend on the model term supplying that rows name.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

Examples

library(mgcv)
## simulate data with concurvity...
set.seed(8);n<- 200
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
(10 * x)^3 * (1 - x)^10
t <- sort(runif(n)) ## first covariate
## make covariate x a smooth function of t + noise...
x <- f2(t) + rnorm(n)*3
## simulate response dependent on t and x...
y <- sin(4*pi*t) + exp(x/20) + rnorm(n)*.3

## fit model...
b <- gam(y ~ s(t,k=15) + s(x,k=15),method="REML")

## assess concurvity between each term and `rest of model'...
concurvity(b)

## ... and now look at pairwise concurvity between terms...
concurvity(b,full=FALSE)
Description

The cox.ph family implements the Cox Proportional Hazards model with Peto’s correction for ties, optional stratification, and estimation by penalized partial likelihood maximization, for use with `gam`. In the model formula, event time is the response. Under stratification the response has two columns: time and a numeric index for stratum. The weights vector provides the censoring information (0 for censoring, 1 for event). cox.ph deals with the case in which each subject has one event/censoring time and one row of covariate values. When each subject has several time dependent covariates see cox.pht.

See example below for conditional logistic regression.

Usage

```r
cox.ph(link = "identity")
```

Arguments

- `link` currently (and possibly for ever) only "identity" supported.

Details

Used with `gam` to fit Cox Proportional Hazards models to survival data. The model formula will have event/censoring times on the left hand side and the linear predictor specification on the right hand side. Censoring information is provided by the weights argument to `gam`, with 1 indicating an event and 0 indicating censoring.

Stratification is possible, allowing for different baseline hazards in different strata. In that case the response has two columns: the first is event/censoring time and the second is a numeric stratum index. See below for an example.

Prediction from the fitted model object (using the predict method) with `type = "response"` will predict on the survivor function scale. This requires evaluation times to be provided as well as covariates (see example). Also see example code below for extracting the cumulative baseline hazard/survival directly. The fitted.values stored in the model object are survival function estimates for each subject at their event/censoring time.

deviance, martingale, score, or schoenfeld residuals can be extracted. See Klein and Moeschberger (2003) for descriptions. The score residuals are returned as a matrix of the same dimension as the model matrix, with a "terms" attribute, which is a list indicating which model matrix columns belong to which model terms. The score residuals are scaled. For parametric terms this is by the standard deviation of associated model coefficient. For smooth terms the sub matrix of score residuals for the term is postmultiplied by the transposed Cholesky factor of the covariance matrix for the term’s coefficients. This is a transformation that makes the coefficients approximately independent, as required to make plots of the score residuals against event time interpretable for checking the proportional hazards assumption (see Klein and Moeschberger, 2003, p376). Penalization causes drift in the score residuals, which is also removed, to allow the residuals to be approximately interpreted as unpenalized score residuals. Schoenfeld and score residuals are computed by strata. See the examples for simple PH assumption checks by plotting score residuals, and Klein and Moeschberger (2003, section 11.4) for details. Note that high correlation between terms can undermine these checks.

Estimation of model coefficients is by maximising the log-partial likelihood penalized by the smoothing penalties. See e.g. Hastie and Tibshirani, 1990, section 8.3. for the partial likelihood used (with Peto’s approximation for ties), but note that optimization of the partial likelihood does
not follow Hastie and Tibshirani. See Klein and Moeschberger (2003) for estimation of residuals, the cumulative baseline hazard, survival function and associated standard errors (the survival standard error expression has a typo).

The percentage deviance explained reported for Cox PH models is based on the sum of squares of the deviance residuals, as the model deviance, and the sum of squares of the deviance residuals when the covariate effects are set to zero, as the null deviance. The same baseline hazard estimate is used for both.

This family deals efficiently with the case in which each subject has one event/censoring time and one row of covariate values. For studies in which there are multiple time varying covariate measures for each subject then the equivalent Poisson model should be fitted to suitable pseudodata using bam(..., discrete=TRUE). See \texttt{cox.pht}.

**Value**

An object inheriting from class \texttt{general.family}.

**References**


**See Also**

\texttt{cox.pht, cnorm}

**Examples**

```r
library(mgcv)
library(survival) ## for data
col1 <- colon[colon$etype==1,] ## concentrate on single event
col1$differ <- as.factor(col1$differ)
col1$sex <- as.factor(col1$sex)

b <- gam(time~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct+adhere,
         family=cox.ph(),data=col1,weights=status)

summary(b)

plot(b,pages=1,all.terms=TRUE) ## plot effects
plot(b$linear.predictors,residuals(b))

## plot survival function for patient j...
np <- 300;j <- 6
newd <- data.frame(time=seq(0,3000,length=np))
dname <- names(col1)
for (n in dname) newd[[n]] <- rep(col1[[n]][j],np)
newd$time <- seq(0,3000,length=np)
fv <- predict(b,newdata=newd,type="response",se=TRUE)
```

plot(newd$time,fv$fit,type="l",ylim=c(0,1),xlab="time",ylab="survival")
lines(newd$time,fv$fit+2*fv$se.fit,col=2)
lines(newd$time,fv$fit-2*fv$se.fit,col=2)

## crude plot of baseline survival...
plot(b$family$data$tr,exp(-b$family$data$h),type="l",ylim=c(0,1),xlab="time",ylab="survival")
lines(b$family$data$tr,exp(-b$family$data$h + 2*b$family$data$q^.5),col=2)
lines(b$family$data$tr,exp(-b$family$data$h - 2*b$family$data$q^.5),col=2)
lines(b$family$data$tr,exp(-b$family$data$km),lty=2) ## Kaplan Meier

## Checking the proportional hazards assumption via scaled score plots as
## in Klein and Moeschberger Section 11.4 p374-376...

ph.resid <- function(b,stratum=1) {
## convenience function to plot scaled score residuals against time,
## by term. Reference lines at 5% exceedance prob for Brownian bridge
## (see KS test statistic distribution).
rs <- residuals(b,"score");term <- attr(rs,"term")
if (is.matrix(b$y)) {
 ii <- b$y[,2] == stratum;b$y <- b$y[ii,1];rs <- rs[ii,]
}
oy <- order(b$y)
for (i in 1:length(term)) {
 ii <- term[ii]; m <- length(ii)
plot(b$y[oy],rs[oy,ii[1]],ylim=c(-3,3),type="l",ylab="score residuals",
  xlab="time",main=names(term)[i])
if (m>1) for (k in 2:m) lines(b$y[oy],rs[oy,ii[k]],col=k);
abline(-1.3581,0,lty=2);abline(1.3581,0,lty=2)
}
}
par(mfrow=c(2,2))
ph.resid(b)

## stratification example, with 2 randomly allocated strata
## so that results should be similar to previous....
coll$strata <- sample(1:2,nrow(coll),replace=TRUE)
bs <- gam(cbind(time,strata)~s(age,by=sex)+sex+s(nodes)+perfor+rx+obstruct
  +adhere,family=cox.ph(),data=coll,weights=status)
plot(bs,pages=1,all.terms=TRUE) ## plot effects

## baseline survival plots by strata...
for (i in 1:2) { ## loop over strata
## create index selecting elements of stored hazard info for stratum i...
ind <- which(bs$family$data$strat == i)
if (i==1) plot(bs$family$data[ind].exp(-bs$family$data$h[ind]),type="l",
ylim=c(0,1),xlab="time",ylab="survival",lwd=2,col=i) else
lines(bs$family$data[ind].exp(-bs$family$data$h[ind]),lwd=2,col=i)
lines(bs$family$data[ind].exp(-bs$family$data$h[ind] +
  2*bs$family$data&q[ind].^+.5),lty=2,col=i) ## upper ci
lines(bs$family$data[ind].exp(-bs$family$data$h[ind] -
  2*bs$family$data&q[ind].^+.5),lty=2,col=i) ## lower ci
lines(bs$family$data[ind].exp(-bs$family$data$km[ind]),col=i) ## KM
}
## Simple simulated known truth example...

```r
ph.weibull.sim <- function(eta, gamma=1, h0=.01, t1=100) {
  lambda <- h0*exp(eta)
  n <- length(eta)
  U <- runif(n)
  t <- (-log(U)/lambda)^(1/gamma)
  d <- as.numeric(t <= t1)
  t[!d] <- t1
  list(t=t, d=d)
}
```

```
n <- 500; set.seed(2)
x0 <- runif(n, 0, 1); x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1); x3 <- runif(n, 0, 1)
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
f3 <- function(x) 0*x
f <- f0(x0) + f1(x1) + f2(x2)
g <- (f-mean(f))/5
surv <- ph.weibull.sim(g)
surv$x0 <- x0; surv$x1 <- x1; surv$x2 <- x2; surv$x3 <- x3

b <- gam(t~s(x0)+s(x1)+s(x2,k=15)+s(x3),family=cox.ph,weights=d, data=surv)
plot(b, pages=1)
```

## Another one, including a violation of proportional hazards for ## effect of x2...

```
set.seed(2)
h <- exp((f0(x0)+f1(x1)+f2(x2)-10)/5)
t <- rexp(n, h); d <- as.numeric(t<20)

## first with no violation of PH in the simulation...

```

```
b <- gam(t~s(x0)+s(x1)+s(x2)+s(x3),family=cox.ph,weights=d)
plot(b, pages=1)
ph.resid(b) ## fine
```

## Now violate PH for x2 in the simulation...

```
ii <- t>1.5
h1 <- exp((f0(x0)+f1(x1)+3*f2(x2)-10)/5)
t[ii] <- 1.5 + rexp(sum(ii), h1[ii]); d <- as.numeric(t<20)

```

```
b <- gam(t~s(x0)+s(x1)+s(x2)+s(x3),family=cox.ph,weights=d)
plot(b, pages=1)
ph.resid(b) ## The checking plot picks up the problem in s(x2)
```

## conditional logistic regression models are often estimated using the ## cox proportional hazards partial likelihood with a strata for each ## case-control group. A dummy vector of times is created (all equal). ## The following compares to 'clogit' for a simple case. Note that ## the gam log likelihood is not exact if there is more than one case ## per stratum, corresponding to clogit's approximate method.

```
library(survival); library(mgcv)
infert$dumt <- rep(1,nrow(infert))
b <- gam(t~s(x0)+s(x1)+s(x2)+s(x3),family=cox.ph,weights=d, data=surv)
plot(b, pages=1)
ph.resid(b) ## The checking plot picks up the problem in s(x2)
```

```
Additive Cox proportional hazard models with time varying covariates

Description

The `cox.ph` family only allows one set of covariate values per subject. If each subject has several time varying covariate measurements then it is still possible to fit a proportional hazards regression model, via an equivalent Poisson model. The recipe is provided by Whitehead (1980) and is equally valid in the smooth additive case. Its drawback is that the equivalent Poisson dataset can be quite large.

The trick is to generate an artificial Poisson observation for each subject in the risk set at each non-censored event time. The corresponding covariate values for each subject are whatever they are at the event time, while the Poisson response is zero for all subjects except those experiencing the event at that time (this corresponds to Peto’s correction for ties). The linear predictor for the model must include an intercept for each event time (the cumulative sum of the exponential of these is the Breslow estimate of the baseline hazard).

Below is some example code employing this trick for the `pbc.sq` data from the `survival` package. It uses `bam` for fitting with the `discrete=TRUE` option for efficiency: there is some approximation involved in doing this, and the exact equivalent to what is done in `cox.ph` is rather obtained by using `gam` with `method="REML"` (taking many times the computational time for the example below). An alternative fits the model as a conditional logistic model using stratified Cox PH with event times as strata (see example). This would be identical in the unpenalized case, but smoothing parameter estimates can differ.

The function `tdpois` in the example code uses crude piecewise constant interpolation for the covariates, in which the covariate value at an event time is taken to be whatever it was the previous time that it was measured. Obviously more sophisticated interpolation schemes might be preferable.

References


Examples

```r
require(mgcv);require(survival)

## First define functions for producing Poisson model data frame

app <- function(x,t,to) {
  ## wrapper to approx for calling from apply...
  y <- if (sum(!is.na(x))<1) rep(NA,length(to)) else approx(t,x,to,method="constant",rule=2)$y
  if (is.factor(x)) factor(levels(x)[y],levels=levels(x)) else y
} ## app
```
tdpois <- function(dat, event="z", et="futime", t="day", status="status1", id="id") {
# dat is data frame. id is patient id; et is event time; t is
# observation time; status is 1 for death 0 otherwise;
# event is name for Poisson response.
if (event %in% names(dat)) warning("event name in use")
require(utils) # for progress bar
te <- sort(unique(dat[[et]][dat[[status]]==1])) # event times
sid <- unique(dat[[id]])
inter <- interactive()
if (inter) prg <- txtProgressBar(min = 0, max = length(sid), initial = 0,
char = " ", width = NA, title="Progress", style = 3)
# create dataframe for poisson model data
dat[[event]] <- 0; start <- 1
dap <- dat[rep(1:length(sid),length(te)),]
for (i in 1:length(sid)) { # work through patients
di <- dat[dat[[id]]==sid[i],] # ith patient's data
tr <- te[te <= di[[et]]][1] # times required for this patient
# Now do the interpolation of covariates to event times...
um <- data.frame(lapply(X=di,FUN=app,t=di[[t]],to=tr))
# Mark the actual event...
if (um[[et]][1]==max(tr)&um[[status]][1]==1) um[[event]][nrow(um)] <- 1
um[[et]] <- tr # reset time to relevant event times
dap[start:(start-1+nrow(um)),] <- um # copy to dap
start <- start + nrow(um)
if (inter) setTxtProgressBar(prg, i)
}
if (inter) close(prg)
dap[1:(start-1),]
} # tdpois

## The following typically takes a minute or less...

## Convert pbcseq to equivalent Poisson form...
pbcseq$status1 <- as.numeric(pbcseq$status==2) # death indicator
pb <- tdpois(pbcseq) # conversion
pb$t <- factor(pb$futime) # add factor for event time

## Fit Poisson model...
b <- bam(z ~ t - 1 + sex + trt + s(sqrt(protime)) + s(platelet) + s(age) +
s(bili) + s(albumin), family=poisson, data=pb, discrete=TRUE, nthreads=2)

pb$df <- rep(1,nrow(pb)) # dummy time

## Fit as conditional logistic...
b1 <- gam(cbind(df, t) ~ sex + trt + s(sqrt(protime)) + s(platelet) +
s(age) + s(bili) + s(albumin), family=cox.ph, data=pb, weights=z)

par(mfrow=c(2,3))
plot(b,scale=0)

## compute residuals...
chaz <- tapply(fitted(b), pb$id, sum) # cum haz by subject
d <- tapply(pb$z, pb$id, sum) # censoring indicator
mrdz <- d - chaz # Martingale
drdz <- sign(mrdz)*sqrt(-2*(mrdz + d*log(chaz))) # deviance
## cSplineDes

### Evaluate cyclic B spline basis

**Description**

Uses splineDesign to set up the model matrix for a cyclic B-spline basis.

**Usage**

```r
cSplineDes(x, knots, ord = 4, derivs=0)
```

**Arguments**

- `x` : covariate values for smooth.
- `knots` : The knot locations: the range of these must include all the data.
- `ord` : order of the basis. 4 is a cubic spline basis. Must be >1.
- `derivs` : order of derivative of the spline to evaluate, between 0 and `ord-1`. Recycled to length of `x`.

**Details**

The routine is a wrapper that sets up a B-spline basis, where the basis functions wrap at the first and last knot locations.

**Value**

A matrix with `length(x)` rows and `length(knots)-1` columns.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

- `cyclic.p.spline`
Examples

```r
require(mgcv)
## create some x's and knots...
n <- 200
x <- 0:(n-1)/(n-1);k<- 0:5/5
X <- cSplineDes(x,k) ## cyclic spline design matrix
## plot evaluated basis functions...
plot(x,X[,1],type="l"); for (i in 2:5) lines(x,X[,i],col=i)
## check that the ends match up....
e <- X[,1]-X[n,];ee
tol <- .Machine$double.eps^.75
if (all.equal(ee,ee*0,tolerance=tol)!=TRUE)
  stop("cyclic spline ends don't match!")
## similar with uneven data spacing...
x <- sort(runif(n)) + 1 ## sorting just makes end checking easy
k <- seq(min(x),max(x),length=8) ## create knots
X <- cSplineDes(x,k) ## get cyclic spline model matrix
plot(x,X[,1],type="l"); for (i in 2:ncol(X)) lines(x,X[,i],col=i)
e <- X[,1]-X[n,];ee ## do ends match??
tol <- .Machine$double.eps^.75
if (all.equal(ee,ee*0,tolerance=tol)!=TRUE)
  stop("cyclic spline ends don't match!")
```

---

*dDeta*  

**Obtaining derivative w.r.t. linear predictor**

**Description**

INTERNAL function. Distribution families provide derivatives of the deviance and link w.r.t. \( \mu = \text{inv}_\text{link}(\eta) \). This routine converts these to the required derivatives of the deviance w.r.t. \( \eta \), the linear predictor.

**Usage**

```r
dDeta(y, mu, wt, theta, fam, deriv = 0)
```

**Arguments**

- `y` vector of observations.
- `mu` if `eta` is the linear predictor, \( \mu = \text{inv}_\text{link}(\eta) \). In a traditional GAM \( \mu = E(y) \).
- `wt` vector of weights.
- `theta` vector of family parameters that are not regression coefficients (e.g. scale parameters).
- `fam` the family object.
- `deriv` the order of derivative of the smoothing parameter score required.

**Value**

A list of derivatives.
Author(s)

Simon N. Wood <simon.wood@r-project.org>.

dpnorm

Stable evaluation of difference between normal c.d.f.s

Description

Evaluates the difference between two $N(0, 1)$ cumulative distribution functions avoiding cancellation error.

Usage

dpnorm(x0, x1)

Arguments

- x0: vector of lower values at which to evaluate standard normal distribution function.
- x1: vector of upper values at which to evaluate standard normal distribution function.

Details

Equivalent to $\text{pnorm}(x_1) - \text{pnorm}(x_0)$, but stable when $x_0$ and $x_1$ values are very close, or in the upper tail of the standard normal.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

```r
require(mgcv)
x <- seq(-10, 10, length=10000)
eps <- 1e-10
y0 <- pnorm(x+eps)-pnorm(x) ## cancellation prone
y1 <- dpnorm(x,x+eps)      ## stable
## illustrate stable computation in black, and
## cancellation prone in red...
par(mfrow=c(1,2),mar=c(4,4,1,1))
plot(log(y1),log(y0),type="l")
lines(log(y1[y>0]),log(y0[y>0]),col=2)
plot(x,log(y1),type="l")
lines(x,log(y0),col=2)
```
exclude.too.far  Exclude prediction grid points too far from data

Description
Takes two arrays defining the nodes of a grid over a 2D covariate space and two arrays defining the location of data in that space, and returns a logical vector with elements TRUE if the corresponding node is too far from data and FALSE otherwise. Basically a service routine for vis.gam and plot.gam.

Usage
exclude.too.far(g1,g2,d1,d2,dist)

Arguments
- `g1`: co-ordinates of grid relative to first axis.
- `g2`: co-ordinates of grid relative to second axis.
- `d1`: co-ordinates of data relative to first axis.
- `d2`: co-ordinates of data relative to second axis.
- `dist`: how far away counts as too far. Grid and data are first scaled so that the grid lies exactly in the unit square, and `dist` is a distance within this unit square.

Details
Linear scalings of the axes are first determined so that the grid defined by the nodes in `g1` and `g2` lies exactly in the unit square (i.e. on [0,1] by [0,1]). These scalings are applied to `g1`, `g2`, `d1` and `d2`. The minimum Euclidean distance from each node to a datum is then determined and if it is greater than `dist` the corresponding entry in the returned array is set to TRUE (otherwise to FALSE). The distance calculations are performed in compiled code for speed without storage overheads.

Value
A logical array with TRUE indicating a node in the grid defined by `g1`, `g2` that is ‘too far’ from any datum.

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References
https://www.maths.ed.ac.uk/~swood34/

See Also
vis.gam
Examples

```r
library(mgcv)
x<-rnorm(100);y<-rnorm(100) # some "data"
n<-40 # generate a grid....
mx<-seq(min(x),max(x),length=n)
ymy<-seq(min(y),max(y),length=n)
gx<-rep(mx,n);gy<-rep(my,rep(n,n))
tf<-exclude.too.far(gx,gy,x,y,0.1)
plot(gx[!tf],gy[!tf],pch=".");points(x,y,col=2)
```

---

**extract.lme.cov**

*Extract the data covariance matrix from an lme object*

**Description**

This is a service routine for **gamm**. Extracts the estimated covariance matrix of the data from an **lme** object, allowing the user control about which levels of random effects to include in this calculation. **extract.lme.cov** forms the full matrix explicitly; **extract.lme.cov2** tries to be more economical than this.

**Usage**

```r
extract.lme.cov(b,data=NULL,start.level=1)
extract.lme.cov2(b,data=NULL,start.level=1)
```

**Arguments**

- `b` A fitted model object returned by a call to **lme**
- `data` The data frame/model frame that was supplied to **lme**, but with any rows removed by the na.action dropped. Uses the data stored in the model object if not supplied.
- `start.level` The level of nesting at which to start including random effects in the calculation. This is used to allow smooth terms to be estimated as random effects, but treated like fixed effects for variance calculations.

**Details**

The random effects, correlation structure and variance structure used for a linear mixed model combine to imply a covariance matrix for the response data being modelled. These routines extracts that covariance matrix. The process is slightly complicated, because different components of the fitted model object are stored in different orders (see function code for details!).

The **extract.lme.cov** calculation is not optimally efficient, since it forms the full matrix, which may in fact be sparse. **extract.lme.cov2** is more efficient. If the covariance matrix is diagonal, then only the leading diagonal is returned; if it can be written as a block diagonal matrix (under some permutation of the original data) then a list of matrices defining the non-zero blocks is returned along with an index indicating which row of the original data each row/column of the block diagonal matrix relates to. The block sizes are defined by the coarsest level of grouping in the random effect structure.
gamm uses extract.lme.cov2.

extract.lme.cov does not currently deal with the situation in which the grouping factors for a correlation structure are finer than those for the random effects. extract.lme.cov2 does deal with this situation.

Value

For extract.lme.cov an estimated covariance matrix.

For extract.lme.cov2 a list containing the estimated covariance matrix and an indexing array. The covariance matrix is stored as the elements on the leading diagonal, a list of the matrices defining a block diagonal matrix, or a full matrix if the previous two options are not possible.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

For lme see:


For details of how GAMMs are set up here for estimation using lme see:


or


https://www.maths.ed.ac.uk/~swood34/

See Also

gamm, formXtViX

Examples

## see also ?formXtViX for use of extract.lme.cov2
require(mgcv)
library(nlme)
data(Rail)
b <- lme(travel~1,Rail,~1|Rail)
extract.lme.cov(b)
extract.lme.cov2(b)
factor.smooth

Factor smooth interactions in GAMs

Description

The interaction of one or more factors with a smooth effect, produces a separate smooth for each factor level. These smooths can have different smoothing parameters, or all have the same smoothing parameter. There are several ways to set them up.

Factor by variables. If the by variables for a smooth (specified using `s`, `te`, `ti` or `t2`) is a factor, then a separate smooth is produced for each factor level. If the factor is ordered, then no smooth is produced for its first level: this is useful for setting up models which have a reference level smooth and then difference to reference smooths for each factor level except the first (which is the reference). Giving the smooth an id forces the same smoothing parameter to be used for all levels of the factor. For example `s(x, by=fac, id=1)` would produce a separate smooth of `x` for each level of `fac`, with each smooth having the same smoothing parameter. See `gam.models` for more.

Sum to zero smooth interactions bs="sz" These factor smooth interactions are specified using `s(..., bs="sz")`. There may be several factors supplied, and a smooth is produced for each combination of factor levels. The smooths are constructed to exclude the ‘main effect’ smooth, or the effects of individual smooths produced for lower order combinations of factor levels. For example, with a single factor, the smooths for the different factor levels are so constrained that the sum over all factor levels of equivalent spline coefficients are all zero. This allows the meaningful and identifiable construction of models with a main effect smooth plus smooths for the difference between each factor level and the main effect. Such a construction is often more natural than the by variable with ordered factors construction. See `smooth.construct.sz.smooth.spec`.

Random wiggly curves bs="fs" This approach produces a smooth curve for each level of a single factor, treating the curves as entirely random. This means that in principle a model can be constructed with a main effect plus factor level smooth deviations from that effect. However the model is not forced to make the main effect do as much of the work as possible, in the way that the "sz" approach does. This approach can be very efficient with `gamm` as it exploits the nested estimation available in `lme`. See `smooth.construct.fs.smooth.spec`.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with input from Matteo Fasiolo.

See Also

`smooth.construct.fs.smooth.spec`, `smooth.construct.sz.smooth.spec`

Examples

```r
library(mgcv)
set.seed(0)
## simulate data...
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x,a=2,b=-1) exp(a * x)+b
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * (10 * x)^3 * (1 - x)^10
n <- 500;nf <- 25
```
fac <- sample(1:nf,n,replace=TRUE)
x0 <- runif(n);x1 <- runif(n);x2 <- runif(n)
a <- rnorm(nf)*.2 + 2;b <- rnorm(nf)*.5
f <- f0(x0) + f1(x1,a[fac],b[fac]) + f2(x2)
fac <- factor(fac)
y <- f + rnorm(n)*2
## so response depends on global smooths of x0 and x2, and a smooth of x1 for each level of fac.

## fit model...
bm <- gamm(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20))
plot(bm$gam,pages=1)
summary(bm$gam)

bd <- bam(y~s(x0)+ s(x1,fac,bs="sz",k=5)+s(x2,k=20),discrete=TRUE)
plot(bd,pages=1)
summary(bd)

## Could also use...
## b <- gam(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20),method="ML")
## ... but its slower (increasingly so with increasing nf)
## b <- gam(y~s(x0)+ t2(x1,fac,bs=c("tp","re"),k=5,full=TRUE)+
## s(x2,k=20),method="ML")
## ... is exactly equivalent.

---

**family.mgcv**

**Distribution families in mgcv**

**Description**

As well as the standard families (of class family) documented in family (see also glm) which can be used with functions gam, bam and gamm, mgcv also supplies some extra families, most of which are currently only usable with gam, although some can also be used with bam. These are described here.

**Details**

The following families (class family) are in the exponential family given the value of a single parameter. They are usable with all modelling functions.

- **Tweedie** An exponential family distribution for which the variance of the response is given by the mean response to the power $p$. $p$ is in $(1,2)$ and must be supplied. Alternatively, see tw to estimate $p$ (gam/bam only).
- **negbin** The negative binomial. Alternatively see nb to estimate the theta parameter of the negative binomial (gam/bam only).

The following families (class extended.family) are for regression type models dependent on a single linear predictor, and with a log likelihood which is a sum of independent terms, each corresponding to a single response observation. Usable with gam, with smoothing parameter estimation by "NCV", "REML" or "ML" (the latter does not integrate the unpenalized and parametric effects out of the marginal likelihood optimized for the smoothing parameters). Also usable with bam.
The above families of class family and extended.family can be combined to model data where different response observations come from different distributions. For example, when modelling the combination of presence-absence and abundance data, binomial and nb families might be used.

The following families (class general.family) implement more general model classes. Usable only with gam and only with REML or NCV smoothing parameter estimation.

- **cox.ph** the Cox Proportional Hazards model for survival data (no NCV).
- **gammals** a gamma location-scale model, where the mean and standard deviation are modelled with separate linear predictors.
- **gaulss** a Gaussian location-scale model where the mean and the standard deviation are both modelled using smooth linear predictors.
- **gevlss** a generalized extreme value (GEV) model where the location, scale and shape parameters are each modelled using a linear predictor.
- **gumbls** a Gumbel location-scale model (2 linear predictors).
- **multinom**: multinomial logistic regression, for unordered categorical responses.
- **mvn**: multivariate normal additive models (no NCV).
- **shash** Sinh-arcsinh location scale and shape model family (4 linear predictors).
- **twlss** Tweedie location scale and variance power model family (3 linear predictors). Can only be fitted using EFS method.
- **ziplss** a ‘two-stage’ zero inflated Poisson model, in which ‘potential-presence’ is modelled with one linear predictor, and Poisson mean abundance given potential presence is modelled with a second linear predictor.

**Author(s)**

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**References**

**FFdes**  
*Level 5 fractional factorial designs*

**Description**

Computes level 5 fractional factorial designs for up to 120 factors using the algorithm of Sanchez and Sanchez (2005), and optionally central composite designs.

**Usage**

```r
FFdes(size=5, ccd=FALSE)
```

**Arguments**

- `size` number of factors up to 120.
- `ccd` if TRUE, adds points along each axis at the same distance from the origin as the points in the fractional factorial design, to create the outer points of a central composite design. Add central points to complete.

**Details**

Basically a translation of the code provided in the appendix of Sanchez and Sanchez (2005).

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**Examples**

```r
require(mgcv)
plot(rbind(0,FFdes(2,TRUE)),xlab="x",ylab="y",
col=c(2,1,1,1,4,4,4,4),pch=19,main="CCD")
FFdes(5)
FFdes(5,TRUE)
```

---

**fix.family.link**  
*Modify families for use in GAM fitting and checking*

**Description**

Generalized Additive Model fitting by ‘outer’ iteration, requires extra derivatives of the variance and link functions to be added to family objects. The first 3 functions add what is needed. Model checking can be aided by adding quantile and random deviate generating functions to the family. The final two functions do this.
fix.family.link(fam)
fix.family.var(fam)
fix.family.ls(fam)
fix.family.qf(fam)
fix.family.rd(fam)

Arguments

fam A family.

Details

Consider the first 3 function first.
Outer iteration GAM estimation requires derivatives of the GCV, UBRE/gAIC, GACV, REML or ML score, which are obtained by finding the derivatives of the model coefficients w.r.t. the log smoothing parameters, using the implicit function theorem. The expressions for the derivatives require the second and third derivatives of the link w.r.t. the mean (and the 4th derivatives if Fisher scoring is not used). Also required are the first and second derivatives of the variance function w.r.t. the mean (plus the third derivative if Fisher scoring is not used). Finally REML or ML estimation of smoothing parameters requires the log saturated likelihood and its first two derivatives w.r.t. the scale parameter. These functions add functions evaluating these quantities to a family.

If the family already has functions dvar, d2var, d3var, d2link, d3link, d4link and for RE/ML ls, then these functions simply return the family unmodified: this allows non-standard links to be used with gam when using outer iteration (performance iteration operates with unmodified families). Note that if you only need Fisher scoring then d4link and d3var can be dummy, as they are ignored. Similarly ls is only needed for RE/ML.

The dvar function is a function of a mean vector, mu, and returns a vector of corresponding first derivatives of the family variance function. The d2link function is also a function of a vector of mean values, mu: it returns a vector of second derivatives of the link, evaluated at mu. Higher derivatives are defined similarly.

If modifying your own family, note that you can often get away with supplying only a dvar and d2var, function if your family only requires links that occur in one of the standard families.

The second two functions are useful for investigating the distribution of residuals and are used by qq.gam. If possible the functions add quantile (qf) or random deviate (rd) generating functions to the family. If a family already has qf or rd functions then it is left unmodified. qf functions are only available for some families, and for quasi families neither type of function is available.

Value

A family object with extra component functions dvar, d2var, d2link, d3link, d4link, ls, and possibly qf and rd, depending on which functions are called. fix.family.var also adds a variable scale set to negative to indicate that family has a free scale parameter.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

gam.fit3, qq.gam
fixDependence

Detect linear dependencies of one matrix on another

Description

Identifies columns of a matrix X2 which are linearly dependent on columns of a matrix X1. Primarily of use in setting up identifiability constraints for nested GAMs.

Usage

fixDependence(X1, X2, tol = .Machine$double.eps^0.5, rank.def = 0, strict = FALSE)

Arguments

X1 A matrix.
X2 A matrix, the columns of which may be partially linearly dependent on the columns of X1.
tol The tolerance to use when assessing linear dependence.
rank.def If the degree of rank deficiency in X2, given X1, is known, then it can be supplied here, and tol is then ignored. Unused unless positive and not greater than the number of columns in X2.
strict if TRUE then only columns individually dependent on X1 are detected, if FALSE then enough columns to make the reduced X2 full rank and independent of X1 are detected.

Details

The algorithm uses a simple approach based on QR decomposition: see Wood (2017, section 5.6.3) for details.

Value

A vector of the columns of X2 which are linearly dependent on columns of X1 (or which need to be deleted to achieve independence and full rank if strict==FALSE). NULL if the two matrices are independent.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Examples

```r
library(mgcv)
nc=20;c1<4;c2<7
X1<-matrix(runif(n*c1),n,c1)
X2<-matrix(runif(n*c2),n,c2)
X2[,3]<-X1[,2]+X2[,4]*.1
X2[,5]<-X1[,1]*.2+X1[,2]*.04
fixDependence(X1,X2)
fixDependence(X1,X2,strict=TRUE)
```

---

**Description**

Description of `gam` formula (see Details), and how to extract it from a fitted `gam` object.

**Usage**

```r
## S3 method for class 'gam'
formula(x,...)
```

**Arguments**

- `x`: fitted model objects of class `gam` (see `gamObject`) as produced by `gam()`.
- `...`: un-used in this case

**Details**

`gam` will accept a formula or, with some families, a list of formulae. Other `mgcv` modelling functions will not accept a list. The list form provides a mechanism for specifying several linear predictors, and allows these to share terms: see below.

The formulae supplied to `gam` are exactly like those supplied to `glm` except that smooth terms, `s`, `te`, `ti` and `t2` can be added to the right hand side (and `. ` is not supported in `gam` formulae).

Smooth terms are specified by expressions of the form:

```
s(x1,x2,...,k=12,fx=FALSE,bs="tp",by=z,id=1)
```

where `x1`, `x2`, etc. are the covariates which the smooth is a function of, and `k` is the dimension of the basis used to represent the smooth term. If `k` is not specified then basis specific defaults are used. Note that these defaults are essentially arbitrary, and it is important to check that they are not so small that they cause oversmoothing (too large just slows down computation). Sometimes the modelling context suggests sensible values for `k`, but if not informal checking is easy: see `choose.k` and `gam.check`.

`fx` is used to indicate whether or not this term should be unpenalized, and therefore have a fixed number of degrees of freedom set by `k` (almost always `k-1`). `bs` indicates the basis to use for the smooth: the built in options are described in `smooth.terms`, and user defined smooths can be added (see `user.defined.smooth`). If `bs` is not supplied then the default "tp" (`tp`) basis is used. `by` can be used to specify a variable by which the smooth should be multiplied. For example `gam(y~s(x,by=z))` would specify a model `E(y) = f(x)z` where `f(·)` is a smooth function. The `by` option is particularly useful for models in which different functions of the same variable are required for each level of a factor and for ‘varying coefficient models’: see `gam.models`. `id` is
used to give smooths identities: smooths with the same identity have the same basis, penalty and smoothing parameter (but different coefficients, so they are different functions).

An alternative for specifying smooths of more than one covariate is e.g.:

```r
te(x,z,bs=c("tp","tp"),m=c(2,3),k=c(5,10))
```

which would specify a tensor product smooth of the two covariates x and z constructed from marginal t.p.r.s. bases of dimension 5 and 10 with marginal penalties of order 2 and 3. Any combination of basis types is possible, as is any number of covariates. ti terms are a variant designed to be used as interaction terms when the main effects (and any lower order interactions) are present. t2 produces tensor product smooths that are the natural low rank analogue of smoothing spline anova models.

s, te, ti and t2 terms accept an sp argument of supplied smoothing parameters: positive values are taken as fixed values to be used, negative to indicate that the parameter should be estimated. If sp is supplied then it over-rides whatever is in the sp argument to gam, if it is not supplied then it defaults to all negative, but does not over-ride the sp argument to gam.

Formulae can involve nested or “overlapping” terms such as

```r
y~s(x)+s(z)+s(x,z)
```
or

```r
y~s(x,z)+s(z,v)
```

but nested models should really be set up using ti terms: see `gam.side` for further details and examples.

Smooth terms in a `gam` formula will accept matrix arguments as covariates (and corresponding by variable), in which case a ‘summation convention’ is invoked. Consider the example of

```r
s(X,Z,by=L)
```

where X, Z and L are n by m matrices. Let F be the n by m matrix that results from evaluating the smooth at the values in X and Z. Then the contribution to the linear predictor from the term will be `rowSums(F*L)` (note the element-wise multiplication). This convention allows the linear predictor of the GAM to depend on (a discrete approximation to) any linear functional of a smooth: see `linear.functional.terms` for more information and examples (including functional linear models/signal regression).

Note that `gam` allows any term in the model formula to be penalized (possibly by multiple penalties), via the `paraPen` argument. See `gam.models` for details and example code.

When several formulae are provided in a list, then they can be used to specify multiple linear predictors for families for which this makes sense (e.g. `mvn`). The first formula in the list must include a response variable, but later formulae need not (depending on the requirements of the family). Let the linear predictors be indexed, 1 to d where d is the number of linear predictors, and the indexing is in the order in which the formulae appear in the list. It is possible to supply extra formulae specifying that several linear predictors should share some terms. To do this a formula is supplied in which the response is replaced by numbers specifying the indices of the linear predictors which will share the terms specified on the r.h.s. For example `1+3~s(x)+z-1` specifies that linear predictors 1 and 3 will share the terms s(x) and z (but we don’t want an extra intercept, as this would usually be unidentifiable). Note that it is possible that a linear predictor only includes shared terms: it must still have its own formula, but the r.h.s. would simply be `-1` (e.g. `y ~ -1` or `~ -1`). See `multinom` for an example.

### Value

Returns the model formula, `x$formula`. Provided so that `anova` methods print an appropriate description of the model.

### WARNING

A `gam` formula should not refer to variables using e.g. `dat[['x']]`. 

---

**formula.gam**

2915
formXtViX

Description
This is a service routine for `gamm`. Given, $V$, an estimated covariance matrix obtained using `extract.lme.cov2` this routine forms a matrix square root of $X^T V^{-1} X$ as efficiently as possible, given the structure of $V$ (usually sparse).

Usage
formXtViX(V, X)

Arguments
- `V`: A data covariance matrix list returned from `extract.lme.cov2`
- `X`: A model matrix.

Details
The covariance matrix returned by `extract.lme.cov2` may be in a packed and re-ordered format, since it is usually sparse. Hence a special service routine is required to form the required products involving this matrix.

Value
A matrix, $R$ such that `crossprod(R)` gives $X^T V^{-1} X$.

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References
For `lme` see:
For details of how GAMMs are set up for estimation using `lme` see:
`https://www.maths.ed.ac.uk/~swood34/`

See Also
`gamm`, `extract.lme.cov2`
Examples

```r
require(mgcv)
library(nlme)
data(ergoStool)
b <- lme(effort ~ Type, data=ergoStool, random=-1|Subject)
V1 <- extract.lme.cov(b, ergoStool)
V2 <- extract.lme.cov2(b, ergoStool)
X <- model.matrix(b, data=ergoStool)
crossprod(formXtViX(V2, X))
t(X)
```

---

**fs.test**  
*FELSPLINE test function*

Description

Implements a finite area test function based on one proposed by Tim Ramsay (2002).

Usage

```r
fs.test(x,y,r0=.1,r=.5,l=3,b=1,exclude=TRUE)
fs.boundary(r0=.1,r=.5,l=3,n.theta=20)
```

Arguments

- `x`, `y` Points at which to evaluate the test function.
- `r0` The test domain is a sort of bent sausage. This is the radius of the inner bend.
- `r` The radius of the curve at the centre of the sausage.
- `l` The length of an arm of the sausage.
- `b` The rate at which the function increases per unit increase in distance along the centre line of the sausage.
- `exclude` Should exterior points be set to NA?
- `n.theta` How many points to use in a piecewise linear representation of a quarter of a circle, when generating the boundary curve.

Details

The function details are not given in the source article: but this is pretty close. The function is modified from Ramsay (2002), in that it bulges, rather than being flat: this makes a better test of the smoother.

Value

`fs.test` returns function evaluations, or NAs for points outside the boundary. `fs.boundary` returns a list of `x`, `y` points to be jointed up in order to define/draw the boundary.

Author(s)

Simon N. Wood <simon.wood@r-project.org>
References


Examples

```r
require(mgcv)
## plot the function, and its boundary...
fsb <- fsboundary()
m<-300;n<-150
xm <- seq(-1,4,length=m);yn<-seq(-1,1,length=n)
xx <- rep(xm,n);yy<-rep(yn,rep(m,n))
tru <- matrix(fs.test(xx,yy),m,n) ## truth
image(xm,yn,tru,col=heat.colors(100),xlab="x",ylab="y")
lines(fsb$x,fsb$y,lwd=3)
contour(xm,yn,tru,levels=seq(-5,5,by=.25),add=TRUE)
```

full.score

GCV/UBRE score for use within nlm

Description

Evaluates GCV/UBRE score for a GAM, given smoothing parameters. The routine calls `gam.fit` to fit the model, and is usually called by `nlm` to optimize the smoothing parameters.

This is basically a service routine for `gam`, and is not usually called directly by users. It is only used in this context for GAMs fitted by outer iteration (see `gam.outer`) when the the outer method is "nlm.fd" (see `gam` argument optimizer).

Usage

```r
full.score(sp,G,family,control,gamma,...)
```

Arguments

- `sp` The logs of the smoothing parameters
- `G` a list returned by `mgcv:::gam.setup`
- `family` The family object for the GAM.
- `control` a list returned be `gam.control`
- `gamma` the degrees of freedom inflation factor (usually 1).
- `...` other arguments, typically for passing on to `gam.fit`.

Value

The value of the GCV/UBRE score, with attribute "full.gam.object" which is the full object returned by `gam.fit`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>
Generalized additive models with integrated smoothness estimation

Description

Fits a generalized additive model (GAM) to data, the term ‘GAM’ being taken to include any quadratically penalized GLM and a variety of other models estimated by a quadratically penalised likelihood type approach (see family.mgcv). The degree of smoothness of model terms is estimated as part of fitting. gam can also fit any GLM subject to multiple quadratic penalties (including estimation of degree of penalization). Confidence/credible intervals are readily available for any quantity predicted using a fitted model.

Smooth terms are represented using penalized regression splines (or similar smoothers) with smoothing parameters selected by GCV/UBRE/AIC/REML/NCV or by regression splines with fixed degrees of freedom (mixtures of the two are permitted). Multi-dimensional smooths are available using penalized thin plate regression splines (isotropic) or tensor product splines (when an isotropic smooth is inappropriate), and users can add smooths. Linear functionals of smooths can also be included in models. For an overview of the smooths available see smooth.terms. For more on specifying models see gam.models, random.effects and linear.functional.terms. For more on model selection see gam.selection. Do read gam.check and choose.k.

For GAMs via the original Hastie and Tibshirani approach (see details for differences to this implementation).

For very large datasets see bam, for mixed GAM see gamm and random.effects.

Usage

gam(formula, family=gaussian(), data=list(), weights=NULL, subset=NULL, na.action, offset=NULL, method="GCV.Cp", optimizer=c("outer","newton"), control=list(), scale=0, select=FALSE, knots=NULL, sp=NULL, min.sp=NULL, H=NULL, gamma=1, fit=TRUE, paraPen=NULL, G=NULL, in.out, drop.unused.levels=TRUE, drop.intercept=NULL, nei=NULL, discrete=FALSE, ...)

Arguments

formula A GAM formula, or a list of formulae (see formula.gam and also gam.models). These are exactly like the formula for a GLM except that smooth terms, s, te, ti and t2, can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).

family This is a family object specifying the distribution and link to use in fitting etc (see glm and family). See family.mgcv for a full list of what is available, which goes well beyond exponential family. Note that quasi families actually result in the use of extended quasi-likelihood if method is set to a RE/ML method (McCullagh and Nelder, 1989, 9.6).

data A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from environment(formula): typically the environment from which gam is called.

weights prior weights on the contribution of the data to the log likelihood. Note that a weight of 2, for example, is equivalent to having made exactly the same observation twice. If you want to re-weight the contributions of each datum without
changing the overall magnitude of the log likelihood, then you should normalize
the weights (e.g. weights <- weights/mean(weights)).

subset
an optional vector specifying a subset of observations to be used in the fitting
process.

na.action
a function which indicates what should happen when the data contain 'NA's.
The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is
unset. The "factory-fresh" default is 'na.omit'.

offset
Can be used to supply a model offset for use in fitting. Note that this offset
will always be completely ignored when predicting, unlike an offset included in
formula (this used to conform to the behaviour of lm and glm).

control
A list of fit control parameters to replace defaults returned by \texttt{gam.control}.
Values not set assume default values.

method
The smoothing parameter estimation method. "GCV.Cp" to use GCV for
unknown scale parameter and Mallows' Cp/UBRE/AIC for known scale. "GACV.Cp" is equivalent, but using GACV in place of GCV. "NCV" for neigh-
bourhood cross-validation using the neighbourhood structure specified by nei
("QNCV" for numerically more robust version). "REML" for REML estimation, in-
cluding of unknown scale, "P-REML" for REML estimation, but using a Pearson
estimate of the scale. "ML" and "P-ML" are similar, but using maximum likeli-
hood in place of REML. Beyond the exponential family "REML" is the default,
and the only other options are "ML", "NCV" or "QNCV".

optimizer
An array specifying the numerical optimization method to use to optimize the
smoothing parameter estimation criterion (given by method). "outer" for the
direct nested optimization approach. "outer" can use several alternative op-
timizers, specified in the second element of optimizer: "newton" (default),
"bfgs", "optim" or "nlm". "efs" for the extended Fellner Schall method of
Wood and Fasiolo (2017).

scale
If this is positive then it is taken as the known scale parameter. Negative signals
that the scale parameter is unknown. 0 signals that the scale parameter is 1 for
Poisson and binomial and unknown otherwise. Note that (RE)ML methods can
only work with scale parameter 1 for the Poisson and binomial cases.

select
If this is TRUE then \texttt{gam} can add an extra penalty to each term so that it can be
penalized to zero. This means that the smoothing parameter estimation that is
part of fitting can completely remove terms from the model. If the corresponding
smoothing parameter is estimated as zero then the extra penalty has no effect.
Use \texttt{gamma} to increase level of penalization.

knots
this is an optional list containing user specified knot values to be used for basis
construction. For most bases the user simply supplies the knots to be used,
which must match up with the k value supplied (note that the number of knots is
not always just k). See \texttt{tprs} for what happens in the "tp"/"ts" case. Different
terms can use different numbers of knots, unless they share a covariate.

sp
A vector of smoothing parameters can be provided here. Smoothig parameters
must be supplied in the order that the smooth terms appear in the model formula.
Negative elements indicate that the parameter should be estimated, and hence a
mixture of fixed and estimated parameters is possible. If smooths share smooth-
ing parameters then \texttt{length(sp)} must correspond to the number of underlying
smoothing parameters.

min.sp
Lower bounds can be supplied for the smoothing parameters. Note that if this
option is used then the smoothing parameters \texttt{full.sp}, in the returned object,
will need to be added to what is supplied here to get the smoothing parameters actually multiplying the penalties. \texttt{length(min.sp)} should always be the same as the total number of penalties (so it may be longer than \texttt{sp}, if smooths share smoothing parameters).

H A user supplied fixed quadratic penalty on the parameters of the GAM can be supplied, with this as its coefficient matrix. A common use of this term is to add a ridge penalty to the parameters of the GAM in circumstances in which the model is close to un-identifiable on the scale of the linear predictor, but perfectly well defined on the response scale.

\texttt{gamma} Increase this beyond 1 to produce smoother models. \texttt{gamma} multiplies the effective degrees of freedom in the GCV or UBRE/AIC. \texttt{coden/gamma} can be viewed as an effective sample size in the GCV score, and this also enables it to be used with REML/ML. Ignored with P-RE/ML or the \texttt{efs} optimizer.

\texttt{fit} If this argument is \texttt{TRUE} then \texttt{gam} sets up the model and fits it, but if it is \texttt{FALSE} then the model is set up and an object \texttt{G} containing what would be required to fit is returned is returned. See argument \texttt{G}.

\texttt{paraPen} optional list specifying any penalties to be applied to parametric model terms. \texttt{gam.models} explains more.

\texttt{G} Usually \texttt{NULL}, but may contain the object returned by a previous call to \texttt{gam} with \texttt{fit=False}, in which case all other arguments are ignored except for \texttt{sp}, \texttt{gamma}, \texttt{in.out}, \texttt{scale}, \texttt{control}, \texttt{method optimizer} and \texttt{fit}.

\texttt{in.out} optional list for initializing outer iteration. If supplied then this must contain two elements: \texttt{sp} should be an array of initialization values for all smoothing parameters (there must be a value for all smoothing parameters, whether fixed or to be estimated, but those for fixed s.p.s are not used); \texttt{scale} is the typical scale of the GCV/UBRE function, for passing to the outer optimizer, or the the initial value of the scale parameter, if this is to be estimated by RE/ML.

\texttt{drop.unused.levels} by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.

\texttt{drop.intercept} Set to \texttt{TRUE} to force the model to really not have a constant in the parametric model part, even with factor variables present. Can be vector when \texttt{formula} is a list.

\texttt{nei} A list specifying the neighbourhood structure for \texttt{NCV}. \texttt{k} is the vector of indices to be dropped for each neighbourhood and \texttt{m} gives the end of each neighbourhood. So \texttt{nei$k[(nei$m[j-1]+1):nei$m[j]]} gives the points dropped for the neighbourhood \texttt{j}. \texttt{i} is the vector of indices of points to predict, with corresponding endpoints \texttt{mi}. So \texttt{nei$i[(nei$mi[j-1]+1):nei$mi[j]]} indexes the points to predict for neighbourhood \texttt{j}. If \texttt{nei==NULL} (or \texttt{k} or \texttt{m} are missing) then leave-one-out cross validation is obtained. If \texttt{jackknife} is supplied then \texttt{TRUE} indicates to use raw jackknife covariances estimator and \texttt{FALSE} to use the conventional Bayes estimate. If not supplied then the estimator accounting for neighbourhood structure is used. \texttt{jackknife} ignored when \texttt{method} is not \texttt{NCV}.

\texttt{discrete} experimental option for setting up models for use with discrete methods employed in \texttt{bam}. Do not modify.

\texttt{...} further arguments for passing on e.g. to \texttt{gam.fit} (such as \texttt{mustart}).
Details

A generalized additive model (GAM) is a generalized linear model (GLM) in which the linear predictor is given by a user specified sum of smooth functions of the covariates plus a conventional parametric component of the linear predictor. A simple example is:

$$\log\{E(y_i)\} = \alpha + f_1(x_{1i}) + f_2(x_{2i})$$

where the (independent) response variables $y_i \sim \text{Poi}$, and $f_1$ and $f_2$ are smooth functions of covariates $x_1$ and $x_2$. The log is an example of a link function. Note that to be identifiable the model requires constraints on the smooth functions. By default these are imposed automatically and require that the function sums to zero over the observed covariate values (the presence of a metric by variable is the only case which usually suppresses this).

If absolutely any smooth functions were allowed in model fitting then maximum likelihood estimation of such models would invariably result in complex over-fitting estimates of $f_1$ and $f_2$. For this reason the models are usually fit by penalized likelihood maximization, in which the model (negative log) likelihood is modified by the addition of a penalty for each smooth function, penalizing its ‘wiggliness’. To control the trade-off between penalizing wiggliness and penalizing badness of fit each penalty is multiplied by an associated smoothing parameter: how to estimate these parameters, and how to practically represent the smooth functions are the main statistical questions introduced by moving from GLMs to GAMs.

The mgcv implementation of gam represents the smooth functions using penalized regression splines, and by default uses basis functions for these splines that are designed to be optimal, given the number basis functions used. The smooth terms can be functions of any number of covariates and the user has some control over how smoothness of the functions is measured.

gam in mgcv solves the smoothing parameter estimation problem by using the Generalized Cross Validation (GCV) criterion

$$nD/(n - DoF)^2$$

or an Un-Biased Risk Estimator (UBRE) criterion

$$D/n + 2sDoF/n - s$$

where $D$ is the deviance, $n$ the number of data, $s$ the scale parameter and $DoF$ the effective degrees of freedom of the model. Notice that UBRE is effectively just AIC rescaled, but is only used when $s$ is known.

Alternatives are GACV, NCV or a Laplace approximation to REML. There is some evidence that the latter may actually be the most effective choice. The main computational challenge solved by the mgcv package is to optimize the smoothness selection criteria efficiently and reliably.

Broadly gam works by first constructing basis functions and one or more quadratic penalty coefficient matrices for each smooth term in the model formula, obtaining a model matrix for the strictly parametric part of the model formula, and combining these to obtain a complete model matrix (design matrix) and a set of penalty matrices for the smooth terms. The linear identifiability constraints are also obtained at this point. The model is fit using gam.fit, gam.fit3 or variants, which are modifications of glm.fit. The GAM penalized likelihood maximization problem is solved by Penalized Iteratively Re-weighted Least Squares (P-IRLS) (see e.g. Wood 2000). Smoothing parameter selection is possible in one of three ways. (i) ‘Performance iteration’ uses the fact that at each P-IRLS step a working penalized linear model is estimated, and the smoothing parameter estimation can be performed for each such working model. Eventually, in most cases, both model parameter estimates and smoothing parameter estimates converge. This option is available in bam and gamm. (ii) Alternatively the P-IRLS scheme is iterated to convergence for each trial set of smoothing parameters, and GCV, UBRE or REML scores are only evaluated on convergence - optimization is then ‘outer’ to the P-IRLS loop: in this case the P-IRLS iteration has to be differentiated,
to facilitate optimization, and \texttt{gam.fit3} or one of its variants is used in place of \texttt{gam.fit}.

(iii) The extended Fellner-Schall algorithm of Wood and Fasiolo (2017) alternates estimation of model co-efficients with simple updates of smoothing parameters, eventually approximately maximizing the marginal likelihood of the model (REML). \texttt{gam} uses the second method, outer iteration, by default.

Several alternative basis-penalty types are built in for representing model smooths, but alternatives can easily be added (see \texttt{smooth.terms} for an overview and \texttt{smooth.construct} for how to add smooth classes). The choice of the basis dimension (k in the \texttt{s}, \texttt{te}, \texttt{ti} and \texttt{t2} terms) is something that should be considered carefully (the exact value is not critical, but it is important not to make it restrictively small, nor very large and computationally costly). The basis should be chosen to be larger than is believed to be necessary to approximate the smooth function concerned. The effective degrees of freedom for the smooth will then be controlled by the smoothing penalty on the term, and (usually) selected automatically (with an upper limit set by k-1 or occasionally k). Of course the k should not be made too large, or computation will be slow (or in extreme cases there will be more coefficients to estimate than there are data).

Note that \texttt{gam} assumes a very inclusive definition of what counts as a GAM: basically any penal-ized GLM can be used: to this end \texttt{gam} allows the non smooth model components to be penal-ized via argument \texttt{paraPen} and allows the linear predictor to depend on general linear functionals of smooths, via the summation convention mechanism described in \texttt{linear.functional.terms}. \texttt{link\{family.mgcv\}} details what is available beyond GLMs and the exponential family.


\texttt{gam()} is not a clone of Trevor Hastie’s original (as supplied in S-PLUS or package \texttt{gam}). The major differences are (i) that by default estimation of the degree of smoothness of model terms is part of model fitting, (ii) a Bayesian approach to variance estimation is employed that makes for easier confidence interval calculation (with good coverage probabilities), (iii) that the model can depend on any (bounded) linear functional of smooth terms, (iv) the parametric part of the model can be penalized, (v) simple random effects can be incorporated, and (vi) the facilities for incorporating smooths of more than one variable are different: specifically there are no \texttt{lo} smooths, but instead (a) \texttt{s} terms can have more than one argument, implying an isotropic smooth and (b) \texttt{te}, \texttt{ti} or \texttt{t2} smooths are provided as an effective means for modelling smooth interactions of any number of variables via scale invariant tensor product smooths. Splines on the sphere, Duchon splines and Gaussian Markov Random Fields are also available. (vii) Models beyond the exponential family are available. See package \texttt{gam}, for GAMs via the original Hastie and Tibshirani approach.

\textbf{Value}

If \texttt{fit=FALSE} the function returns a list \texttt{G} of items needed to fit a GAM, but doesn’t actually fit it.

Otherwise the function returns an object of class "gam" as described in \texttt{gamObject}.

\textbf{WARNINGS}

The default basis dimensions used for smooth terms are essentially arbitrary, and it should be checked that they are not too small. See \texttt{choose.k} and \texttt{gam.check}.

Automatic smoothing parameter selection is not likely to work well when fitting models to very few response data.

For data with many zeroes clustered together in the covariate space it is quite easy to set up GAMs which suffer from identifiability problems, particularly when using Poisson or binomial families. The problem is that with e.g. log or logit links, mean value zero corresponds to an infinite range on the linear predictor scale.
Author(s)

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Front end design inspired by the S function of the same name based on the work of Hastie and Tibshirani (1990). Underlying methods owe much to the work of Wahba (e.g. 1990) and Gu (e.g. 2002).

References

Key References on this implementation:


Key Reference on GAMs and related models:


Wahba (1990) Spline Models of Observational Data. SIAM


Background References:


https://www.maths.ed.ac.uk/~swood34/

See Also

mgcv-package, gamObject, gam.models, smooth.terms, linear.functional.terms, s, te predict.gam, plot.gam, summary.gam, gam.side, gam.selection, gam.control gam.check, linear.functional.terms negbin, magic, vis.gam

Examples

## see also examples in ?gam.models (e.g. 'by' variables, ## random effects and tricks for large binary datasets)

library(mgcv)
set.seed(2) ## simulate some data...
dat <- gamSim(1,n=400,dist="normal",scale=2)
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
summary(b)
plot(b,pages=1,residuals=TRUE) ## show partial residuals
plot(b,pages=1,seWithMean=TRUE) ## `with intercept' CIs
## run some basic model checks, including checking ## smoothing basis dimensions...
gam.check(b)

## same fit in two parts ..... G <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),fit=FALSE,data=dat)
b <- gam(G=G)
print(b)

## 2 part fit enabling manipulation of smoothing parameters...
G <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),fit=FALSE,data=dat,sp=b$sp)
G$lsp0 <- log(b$sp*10) ## provide log of required sp vec
gam(G=G) ## it's smoother

## change the smoothness selection method to REML
b0 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML")
## use alternative plotting scheme, and way intervals include ## smoothing parameter uncertainty...
plot(b0,pages=1,scheme=1,unconditional=TRUE)

## Would a smooth interaction of x0 and x1 be better?
## Use tensor product smooth of x0 and x1, basis ## dimension 49 (see ?te for details, also ?t2).
b1 <- gam(y~te(x0,x1,k=7)+s(x2)+s(x3),data=dat,method="REML")
plot(b1,pages=1)
plot(b1,pages=1,scheme=2) ## alternative visualization
AIC(b0,b1) ## interaction worse than additive
## Alternative: test for interaction with a smooth ANOVA decomposition (this time between x2 and x1)

```r
b0 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3)+ti(x1,x2,k=6),
        data=dat,method="REML")
summary(b0)
```

## If it is believed that x0 and x1 are naturally on the same scale, and should be treated isotropically then could try...

```r
bs <- gam(y~s(x0,x1,k=40)+s(x2)+s(x3),data=dat,method="REML")
plot(bs,pages=1)
AIC(b0,bt,bs) # additive still better.
```

## Now do automatic terms selection as well

```r
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML",select=TRUE)
plot(b1,pages=1)
```

## set the smoothing parameter for the first term, estimate rest ...

```r
bp <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),sp=c(0.01,-1,-1,-1),data=dat)
plot(bp,pages=1,scheme=1)
```

## alternatively...

```r
bp <- gam(y~s(x0,sp=.01)+s(x1)+s(x2)+s(x3),data=dat)
```

# set lower bounds on smoothing parameters ....

```r
bp<p<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),
        min.sp=c(0.001,0.01,0,10),data=dat)
print(b);print(bp)
```

# same with REML

```r
bp<p<gam(y~s(x0)+s(x1)+s(x2)+s(x3),
        min.sp=c(0.1,0.1,0,10),data=dat,method="REML")
print(b0);print(bp)
```

## now a GAM with 3df regression spline term & 2 penalized terms

```r
b0 <- gam(y~s(x0,k=4,fx=TRUE,bs="tp") + s(x1,k=12)+s(x2,k=15),data=dat)
plot(b0,pages=1)
```

## now simulate poisson data...

```r
set.seed(6)
dat <- gamSim(1,n=2000,dist="poisson",scale=.1)
```

## use "cr" basis to save time, with 2000 data...

```r
b2<gam(y~s(x0,bs="cr") + s(x1,bs="cr") + s(x2,bs="cr") +
      s(x3,bs="cr"),family=poisson,data=dat,method="REML")
plot(b2,pages=1)
```

## drop x3, but initialize sp's from previous fit, to save more time...

```r
b2a<-gam(y~s(x0,bs="cr") + s(x1,bs="cr") + s(x2,bs="cr"),
```
family=poisson, data=dat, method="REML",
in.out=list(sp=b2$sp[1:3], scale=1))
par(mfrow=c(2,2))
plot(b2a)

par(mfrow=c(1,1))
## similar example using GACV...
dat <- gamSim(1, n=400, dist="poisson", scale=.25)
b4<-gam(y~s(x0)+s(x1)+s(x2)+s(x3), family=poisson,
data=dat, method="GACV.Cp", scale=-1)
plot(b4, pages=1)
## repeat using REML as in Wood 2011...
b5<-gam(y~s(x0)+s(x1)+s(x2)+s(x3), family=poisson, 
data=dat, method="REML")
plot(b5, pages=1)

## a binary example (see ?gam.models for large dataset version)...
dat <- gamSim(1, n=400, dist="binary", scale=.33)
lr.fit <- gam(y~s(x0)+s(x1)+s(x2)+s(x3), family=binomial, 
data=dat, method="REML")

## plot model components with truth overlaid in red
op <- par(mfrow=c(2,2))
fn <- c("f0", "f1", "f2", "f3"); xn <- c("x0", "x1", "x2", "x3")
for (k in 1:4) {
  plot(lr.fit, residuals=TRUE, select=k)
  ff <- dat[[fn[k]]]; xx <- dat[[xn[k]]]
  ind <- sort.int(xx, index.return=TRUE)$ix
  lines(xx[ind], (ff-mean(ff))[ind]*.33, col=2)
}
par(op)
anova(lr.fit)
lr.fit1 <- gam(y~s(x0)+s(x1)+s(x2), family=binomial, 
data=dat, method="REML")
lr.fit2 <- gam(y~s(x1)+s(x2), family=binomial, 
data=dat, method="REML")
AIC(lr.fit, lr.fit1, lr.fit2)
## For a Gamma example, see ?summary.gam...
## For inverse Gaussian, see ?rig
## now 2D smoothing...
eg <- gamSim(2, n=500, scale=.1)
attach(eg)
op <- par(mfrow=c(2,2), mar=c(4,4,1,1))
contour(truth$x, truth$z, truth$f)  ## contour truth
```r
b4 <- gam(y~s(x,z),data=data) ## fit model
fit1 <- matrix(predict.gam(b4,pr,se=FALSE),40,40)
contour(truth$x,truth$z,fit1) ## contour fit
persp(truth$x,truth$z,truth$f) ## persp truth
vis.gam(b4) ## persp fit
detach(eg)
par(op)

#########################################################
## largish dataset example with user defined knots
#########################################################
par(mfrow=c(2,2))
n <- 5000
eg <- gamSim(2,n=n,scale=.5)
attach(eg)
ind<-sample(1:n,200,replace=FALSE)
b5<-gam(y~s(x,z,k=40),data=data,
knots=list(x=data$x[ind],z=data$z[ind]))
## various visualizations
vis.gam(b5,theta=30,phi=30)
plot(b5)
plot(b5,scheme=1,theta=50,phi=20)
plot(b5,scheme=2)
par(mfrow=c(1,1))
## and a pure "knot based" spline of the same data
b6<-gam(y~s(x,z,k=64),data=data,knots=list(x= rep((1:8-0.5)/8,8),
    z=rep((1:8-0.5)/8,rep(8,8))))
vis.gam(b6,color="heat",theta=30,phi=30)
## varying the default large dataset behaviour via `xt`
b7 <- gam(y~s(x,z,k=40,xt=list(max.knots=500,seed=2)),data=data)
vis.gam(b7,theta=30,phi=30)
detach(eg)
```

---

**Description**

Takes a fitted gam object produced by `gam()` and produces some diagnostic information about the fitting procedure and results. The default is to produce 4 residual plots, some information about the convergence of the smoothness selection optimization, and to run diagnostic tests of whether the basis dimension choices are adequate. Care should be taken in interpreting the results when applied to gam objects returned by `gamm`.

**Usage**

```r
gam.check(b, old.style=FALSE,
type=c("deviance","pearson","response"),
    k.sample=5000,k.rep=200,
    rep=0, level=.9, r1.col=2, rep.col="gray80", ...)
```
**Arguments**

- **b**: A fitted `gam` object as produced by `gam()`.
- **old.style**: If you want old-fashioned plots, exactly as in Wood, 2006, set to `TRUE`.
- **type**: Type of residuals, see `residuals.gam`, used in all plots.
- **k.sample**: Above this k testing uses a random sub-sample of data.
- **k.rep**: How many re-shuffles to do to get p-value for k testing.
- **rep, level, rl.col, rep.col**: Arguments passed to `qq.gam()` when `old.style` is false, see there.
- **...**: Extra graphics parameters to pass to plotting functions.

**Details**

Checking a fitted `gam` is like checking a fitted `glm`, with two main differences. Firstly, the basis dimensions used for smooth terms need to be checked, to ensure that they are not so small that they force oversmoothing: the defaults are arbitrary. `choose.k` provides more detail, but the diagnostic tests described below and reported by this function may also help. Secondly, fitting may not always be as robust to violation of the distributional assumptions as would be the case for a regular GLM, so slightly more care may be needed here. In particular, the theory of quasi-likelihood implies that if the mean variance relationship is OK for a GLM, then other departures from the assumed distribution are not problematic: GAMs can sometimes be more sensitive. For example, un-modelled overdispersion will typically lead to overfit, as the smoothness selection criterion tries to reduce the scale parameter to the one specified. Similarly, it is not clear how sensitive REML and ML smoothness selection will be to deviations from the assumed response distribution. For these reasons this routine uses an enhanced residual QQ plot.

This function plots 4 standard diagnostic plots, some smoothing parameter estimation convergence information and the results of tests which may indicate if the smoothing basis dimension for a term is too low.

Usually the 4 plots are various residual plots. For the default optimization methods the convergence information is summarized in a readable way, but for other optimization methods, whatever is returned by way of convergence diagnostics is simply printed.

The test of whether the basis dimension for a smooth is adequate (Wood, 2017, section 5.9) is based on computing an estimate of the residual variance based on differencing residuals that are near neighbours according to the (numeric) covariates of the smooth. This estimate divided by the residual variance is the k-index reported. The further below 1 this is, the more likely it is that there is missed pattern left in the residuals. The p-value is computed by simulation: the residuals are randomly re-shuffled k.rep times to obtain the null distribution of the differencing variance estimator, if there is no pattern in the residuals. For models fitted to more than k.sample data, the tests are based of k.sample randomly sampled data. Low p-values may indicate that the basis dimension, k, has been set too low, especially if the reported edf is close to k', the maximum possible EDF for the term. Note the disconcerting fact that if the test statistic itself is based on random resampling and the null is true, then the associated p-values will of course vary widely from one replicate to the next. Currently smooths of factor variables are not supported and will give an NA p-value.

Doubling a suspect k and re-fitting is sensible: if the reported edf increases substantially then you may have been missing something in the first fit. Of course p-values can be low for reasons other than a too low k. See `choose.k` for fuller discussion.

The QQ plot produced is usually created by a call to `qq.gam`, and plots deviance residuals against approximate theoretical quantiles of the deviance residual distribution, according to the fitted model. If this looks odd then investigate further using `qq.gam`. Note that residuals for models fitted to
binary data contain very little information useful for model checking (it is necessary to find some way of aggregating them first), so the QQ plot is unlikely to be useful in this case.

Take care when interpreting results from applying this function to a model fitted using \texttt{gamm}. In this case the returned \texttt{gam} object is based on the working model used for estimation, and will treat all the random effects as part of the error. This means that the residuals extracted from the \texttt{gam} object are not standardized for the family used or for the random effects or correlation structure. Usually it is necessary to produce your own residual checks based on consideration of the model structure you have used.

\textbf{Value}

A vector of reference quantiles for the residual distribution, if these can be computed.

\textbf{Author(s)}

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\textbf{References}


https://www.maths.ed.ac.uk/~swood34/

\textbf{See Also}

\texttt{choose.k}, \texttt{gam}, \texttt{magic}

\textbf{Examples}

library(mgcv)
set.seed(0)
dat <- gamSim(1,n=200)
b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)
gam.check(b,pch=19,cex=.3)
gam.control

Usage

gam.control(nthreads=1, ncv.threads=1, irls.reg=0.0, epsilon = 1e-07, maxit = 200, mgcv.tol=1e-7, mgcv.half=15, trace = FALSE, rank.tol=.Machine$double.eps^0.5, nlm=list(), optim=list(), newton=list(), idLinksBases=TRUE, scalePenalty=TRUE, efs.lspmax=15, efs.tol=.1, keepData=FALSE, scale.est="fletcher", edge.correct=FALSE)

Arguments

nthreads Some parts of some smoothing parameter selection methods (e.g. REML) can use some parallelization in the C code if your R installation supports openMP, and nthreads is set to more than 1. Note that it is usually better to use the number of physical cores here, rather than the number of hyper-threading cores.

ncv.threads The computations for neighbourhood cross-validation (NCV) typically scale better than the rest of the GAM computations and are worth parallelizing. ncv.threads allows you to set the number of threads to use separately.

irls.reg For most models this should be 0. The iteratively re-weighted least squares method by which GAMs are fitted can fail to converge in some circumstances. For example, data with many zeroes can cause problems in a model with a log link, because a mean of zero corresponds to an infinite range of linear predictor values. Such convergence problems are caused by a fundamental lack of identifiability, but do not show up as lack of identifiability in the penalized linear model problems that have to be solved at each stage of iteration. In such circumstances it is possible to apply a ridge regression penalty to the model to impose identifiability, and irls.reg is the size of the penalty.

epsilon This is used for judging conversion of the GLM IRLS loop in gam.fit or gam.fit3.

maxit Maximum number of IRLS iterations to perform.

mgcv.tol The convergence tolerance parameter to use in GCV/UBRE optimization.

mgcv.half If a step of the GCV/UBRE optimization method leads to a worse GCV/UBRE score, then the step length is halved. This is the number of halvings to try before giving up.

trace Set this to TRUE to turn on diagnostic output.

rank.tol The tolerance used to estimate the rank of the fitting problem.

nlm list of control parameters to pass to nlm if this is used for outer estimation of smoothing parameters (not default). See details.

optim list of control parameters to pass to optim if this is used for outer estimation of smoothing parameters (not default). See details.

newton list of control parameters to pass to default Newton optimizer used for outer estimation of log smoothing parameters. See details.

idLinksBases If smooth terms have their smoothing parameters linked via the id mechanism (see s), should they also have the same bases. Set this to FALSE only if you are sure you know what you are doing (you should almost surely set scalePenalty to FALSE as well in this case).

scalePenalty gamm is somewhat sensitive to the absolute scaling of the penalty matrices of a smooth relative to its model matrix. This option rescales the penalty matrices
to accomodate this problem. Probably should be set to FALSE if you are linking smoothing parameters but have set idLinkBases to FALSE.

**efs.lspmax**
maximum log smoothing parameters to allow under extended Fellner Schall smoothing parameter optimization.

**efs.tol**
change in REML to count as negligible when testing for EFS convergence. If the step is small and the last 3 steps led to a REML change smaller than this, then stop.

**keepData**
Should a copy of the original data argument be kept in the gam object? Strict compatibility with class glm would keep it, but it wastes space to do so.

**scale.est**
How to estimate the scale parameter for exponential family models estimated by outer iteration. See **gam.scale**.

**edge.correct**
With RE/ML smoothing parameter selection in gam using the default Newton RE/ML optimizer, it is possible to improve inference at the ‘completely smooth’ edge of the smoothing parameter space, by decreasing smoothing parameters until there is a small increase in the negative RE/ML (e.g. 0.02). Set to TRUE or to a number representing the target increase to use. Only changes the corrected smoothing parameter matrix, Vc.

**Details**

Outer iteration using newton is controlled by the list newton with the following elements: conv.tol (default 1e-6) is the relative convergence tolerance; maxNstep is the maximum length allowed for an element of the Newton search direction (default 5); maxSstep is the maximum length allowed for an element of the steepest descent direction (only used if Newton fails - default 2); maxHalf is the maximum number of step halvings to permit before giving up (default 30).

If outer iteration using nlm is used for fitting, then the control list nlm stores control arguments for calls to routine nlm. The list has the following named elements: (i) ndigit is the number of significant digits in the GCV/UBRE score - by default this is worked out from epsilon; (ii) gradtol is the tolerance used to judge convergence of the gradient of the GCV/UBRE score to zero - by default set to 1e-epsillon; (iii) stepmax is the maximum allowable log smoothing parameter step - defaults to 2; (iv) steptol is the minimum allowable step length - defaults to 1e-4; (v) iterlim is the maximum number of optimization steps allowed - defaults to 200; (vi) check.analyticals indicates whether the built in exact derivative calculations should be checked numerically - defaults to FALSE. Any of these which are not supplied and named in the list are set to their default values.

Outer iteration using optim is controlled using list optim, which currently has one element: factr which takes default value 1e7.

**Author(s)**

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**References**


[https://www.maths.ed.ac.uk/~swood34/](https://www.maths.ed.ac.uk/~swood34/)
gam.convergence

See Also
gam, gam.fit, glm.control

Description

When fitting GAMs there is a tradeoff between speed of fitting and probability of fit convergence. The fitting methods used by gam opt for certainty of convergence over speed of fit. bam opts for speed.

gam uses a nested iteration method (see gam outer), in which each trial set of smoothing parameters proposed by an outer Newton algorithm require an inner Newton algorithm (penalized iteratively re-weighted least squares, PIRLS) to find the corresponding best fit model coefficients. Implicit differentiation is used to find the derivatives of the coefficients with respect to log smoothing parameters, so that the derivatives of the smoothness selection criterion can be obtained, as required by the outer iteration. This approach is less expensive than it at first appears, since excellent starting values for the inner iteration are available as soon as the smoothing parameters start to converge. See Wood (2011) and Wood, Pya and Saefken (2016).

bam uses an alternative approach similar to ‘performance iteration’ or ‘PQL’. A single PIRLS iteration is run to find the model coefficients. At each step this requires the estimation of a working penalized linear model. Smoothing parameter selection is applied directly to this working model at each step (as if it were a Gaussian additive model). This approach is more straightforward to code and in principle less costly than the nested approach. However it is not guaranteed to converge, since the smoothness selection criterion is changing at each iteration. It is sometimes possible for the algorithm to cycle around a small set of smoothing parameter, coefficient combinations without ever converging. bam includes some checks to limit this behaviour, and the further checks in the algorithm used by bam(..., discrete=TRUE) actually guarantee convergence in some cases, but in general guarantees are not possible. See Wood, Goude and Shaw (2015) and Wood et al. (2017).

gam when used with ‘general’ families (such as multinom or cox.ph) can also use a potentially faster scheme based on the extended Fellner-Schall method (Wood and Fasiolo, 2017). This also operates with a single iteration and is not guaranteed to converge, theoretically.

There are three things that you can try to speed up GAM fitting. (i) if you have large numbers of smoothing parameters in the generalized case, then try the "bfgs" method option in gam argument optimizer: this can be faster than the default. (ii) Try using bam (iii) For large datasets it may be worth changing the smoothing basis to use bs="cr" (see s for details) for 1-d smooths, and to use te smooths in place of s smooths for smooths of more than one variable. This is because the default thin plate regression spline basis "tp" is costly to set up for large datasets.

If you have convergence problems, it’s worth noting that a GAM is just a (penalized) GLM and the IRLS scheme used to estimate GLMs is not guaranteed to converge. Hence non convergence of a GAM may relate to a lack of stability in the basic IRLS scheme. Therefore it is worth trying to establish whether the IRLS iterations are capable of converging. To do this fit the problematic GAM with all smooth terms specified with fx=TRUE so that the smoothing parameters are all fixed at zero. If this ‘largest’ model can converge then, then the maintainer would quite like to know about your problem! If it doesn’t converge, then its likely that your model is just too flexible for the IRLS process itself. Having tried increasing maxit in gam.control, there are several other possibilities for stabilizing the iteration. It is possible to try (i) setting lower bounds on the smoothing parameters using the min.sp argument of gam: this may or may not change the model being fitted; (ii) reducing
the flexibility of the model by reducing the basis dimensions $k$ in the specification of $s$ and $te$ model terms: this obviously changes the model being fitted somewhat.

Usually, a major contributor to fitting difficulties is that the model is a very poor description of the data.

Please report convergence problems, especially if you there is no obvious pathology in the data/model that suggests convergence should fail.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Key References on this implementation:


gam.fit

GAM P-IRLS estimation with GCV/UBRE smoothness estimation

Description

This is an internal function of package mgcv. It is a modification of the function glm.fit, designed to be called from gam when performance iteration is selected (not the default). The major modification is that rather than solving a weighted least squares problem at each IRLS step, a weighted, penalized least squares problem is solved at each IRLS step with smoothing parameters associated with each penalty chosen by GCV or UBRE, using routine magic. For further information on usage see code for gam. Some regularization of the IRLS weights is also permitted as a way of addressing identifiability related problems (see gam.control). Negative binomial parameter estimation is supported.

The basic idea of estimating smoothing parameters at each step of the P-IRLS is due to Gu (1992), and is termed ‘performance iteration’ or ‘performance oriented iteration’.
**gam.fit**

**Usage**

```r
gam.fit(G, start = NULL, etastart = NULL, mustart = NULL, family = gaussian(), control = gam.control(), gamma = 1, fixedSteps = (control$maxit+1), ...)
```

**Arguments**

- `G` An object of the type returned by `gam` when `fit=FALSE`.
- `start` Initial values for the model coefficients.
- `etastart` Initial values for the linear predictor.
- `mustart` Initial values for the expected response.
- `family` The family object, specifying the distribution and link to use.
- `control` Control option list as returned by `gam.control`.
- `gamma` Parameter which can be increased to up the cost of each effective degree of freedom in the GCV or AIC/UBRE objective.
- `fixedSteps` How many steps to take: useful when only using this routine to get rough starting values for other methods.
- `...` Other arguments: ignored.

**Value**

A list of fit information.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**See Also**

`gam.fit3`, `gam`, `magic`
Description

Estimation of GAM smoothing parameters is most stable if optimization of the UBRE/AIC, GCV, GACV, REML or ML score is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters.

This routine estimates a GAM (any quadratically penalized GLM) given log smoothing parameters, and evaluates derivatives of the smoothness selection scores of the model with respect to the log smoothing parameters. Calculation of exact derivatives is generally faster than approximating them by finite differencing, as well as generally improving the reliability of GCV/UBRE/AIC/REML score minimization.

The approach is to run the P-IRLS to convergence, and only then to iterate for first and second derivatives.

Not normally called directly, but rather service routines for `gam`.

Usage

```r
gam.fit3(x, y, sp, Eb, UrS=list(),
          weights = rep(1, nobs), start = NULL, etastart = NULL,
          mustart = NULL, offset = rep(0, nobs), U1 = diag(ncol(x)),
          Mp = -1, family = gaussian(), control = gam.control(),
          intercept = TRUE, deriv=2, gamma=1, scale=1,
          printWarn=TRUE, scoreType="REML", null.coef=rep(0,ncol(x)),
          pearson.extra=0, dev.extra=0, n.true=-1, S1=NULL, nei=NULL,...)
```

Arguments

- `x` The model matrix for the GAM (or any penalized GLM).
- `y` The response variable.
- `sp` The log smoothing parameters.
- `Eb` A balanced version of the total penalty matrix: used for numerical rank determination.
- `UrS` List of square root penalties premultiplied by transpose of orthogonal basis for the total penalty.
- `weights` prior weights for fitting.
- `start` optional starting parameter guesses.
- `etastart` optional starting values for the linear predictor.
- `mustart` optional starting values for the mean.
- `offset` the model offset.
- `U1` An orthogonal basis for the range space of the penalty — required for ML smoothness estimation only.
- `Mp` The dimension of the total penalty null space — required for ML smoothness estimation only.
family the family - actually this routine would never be called with gaussian()
control control list as returned from glm.control
intercept does the model have an intercept, TRUE or FALSE
deriv Should derivatives of the GCV and UBRE/AIC scores be calculated? 0, 1 or 2, indicating the maximum order of differentiation to apply.
gamma The weight given to each degree of freedom in the GCV and UBRE scores can be varied (usually increased) using this parameter.
scale The scale parameter - needed for the UBRE/AIC score.
printWarn Set to FALSE to suppress some warnings. Useful in order to ensure that some warnings are only printed if they apply to the final fitted model, rather than an intermediate used in optimization.
scoreType specifies smoothing parameter selection criterion to use.
null.coef coefficients for a model which gives some sort of upper bound on deviance. This allows immediate divergence problems to be controlled.
pearson.extra Extra component to add to numerator of pearson statistic in P-REML/P-ML smoothness selection criteria.
dev.extra Extra component to add to deviance for REML/ML type smoothness selection criteria.
n.true Number of data to assume in smoothness selection criteria. <=0 indicates that it should be the number of rows of X.
S1 A smooth list suitable for passing to gam.fit5.
nei List specifying neighbourhood structure if NCV used. See gam.
... Other arguments: ignored.

Details
This routine is basically glm.fit with some modifications to allow (i) for quadratic penalties on the log likelihood; (ii) derivatives of the model coefficients with respect to log smoothing parameters to be obtained by use of the implicit function theorem and (iii) derivatives of the GAM GCV, UBRE/AIC, REML or ML scores to be evaluated at convergence.
In addition the routines apply step halving to any step that increases the penalized deviance substantially.
The most costly parts of the calculations are performed by calls to compiled C code (which in turn calls LAPACK routines) in place of the compiled code that would usually perform least squares estimation on the working model in the IRLS iteration.
Estimation of smoothing parameters by optimizing GCV scores obtained at convergence of the P-IRLS iteration was proposed by O’Sullivan et al. (1986), and is here termed ‘outer’ iteration.
Note that use of non-standard families with this routine requires modification of the families as described in fix.family.link.

Author(s)
Simon N. Wood <simon.wood@r-project.org>
The routine has been modified from glm.fit in R 2.0.1, written by the R core (see glm.fit for further credits).
References


https://www.maths.ed.ac.uk/~swood34/

See Also

gam.fit, gam, magic

gam.fit5.post.proc Post-processing output of gam.fit5

Description

INTERNAL function for post-processing the output of gam.fit5.

Usage

gam.fit5.post.proc(object, Sl, L, lsp0, S, off, gamma)

Arguments

object output of gam.fit5.
Sl penalty object, output of Sl.setup.
L matrix mapping the working smoothing parameters.
lsp0 log smoothing parameters.
S penalty matrix.
off vector of offsets.
gamma parameter for increasing model smoothness in fitting.

Value

A list containing:

• R: unpivoted Choleski of estimated expected hessian of log-likelihood.
• Vb: the Bayesian covariance matrix of the model parameters.
• Ve: “frequentist” alternative to Vb.
• Vc: corrected covariance matrix.
• F: matrix of effective degrees of freedom (EDF).
• edf: diag(F).
• edf2: diag(2F-FF).

Author(s)

Simon N. Wood <simon.wood@r-project.org>.
Simple posterior simulation with gam fits

Description

GAM coefficients can be simulated directly from the Gaussian approximation to the posterior for the coefficients, or using a simple Metropolis Hastings sampler. See also ginla.

Usage

```r
gam.mh(b, ns=10000, burn=1000, t.df=40, rw.scale=.25, thin=1)
```

Arguments

- `b`: a fitted model object from `gam`, `bam` fits are not supported.
- `ns`: the number of samples to generate.
- `burn`: the length of any initial burn in period to discard (in addition to codens).
- `t.df`: degrees of freedom for static multivariate t proposal. Lower for heavier tailed proposals.
- `rw.scale`: Factor by which to scale posterior covariance matrix when generating random walk proposals. Negative or non finite to skip the random walk step.
- `thin`: retain only every `thin` samples.

Details

Posterior simulation is particularly useful for making inferences about non-linear functions of the model coefficients. Simulate random draws from the posterior, compute the function for each draw, and you have a draw from the posterior for the function. In many cases the Gaussian approximation to the posterior of the model coefficients is accurate, and samples generated from it can be treated as samples from the posterior for the coefficients. See example code below. This approach is computationally very efficient.

In other cases the Gaussian approximation can become poor. A typical example is in a spatial model with a log or logit link when there is a large area of observations containing only zeroes. In this case the linear predictor is poorly identified and the Gaussian approximation can become useless (an example is provided below). In that case it can sometimes be useful to simulate from the posterior using a Metropolis Hastings sampler. A simple approach alternates fixed proposals, based on the Gaussian approximation to the posterior, with random walk proposals, based on a shrunken version of the approximate posterior covariance matrix. `gam.mh` implements this. The fixed proposal often promotes rapid mixing, while the random walk component ensures that the chain does not become stuck in regions for which the fixed Gaussian proposal density is much lower than the posterior density.

The function reports the acceptance rate of the two types of step. If the random walk acceptance probability is higher than a quarter then `rw.step` should probably be increased. Similarly if the acceptance rate is too low, it should be decreased. The random walk steps can be turned off altogether (see above), but it is important to check the chains for stuck sections if this is done.

Value

A list containing the retained simulated coefficients in matrix `bs` and two entries for the acceptance probabilities.
library(mgcv)
set.seed(3);n <- 400

### First example: simulated Tweedie model...
### First example: simulated Tweedie model...

dat <- gamSim(1,n=n,dist="poisson",scale=.2)
dat$y <- rTweedie(exp(dat$f),p=1.3,phi=.5) ## Tweedie response
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=tw(),
data=dat,method="REML")

## simulate directly from Gaussian approximate posterior...
br <- rmvn(1000,coef(b),vcov(b))

## Alternatively use MH sampling...
br <- gam.mh(b,thin=2,ns=2000,rw.scale=.15)$bs

## If 'coda' installed, can check effective sample size
## require(coda);effectiveSize(as.mcmc(br))

## Now compare simulation results and Gaussian approximation for
## smooth term confidence intervals...
x <- seq(0,1,length=100)
px <- data.frame(x0=x,x1=x,x2=x,x3=x)
X <- predict(b,newdata=px,type="lpmatrix")
par(mfrow=c(2,2))
for(i in 1:4) {
  plot(b,select=i,scale=0,scheme=1)
i1 <- b$s[[i]]$first.parabps[[i]]$last.paraf
f <- X[,i1]T(br[i,j]) ## posterior curve sample
fq <- apply(ff,1,quantile,probs=$.025,.16,.84,.975))
lines(x,fq[1,],col=2,lty=2);lines(x,fq[4,],col=2,lty=2)
lines(x,fq[2,],col=2);lines(x,fq[3,],col=2)
}

## Second example, where Gaussian approximation is a failure...
## Second example, where Gaussian approximation is a failure...
y <- c(rep(0, 89), 1, 0, 1, 0, 1, rep(0, 13), 1, 0, 0, 1,
rep(0, 10), 1, 0, 0, 1, 1, 0, 1, rep(0, 4), 1, rep(0, 3),
1, rep(0, 3), 1, rep(0, 10), 1, rep(0, 4), 1, 0, 1, 0, 0,
rep(1, 4), 0, rep(1, 5), rep(0, 4), 1, 1, rep(0, 46))
set.seed(3);x <- sort(c(0:10+5,rnorm(length(y)-11)*20+100))
b <- gam(y ~ s(x, k = 15),method = "REML", family = binomial)
br <- gam.mh(b,thin=2,ns=2000,rw.scale=.4)$bs
X <- model.matrix(b)
gam.models

Specifying generalized additive models

Description

This page is intended to provide some more information on how to specify GAMs. A GAM is a
GLM in which the linear predictor depends, in part, on a sum of smooth functions of predictors and
(possibly) linear functionals of smooth functions of (possibly dummy) predictors. Specifically let \( y_i \) denote an independent random variable with mean \( \mu_i \) and an exponential family
distribution, or failing that a known mean variance relationship suitable for use of quasi-likelihood
methods. Then the linear predictor of a GAM has a structure something like

\[
g(\mu_i) = X_i \beta + f_1(x_{1i}, x_{2i}) + f_2(x_{3i}) + L_i f_3(x_{4i}) + \ldots
\]

where \( g \) is a known smooth monotonic ‘link’ function, \( X_i \beta \) is the parametric part of the linear
predictor, the \( x_j \) are predictor variables, the \( f_j \) are smooth functions and \( L_i \) is some linear functional
of \( f_3 \). There may of course be multiple linear functional terms, or none.

The key idea here is that the dependence of the response on the predictors can be represented as
a parametric sub-model plus the sum of some (functionals of) smooth functions of one or more
of the predictor variables. Thus the model is quite flexible relative to strictly parametric linear or
generalized linear models, but still has much more structure than the completely general model that
says that the response is just some smooth function of all the covariates.

Note one important point. In order for the model to be identifiable the smooth functions usually
have to be constrained to have zero mean (usually taken over the set of covariate values). The
constraint is needed if the term involving the smooth includes a constant function in its span. \texttt{gam}
always applies such constraints unless there is a by variable present, in which case an assessment is
made of whether the constraint is needed or not (see below).

The following sections discuss specifying model structures for gam. Specification of the distribution
and link function is done using the \texttt{family} argument to \texttt{gam} and works in the same way as for \texttt{glm}.
This page therefore concentrates on the model formula for \texttt{gam}.
Models with simple smooth terms

Consider the example model.
\[ g(\mu_i) = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + f_1(x_{3i}) + f_2(x_{4i}, x_{5i}) \]
where the response variables \( y_i \) has expectation \( \mu_i \) and \( g \) is a link function.

The \texttt{gam} formula for this would be
\[ y \sim x1 + x2 + s(x3) + s(x4, x5) \]
This would use the default basis for the smooths (a thin plate regression spline basis for each), with automatic selection of the effective degrees of freedom for both smooths. The dimension of the smoothing basis is given a default value as well (the dimension of the basis sets an upper limit on the maximum possible degrees of freedom for the basis - the limit is typically one less than basis dimension). Full details of how to control smooths are given in \texttt{s} and \texttt{te}, and further discussion of basis dimension choice can be found in \texttt{choose.k}. For the moment suppose that we would like to change the basis of the first smooth to a cubic regression spline basis with a dimension of 20, while fixing the second term at 25 degrees of freedom. The appropriate formula would be:
\[ y \sim x1 + x2 + s(x3, bs="cr", k=20) + s(x4, x5, k=26, fx=TRUE) \]
The above assumes that \( x_4 \) and \( x_5 \) are naturally on similar scales (e.g. they might be co-ordinates), so that isotropic smoothing is appropriate. If this assumption is false then tensor product smoothing might be better (see \texttt{te}).
\[ y \sim x1 + x2 + s(x3) + te(x4, x5) \]
would generate a tensor product smooth of \( x_4 \) and \( x_5 \). By default this smooth would have basis dimension 25 and use cubic regression spline marginals. Varying the defaults is easy. For example
\[ y \sim x1 + x2 + s(x3) + te(x4, x5, bs="cr", ps", k=c(6,7)) \]
specifies that the tensor product should use a rank 6 cubic regression spline marginal and a rank 7 P-spline marginal to create a smooth with basis dimension 42.

Nested terms/functional ANOVA

Sometimes it is interesting to specify smooth models with a main effects + interaction structure such as
\[ E(y_i) = f_1(x_i) + f_2(z_i) + f_3(x_i, z_i) \]
or
\[ E(y_i) = f_1(x_i) + f_2(z_i) + f_3(v_i) + f_4(x_i, z_i) + f_5(z_i, v_i) + f_6(z_i, v_i) + f_7(x_i, z_i, v_i) \]
for example. Such models should be set up using \texttt{ti} terms in the model formula. For example:
\[ y \sim ti(x) + ti(z) + ti(x, z), \text{ or} \]
\[ y \sim ti(x) + ti(z) + ti(v) + ti(x, z) + ti(x, v) + ti(z, v) + ti(x, z, v). \]
The \texttt{ti} terms produce interactions with the component main effects excluded appropriately. (There is in fact no need to use \texttt{ti} terms for the main effects here, \texttt{s} terms could also be used.)
\texttt{gam} allows nesting (or ‘overlap’) of \texttt{te} and \texttt{s} smooths, and automatically generates side conditions to make such models identifiable, but the resulting models are much less stable and interpretable than those constructed using \texttt{ti} terms.

‘by’ variables

by variables are the means for constructing ‘varying-coefficient models’ (geographic regression models) and for letting smooths ‘interact’ with factors or parametric terms. They are also the key to specifying general linear functionals of smooths.

The \texttt{s} and \texttt{te} terms used to specify smooths accept an argument \texttt{by}, which is a numeric or factor variable of the same dimension as the covariates of the smooth. If a \texttt{by} variable is numeric, then its \( i^{th} \) element multiples the \( i^{th} \) row of the model matrix corresponding to the smooth term concerned.
Factor smooth interactions (see also factor.smooth.interaction). If a by variable is a factor then it generates an indicator vector for each level of the factor, unless it is an ordered factor. In the non-ordered case, the model matrix for the smooth term is then replicated for each factor level, and each copy has its rows multiplied by the corresponding rows of its indicator variable. The smoothness penalties are also duplicated for each factor level. In short a different smooth is generated for each factor level (the id argument to s and te can be used to force all such smooths to have the same smoothing parameter). ordered by variables are handled in the same way, except that no smooth is generated for the first level of the ordered factor (see b3 example below). This is useful for setting up identifiable models when the same smooth occurs more than once in a model, with different factor by variables.

As an example, consider the model

\[ E(y_i) = \beta_0 + f(x_i)z_i \]

where \( f \) is a smooth function, and \( z_i \) is a numeric variable. The appropriate formula is:
\[ y \sim s(x, by=z) \]
- the by argument ensures that the smooth function gets multiplied by covariate \( z \). Note that when using factor by variables, centering constraints are applied to the smooths, which usually means that the by variable should be included as a parametric term, as well.

The example code below also illustrates the use of factor by variables.

by variables may be supplied as numeric matrices as part of specifying general linear functional terms.

If a by variable is present and numeric (rather than a factor) then the corresponding smooth is only subjected to an identifiability constraint if (i) the by variable is a constant vector, or, (ii) for a matrix by variable, \( L, \) if \( L %*% rep(1, ncol(L)) \) is constant or (iii) if a user defined smooth constructor supplies an identifiability constraint explicitly, and that constraint has an attribute "always.apply".

**Linking smooths with ‘id’**

It is sometimes desirable to insist that different smooth terms have the same degree of smoothness. This can be done by using the id argument to s or te terms. Smooths which share an id will have the same smoothing parameter. Really this only makes sense if the smooths use the same basis functions, and the default behaviour is to force this to happen: all smooths sharing an id have the same basis functions as the first smooth occurring with that id. Note that if you want exactly the same function for each smooth, then this is best achieved by making use of the summation convention covered under ‘linear functional terms’.

As an example suppose that \( E(y_i) \equiv \mu_i \) and

\[ g(\mu_i) = f_1(x_{i1}) + f_2(x_{i2}, x_{i3}) + f_3(x_{i4}) \]

but that \( f_1 \) and \( f_3 \) should have the same smoothing parameters (and \( x_2 \) and \( x_3 \) are on different scales). Then the gam formula

\[ y \sim s(x1, id=1) + te(x_2, x_3) + s(x4, id=1) \]

would achieve the desired result. id can be numbers or character strings. Giving an id to a term with a factor by variable causes the smooths at each level of the factor to have the same smoothing parameter.

Smooth term ids are not supported by gamm.

**Linear functional terms**

General linear functional terms have a long history in the spline literature including in the penalized GLM context (see e.g. Wahba 1990). Such terms encompass varying coefficient models/ geographic
regression, functional GLMs (i.e. GLMs with functional predictors), GLASS models, etc, and allow smoothing with respect to aggregated covariate values, for example.

Such terms are implemented in mgcv using a simple ‘summation convention’ for smooth terms: If the covariates of a smooth are supplied as matrices, then summation of the evaluated smooth over the columns of the matrices is implied. Each covariate matrix and any by variable matrix must be of the same dimension. Consider, for example the term

\[ s(X, Z, \text{by}=L) \]

where \( X, Z \) and \( L \) are \( n \times p \) matrices. Let \( f \) denote the thin plate regression spline specified. The resulting contribution to the \( i^{th} \) element of the linear predictor is

\[ L_{ij} f(X_{ij}, Z_{ij}) \]

If no \( L \) is supplied then all its elements are taken as 1. In R code terms, let \( F \) denote the \( n \times p \) matrix obtained by evaluating the smooth at the values in \( X \) and \( Z \). Then the contribution of the term to the linear predictor is \( \text{rowSums}(L \times F) \) (note that it’s element by element multiplication here!).

The summation convention applies to \( te \) terms as well as \( s \) terms. More details and examples are provided in \texttt{linear.functional.terms}.

### Random effects

Random effects can be added to \texttt{gam} models using \( s(...) \text{,bs="re"} \) terms (see \texttt{smooth.construct.re.smooth.spec}), or the \texttt{paraPen} argument to \texttt{gam} covered below. See \texttt{gam.vcomp}, \texttt{random.effects} and \texttt{smooth.construct.re.smooth.spec} for further details. An alternative is to use the approach of \texttt{gamm}.

### Penalizing the parametric terms

In case the ability to add smooth classes, smooth identities, by variables and the summation convention are still not sufficient to implement exactly the penalized GLM that you require, \texttt{gam} also allows you to penalize the parametric terms in the model formula. This is mostly useful in allowing one or more matrix terms to be included in the formula, along with a sequence of quadratic penalty matrices for each.

Suppose that you have set up a model matrix \( X \), and want to penalize the corresponding coefficients, \( \beta \) with two penalties \( \beta^T S_1 \beta \) and \( \beta^T S_2 \beta \). Then something like the following would be appropriate:

\[
\text{gam}(y \sim X - 1, \text{paraPen}=\text{list}(X=\text{list}(S_1,S_2)))
\]

The \texttt{paraPen} argument should be a list with elements having names corresponding to the terms being penalized. Each element of \texttt{paraPen} is itself a list, with optional elements \( L, \text{rank} \) and \( \text{sp} \): all other elements must be penalty matrices. If present, \( \text{rank} \) is a vector giving the rank of each penalty matrix (if absent this is determined numerically). \( L \) is a matrix that maps underlying log smoothing parameters to the log smoothing parameters that actually multiply the individual quadratic penalties: taken as the identity if not supplied. \( \text{sp} \) is a vector of (underlying) smoothing parameter values: positive values are taken as fixed, negative to signal that the smoothing parameter should be estimated. Taken as all negative if not supplied.

An obvious application of \texttt{paraPen} is to incorporate random effects, and an example of this is provided below. In this case the supplied penalty matrices will be (generalized) inverse covariance matrices for the random effects — i.e. precision matrices. The final estimate of the covariance matrix corresponding to one of these penalties is given by the (generalized) inverse of the penalty matrix multiplied by the estimated scale parameter and divided by the estimated smoothing parameter for the penalty. For example, if you use an identity matrix to penalize some coefficients that are to be viewed as i.i.d. Gaussian random effects, then their estimated variance will be the estimated
scale parameter divided by the estimate of the smoothing parameter, for this penalty. See the ‘rail’ example below.

P-values for penalized parametric terms should be treated with caution. If you must have them, then use the option freq=TRUE in anova.gam and summary.gam, which will tend to give reasonable results for random effects implemented this way, but not for terms with a rank deficient penalty (or penalties with a wide eigen-spectrum).

Author(s)

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References

Wahba (1990) Spline Models of Observational Data SIAM.

Examples

```r
require(mgcv)
set.seed(10)
## simulate date from y = f(x2)*x1 + error
dat <- gamSim(3,n=400)
b <- gam(y ~ s(x2,by=x1),data=dat)
plot(b,pages=1)
summary(b)

## Factor 'by' variable example (with a spurious covariate x0)
## simulate data...
dat <- gamSim(4)
## fit model...
b <- gam(y ~ fac+s(x2,by=fac)+s(x0),data=dat)
plot(b,pages=1)
summary(b)

## repeat forcing all s(x2) terms to have the same smoothing param
## (not a very good idea for these data!)
b2 <- gam(y ~ fac+s(x2,by=fac,id=1)+s(x0),data=dat)
plot(b2,pages=1)
summary(b2)

## now repeat with a single reference level smooth, and
## two 'difference' smooths...
dat$fac <- ordered(dat$fac)
b3 <- gam(y ~ fac+s(x2)+s(x2,by=fac)+s(x0),data=dat,method="REML")
```
## An example of a simple random effects term implemented via penalization of the parametric part of the model...

dat <- gamSim(1,n=400,scale=2) ## simulate 4 term additive truth
## Now add some random effects to the simulation. Response is grouped into one of 20 groups by `fac` and each groups has a random effect added....
fac <- as.factor(sample(1:20,400,replace=TRUE))
dat$X <- model.matrix(~fac-1)
b <- rnorm(20)*.5
dat$y <- dat$y + dat$X%*%b
## now fit appropriate random effect model...
PP <- list(X=list(rank=20,diag(20))
rm <- gam(y~ X+s(x0)+s(x1)+s(x2)+s(x3),data=dat,paraPen=PP)
## Get estimated random effects standard deviation...
sig.b <- sqrt(rm$sig2/rm$sp[1]);sig.b
## a much simpler approach uses "re" terms...
m1 <- gam(y ~ s(fac,bs="re") + s(x0) + s(x1) + s(x2) + s(x3),data=dat,method="ML")
gam.vcomp(m1)
## Simple comparison with lme, using Rail data.
## See ?random.effects for a simpler method
require(nlme)
b0 <- lme(travel~1,data=Rail,~1|Rail,method="ML")
Z <- model.matrix(~Rail-1,data=Rail,
contrasts.arg=list(Rail="contr.treatment"))
b <- gam(travel~Z,data=Rail,paraPen=list(Z=list(diag(6))),method="ML")
b0
(b$reml.scale/b$sp)^.5 ## 'gam' ML estimate of Rail sd
b$reml.scale^.5 ## 'gam' ML estimate of residual sd
b0 <- lme(travel~1,data=Rail,~1|Rail,method="REML")
Z <- model.matrix(~Rail-1,data=Rail,
contrasts.arg=list(Rail="contr.treatment"))
b <- gam(travel~Z,data=Rail,paraPen=list(Z=list(diag(6))),method="REML")
b0
(b$reml.scale/b$sp)^.5 ## 'gam' REML estimate of Rail sd
b$reml.scale^.5 ## 'gam' REML estimate of residual sd

# Approximate large dataset logistic regression for rare events
# based on subsampling the zeroes, and adding an offset to approximately allow for this.
# Doing the same thing, but upweighting the sampled zeroes
# leads to problems with smoothness selection, and CIs.
n <- 50000  # simulate n data
dat <- gamSim(1, n=n, dist="binary", scale=.33)
p <- binomial()$linkinv(dat$f-6)  # make 1's rare
dat$y <- rbinom(p,1,p)  # re-simulate rare response

## Now sample all the 1's but only proportion S of the 0's
S <- 0.02  # sampling fraction of zeroes
dat <- dat[dat$y==1 | runif(n) < S,]  # sampling

## Create offset based on total sampling fraction
dat$s <- rep(log(nrow(dat)/n), nrow(dat))

lr.fit <- gam(y ~ s(x0,bs="cr") + s(x1,bs="cr") + s(x2,bs="cr") + s(x3,bs="cr") + offset(s), family=binomial, data=dat, method="REML")

## plot model components with truth overlaid in red
op <- par(mfrow=c(2,2))
fn <- c("f0","f1","f2","f3"); xn <- c("x0","x1","x2","x3")
for (k in 1:4) {
  plot(lr.fit, select=k, scale=0)
  ff <- dat[[fn[k]]]; xx <- dat[[xn[k]]]
  ind <- sort.int(xx, index.return=TRUE)$ix
  lines(xx[ind], (ff-mean(ff))[ind]*.33, col=2)
}
par(op)
rm(dat)

## A Gamma example, by modify `gamSim` output...
dat <- gamSim(1, n=400, dist="normal", scale=1)
dat$f <- dat$f/4  # true linear predictor
Ey <- exp(dat$f); scale <- .5  # mean and GLM scale parameter
# Note that 'shape' and 'scale' in 'rgamma' are almost
# opposite terminology to that used with GLM/GAM...
dat$y <- rgamma(Ey*6, shape=1/scale, scale=Ey*scale)
bg <- gam(y ~ s(x0)*s(x1)*s(x2)+s(x3), family=Gamma(link=log),
  data=dat, method="REML")
plot(bg, pages=1, scheme=1)

---

**gam.outer**

Minimize GCV or UBRE score of a GAM using 'outer' iteration

**Description**

Estimation of GAM smoothing parameters is most stable if optimization of the smoothness selection score (GCV, GACV, UBRE/AIC, REML, ML etc) is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters. This routine optimizes a smoothness selection score in this way. Basically the score is evaluated for each trial set of smoothing parameters by estimating the GAM for those smoothing parameters. The score is minimized w.r.t. the parameters numerically, using newton (default), bfgs, optim or nlm. Exact (first and second) derivatives of the score can be used by fitting with gam.fit3. This improves efficiency and reliability relative to relying on finite difference derivatives. Not normally called directly, but rather a service routine for gam.
Usage

```r
gam.outer(lsp, fscale, family, control, method, optimizer, 
    criterion, scale, gamma, G, start = NULL, nei = NULL, ...)
```

Arguments

- `lsp` The log smoothing parameters.
- `fscale` Typical scale of the GCV or UBRE/AIC score.
- `family` the model family.
- `control` control argument to pass to `gam.fit` if pure finite differencing is being used.
- `method` method argument to `gam` defining the smoothness criterion to use (but depending on whether or not scale known).
- `optimizer` The argument to `gam` defining the numerical optimization method to use.
- `criterion` Which smoothness selection criterion to use. One of "UBRE", "GCV", "GACV", "REML" or "P-REML".
- `scale` Supplied scale parameter. Positive indicates known.
- `gamma` The degree of freedom inflation factor for the GCV/UBRE/AIC score.
- `G` List produced by `mgcv:::gam.setup`, containing most of what’s needed to actually fit a GAM.
- `start` starting parameter values.
- `nei` List specifying neighbourhood structure if NCV used. See `gam`.
- `...` other arguments, typically for passing on to `gam.fit3` (ultimately).

Details

See Wood (2008) for full details on ‘outer iteration’.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


https://www.maths.ed.ac.uk/~swood34/

See Also

`gam.fit3`, `gam.magic`
Finding stable orthogonal re-parameterization of the square root penalty.

Description

INTERNAL function for finding an orthogonal re-parameterization which avoids "dominant machine zero leakage" between components of the square root penalty.

Usage

gam.reparam(rS, lsp, deriv)

Arguments

- **rS**
  - list of the square root penalties: last entry is root of fixed penalty, if fixed.penalty==TRUE (i.e. length(rS)>length(sp)). The assumption here is that rS[[i]] are in a null space of total penalty already; see e.g. totalPenaltySpace and mini.roots.

- **lsp**
  - vector of log smoothing parameters.

- **deriv**
  - if deriv==1 also the first derivative of the log-determinant of the penalty matrix is returned, if deriv>1 also the second derivative is returned.

Value

A list containing

- **S**: the total penalty matrix similarity transformed for stability.
- **rS**: the component square roots, transformed in the same way.
- **Qs**: the orthogonal transformation matrix $S = t(Qs)\%*\%S0\%*\%Qs$, where $S0$ is the untransformed total penalty implied by sp and rS on input.
- **det**: log|S|.
- **det1**: dlog|S|/dlog(sp) if deriv>0.
- **det2**: hessian of log|S| wrt log(sp) if deriv>1.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.
Scale parameter estimation in GAMs

Description

Scale parameter estimation in `gam` depends on the type of family. For extended families then the RE/ML estimate is used. For conventional exponential families, estimated by the default outer iteration, the scale estimator can be controlled using argument `scale.est` in `gam.control`. The options are "fletcher" (default), "pearson" or "deviance". The Pearson estimator is the (weighted) sum of squares of the Pearson residuals, divided by the effective residual degrees of freedom. The Fletcher (2012) estimator is an improved version of the Pearson estimator. The deviance estimator simply substitutes deviance residuals for Pearson residuals.

Usually the Pearson estimator is recommended for GLMs, since it is asymptotically unbiased. However, it can also be unstable at finite sample sizes, if a few Pearson residuals are very large. For example, a very low Poisson mean with a non zero count can give a huge Pearson residual, even though the deviance residual is much more modest. The Fletcher (2012) estimator is designed to reduce these problems.

For performance iteration the Pearson estimator is always used.

`gamm` uses the estimate of the scale parameter from the underlying call to `lme`. `bam` uses the REML estimator if the method is "fREML". Otherwise the estimator is a Pearson estimator.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with help from Mark Bravington and David Peel

References


See Also

`gam.control`

generalized Additive Model Selection

Description

This page is intended to provide some more information on how to select GAMs. In particular, it gives a brief overview of smoothness selection, and then discusses how this can be extended to select inclusion/exclusion of terms. Hypothesis testing approaches to the latter problem are also discussed.
Smoothness selection criteria

Given a model structure specified by a gam model formula, `gam()` attempts to find the appropriate smoothness for each applicable model term using prediction error criteria or likelihood based methods. The prediction error criteria used are Generalized (Approximate) Cross Validation (GCV or GACV) when the scale parameter is unknown or an Un-Biased Risk Estimator (UBRE) when it is known. UBRE is essentially scaled AIC (Generalized case) or Mallows’ Cp (additive model case). GCV and UBRE are covered in Craven and Wahba (1979) and Wahba (1990). Alternatively REML of maximum likelihood (ML) may be used for smoothness selection, by viewing the smooth components as random effects (in this case the variance component for each smooth random effect will be given by the scale parameter divided by the smoothing parameter — for smooths with multiple penalties, there will be multiple variance components). The method argument to `gam` selects the smoothness selection criterion.

Automatic smoothness selection is unlikely to be successful with few data, particularly with multiple terms to be selected. In addition GCV and UBRE/AIC score can occasionally display local minima that can trap the minimisation algorithms. GCV/UBRE/AIC scores become constant with changing smoothing parameters at very low or very high smoothing parameters, and on occasion these ‘flat’ regions can be separated from regions of lower score by a small ‘lip’. This seems to be the most common form of local minimum, but is usually avoidable by avoiding extreme smoothing parameters as starting values in optimization, and by avoiding big jumps in smoothing parameters while optimizing. Never the less, if you are suspicious of smoothing parameter estimates, try changing fit method (see `gam` arguments `method` and `optimizer`) and see if the estimates change, or try changing some or all of the smoothing parameters ‘manually’ (argument `sp` of `gam`, or `sp` arguments to `s` or `te`).

REML and ML are less prone to local minima than the other criteria, and may therefore be preferable.

Automatic term selection

Unmodified smoothness selection by GCV, AIC, REML etc. will not usually remove a smooth from a model. This is because most smoothing penalties view some space of (non-zero) functions as ‘completely smooth’ and once a term is penalized heavily enough that it is in this space, further penalization does not change it.

However it is straightforward to modify smooths so that under heavy penalization they are penalized to the zero function and thereby ‘selected out’ of the model. There are two approaches.

The first approach is to modify the smoothing penalty with an additional shrinkage term. Smooth classes `cs.smooth` and `tprs.smooth` (specified by "cs" and "ts" respectively) have smoothness penalties which include a small shrinkage component, so that for large enough smoothing parameters the smooth becomes identically zero. This allows automatic smoothing parameter selection methods to effectively remove the term from the model altogether. The shrinkage component of the penalty is set at a level that usually makes negligible contribution to the penalization of the model, only becoming effective when the term is effectively ‘completely smooth’ according to the conventional penalty.

The second approach leaves the original smoothing penalty unchanged, but constructs an additional penalty for each smooth, which penalizes only functions in the null space of the original penalty (the ‘completely smooth’ functions). Hence, if all the smoothing parameters for a term tend to infinity, the term will be selected out of the model. This latter approach is more expensive computationally, but has the advantage that it can be applied automatically to any smooth term. The `select` argument to `gam` turns on this method.

In fact, as implemented, both approaches operate by eigen-decomposing the original penalty matrix. A new penalty is created on the null space: it is the matrix with the same eigenvectors as
the original penalty, but with the originally positive eigenvalues set to zero, and the originally zero
eigenvalues set to something positive. The first approach just adds a multiple of this penalty to the
original penalty, where the multiple is chosen so that the new penalty cannot dominate the original.
The second approach treats the new penalty as an extra penalty, with its own smoothing parameter.

Of course, as with all model selection methods, some care must be taken to ensure that the automatic
selection is sensible, and a decision about the effective degrees of freedom at which to declare a
term ‘negligible’ has to be made.

Interactive term selection

In general the most logically consistent method to use for deciding which terms to include in the
model is to compare GCV/UBRE/ML scores for models with and without the term (REML scores
should not be used to compare models with different fixed effects structures). When UBRE is the
smoothness selection method this will give the same result as comparing by AIC (the AIC in this
case uses the model EDF in place of the usual model DF). Similarly, comparison via GCV score
and via AIC seldom yields different answers. Note that the negative binomial with estimated \theta
parameter is a special case: the GCV score is not informative, because of the \theta estimation
scheme used. More generally the score for the model with a smooth term can be compared to the
score for the model with the smooth term replaced by appropriate parametric terms. Candidates for
replacement by parametric terms are smooth terms with estimated degrees of freedom close to their
minimum possible.

Candidates for removal can also be identified by reference to the approximate p-values provided
by summary.gam, and by looking at the extent to which the confidence band for an estimated term
includes the zero function. It is perfectly possible to perform backwards selection using p-values
in the usual way: that is by sequentially dropping the single term with the highest non-significant
p-value from the model and re-fitting, until all terms are significant. This suffers from the same
problems as stepwise procedures for any GLM/LM, with the additional caveat that the p-values are
only approximate. If adopting this approach, it is probably best to use ML smoothness selection.

Note that GCV and UBRE are not appropriate for comparing models using different families: in
that case AIC should be used.

Caveats/platitudes

Formal model selection methods are only appropriate for selecting between reasonable models. If
formal model selection is attempted starting from a model that simply doesn’t fit the data, then it is
unlikely to provide meaningful results.

The more thought is given to appropriate model structure up front, the more successful model
selection is likely to be. Simply starting with a hugely flexible model with ‘everything in’ and
hoping that automatic selection will find the right structure is not often successful.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Marra, G. and S.N. Wood (2011) Practical variable selection for generalized additive models. Com-
putational Statistics and Data Analysis 55,2372-2387.
Wahba (1990) Spline Models of Observational Data. SIAM.
gam.side


https://www.maths.ed.ac.uk/~swood34/

See Also
gam, step.gam

Examples

## an example of automatic model selection via null space penalization
library(mgcv)
set.seed(3);n<-200
data <- gamSim(1,n=n,scale=.15,dist="poisson") # simulate data
data$x4 <- rnorm(n, 0, 1);data$x5 <- rnorm(n, 0, 1) # spurious

b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3)+s(x4)+s(x5),data=data,family=poisson,select=TRUE,method="REML")
summary(b)
plot(b,pages=1)

---

**gam.side**

Identifiability side conditions for a GAM

**Description**

GAM formulae with repeated variables may only correspond to identifiable models given some side conditions. This routine works out appropriate side conditions, based on zeroing redundant parameters. It is called from mgcv:::gam.setup and is not intended to be called by users.

The method identifies nested and repeated variables by their names, but numerically evaluates which constraints need to be imposed. Constraints are always applied to smooths of more variables in preference to smooths of fewer variables. The numerical approach allows appropriate constraints to be applied to models constructed using any smooths, including user-defined smooths.

**Usage**

```r
 gam.side(sm,Xp,tol=Machine$double.eps*.5,with.pen=FALSE)
```

**Arguments**

- **sm** A list of smooth objects as returned by smooth.construct.
- **Xp** The model matrix for the strictly parametric model components.
- **tol** The tolerance to use when assessing linear dependence of smooths.
- **with.pen** Should the computation of dependence consider the penalties or not. Doing so will lead to fewer constraints.
Details

Models such as \( y = s(x) + s(z) + s(x,z) \) can be estimated by `gam`, but require identifiability constraints to be applied, to make them identifiable. This routine does this, effectively setting redundant parameters to zero. When the redundancy is between smooths of lower and higher numbers of variables, the constraint is always applied to the smooth of the higher number of variables.

Dependent smooths are identified symbolically, but which constraints are needed to ensure identifiability of these smooths is determined numerically, using `fixDependence`. This makes the routine rather general, and not dependent on any particular basis.

`Xp` is used to check whether there is a constant term in the model (or columns that can be linearly combined to give a constant). This is because centred smooths can appear independent, when they would be dependent if there is a constant in the model, so dependence testing needs to take account of this.

Value

A list of smooths, with model matrices and penalty matrices adjusted to automatically impose the required constraints. Any smooth that has been modified will have an attribute "del.index", listing the columns of its model matrix that were deleted. This index is used in the creation of prediction matrices for the term.

WARNINGS

Much better statistical stability will be obtained by using models like \( y = s(x) + s(z) + ti(x,z) \) or \( y = ti(x) + ti(z) + ti(x,z) \) rather than \( y = s(x) + s(z) + s(x,z) \), since the former are designed not to require further constraint.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

ti, gam.models

Examples

```r
## The first two examples here illustrate models that cause
## gam.side to impose constraints, but both are a bad way
## of estimating such models. The 3rd example is the right
## way....
set.seed(7)
require(mgcv)
dat <- gamSim(n=400,scale=2) ## simulate data
## estimate model with redundant smooth interaction (bad idea).
b <- gam(y~s(x0)+s(x1)+s(x0,x1)+s(x2),data=dat)
plot(b,pages=1)

## Simulate data with real interaction...
dat <- gamSim(2,n=500,scale=.1)
old.par <- par(mfrow=c(2,2))

## a fully nested tensor product example (bad idea)
b <- gam(y~s(x,bs="cr",k=6)+s(z,bs="cr",k=6)+te(x,z,k=6),
        data=dat$data)
```
plot(b)
old.par<par(mfrow=c(2,2))
## A fully nested tensor product example, done properly,
## so that gam.side is not needed to ensure identifiability.
## ti terms are designed to produce interaction smooths
## suitable for adding to main effects (we could also have
## used s(x) and s(z) without a problem, but not s(z,x)
## or te(z,x)).
b <- gam(y ~ ti(x,k=6) + ti(z,k=6) + ti(x,z,k=6),
  data=dat$data)
plot(b)
par(old.par)
rm(dat)

---

**gam.vcomp**  
Report gam smoothness estimates as variance components

### Description

GAMs can be viewed as mixed models, where the smoothing parameters are related to variance components. This routine extracts the estimated variance components associated with each smooth term, and if possible returns confidence intervals on the standard deviation scale.

### Usage

```
gam.vcomp(x,rescale=TRUE,conf.lev=.95)
```

### Arguments

- **x**: a fitted model object of class `gam` as produced by `gam()`.
- **rescale**: the penalty matrices for smooths are rescaled before fitting, for numerical stability reasons, if `TRUE` this rescaling is reversed, so that the variance components are on the original scale.
- **conf.lev**: when the smoothing parameters are estimated by REML or ML, then confidence intervals for the variance components can be obtained from large sample likelihood results. This gives the confidence level to work at.

### Details

The (pseudo) inverse of the penalty matrix penalizing a term is proportional to the covariance matrix of the term’s coefficients, when these are viewed as random. For single penalty smooths, it is possible to compute the variance component for the smooth (which multiplies the inverse penalty matrix to obtain the covariance matrix of the smooth’s coefficients). This variance component is given by the scale parameter divided by the smoothing parameter.

This routine computes such variance components, for `gam` models, and associated confidence intervals, if smoothing parameter estimation was likelihood based. Note that variance components are also returned for tensor product smooths, but that their interpretation is not so straightforward.

The routine is particularly useful for model fitted by `gam` in which random effects have been incorporated.
Value

Either a vector of variance components for each smooth term (as standard deviations), or a matrix. The first column of the matrix gives standard deviations for each term, while the subsequent columns give lower and upper confidence bounds, on the same scale.

For models in which there are more smoothing parameters than actually estimated (e.g. if some were fixed, or smoothing parameters are linked) then a list is returned. The vc element is as above, the all element is a vector of variance components for all the smoothing parameters (estimated + fixed or replicated).

The routine prints a table of estimated standard deviations and confidence limits, if these can be computed, and reports the numerical rank of the covariance matrix.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

smooth.construct.re.smooth.spec

Examples

set.seed(3)
require(mgcv)
## simulate some data, consisting of a smooth truth + random effects
dat <- gamSim(1,n=400,dist="normal",scale=2)
a <- factor(sample(1:10,400,replace=TRUE))
b <- factor(sample(1:7,400,replace=TRUE))
Xa <- model.matrix(~a-1)  ## random main effects
Xb <- model.matrix(~b-1)
Xab <- model.matrix(~a:b-1)  ## random interaction
dat$y <- dat$y + Xa%*%rnorm(10)*.5 +
       Xb%*%rnorm(7)*.3 + Xab%*%rnorm(70)*.7
dat$a <- a;dat$b <- b

## Fit the model using "re" terms, and smoother linkage
mod <- gam(y~s(a,bs="re")+s(b,bs="re")+s(a,b,bs="re")+s(x0,bs="re")+s(x1,bs="re")+s(x2,k=15)+s(x3),data=dat,method="ML")
gam.vcomp(mod)
gam2objective

Objective functions for GAM smoothing parameter estimation

Description

Estimation of GAM smoothing parameters is most stable if optimization of the UBRE/AIC or GCV score is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters. These functions evaluate the GCV/UBRE/AIC score of a GAM model, given smoothing parameters, in a manner suitable for use by optim or nlm. Not normally called directly, but rather service routines for gam.outer.

Usage

gam2objective(lsp, args, ...)
gam2derivative(lsp, args, ...)

Arguments

lsp
  The log smoothing parameters.
args
  List of arguments required to call gam.fit3.
...
  Other arguments for passing to gam.fit3.

Details

gam2objective and gam2derivative are functions suitable for calling by optim, to evaluate the GCV/UBRE/AIC score and its derivatives w.r.t. log smoothing parameters.
gam4objective is an equivalent to gam2objective, suitable for optimization by nlm - derivatives of the GCV/UBRE/AIC function are calculated and returned as attributes.

The basic idea of optimizing smoothing parameters ‘outer’ to the P-IRLS loop was first proposed in O’Sullivan et al. (1986).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

See Also

gam.fit3, gam, magic
gamlss.etamu

Transform derivatives wrt mu to derivatives wrt linear predictor

Description

Mainly intended for internal use in specifying location scale models. Let \( g(\mu) = \beta \), where \( \beta \) is the linear predictor, and \( g \) is the link function. Assume that we have calculated the derivatives of the log-likelihood wrt \( \mu \). This function uses the chain rule to calculate the derivatives of the log-likelihood wrt \( \beta \). See \texttt{trind.generator} for array packing conventions.

Usage

\[
gamlss.etamu(l1, l2, l3 = \text{NULL}, l4 = \text{NULL}, ig1, g2, g3 = \text{NULL},
g4 = \text{NULL}, i2, i3 = \text{NULL}, i4 = \text{NULL}, \text{deriv} = 0)
\]

Arguments

- \( l1 \): array of 1st order derivatives of log-likelihood wrt \( \mu \).
- \( l2 \): array of 2nd order derivatives of log-likelihood wrt \( \mu \).
- \( l3 \): array of 3rd order derivatives of log-likelihood wrt \( \mu \).
- \( l4 \): array of 4th order derivatives of log-likelihood wrt \( \mu \).
- \( ig1 \): reciprocal of the first derivative of the link function wrt the linear predictor.
- \( g2 \): array containing the 2nd order derivative of the link function wrt the linear predictor.
- \( g3 \): array containing the 3rd order derivative of the link function wrt the linear predictor.
- \( g4 \): array containing the 4th order derivative of the link function wrt the linear predictor.
- \( i2 \): two-dimensional index array, such that \( l2[, i2[i,j]] \) contains the partial w.r.t. params indexed by \( i,j \) with no restriction on the index values (except that they are in \( 1, \ldots, \text{ncol}(l1) \)).
- \( i3 \): third-dimensional index array, such that \( l3[, i3[i,j,k]] \) contains the partial w.r.t. params indexed by \( i,j,k \).
- \( i4 \): third-dimensional index array, such that \( l4[, i4[i,j,k,l]] \) contains the partial w.r.t. params indexed by \( i,j,k,l \).
- \( \text{deriv} \): if \( \text{deriv}==0 \) only first and second order derivatives will be calculated. If \( \text{deriv}==1 \) the function goes up to 3rd order, and if \( \text{deriv}==2 \) it provides also 4th order derivatives.

Value

A list where the arrays \( l1, l2, l3, l4 \) contain the derivatives (up to order four) of the log-likelihood wrt the linear predictor.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.
See Also

trind.generator

### gamlss.gH

**Calculating derivatives of log-likelihood wrt regression coefficients**

**Description**

Mainly intended for internal use with location scale model families. Given the derivatives of the log-likelihood wrt the linear predictor, this function obtains the derivatives and Hessian wrt the regression coefficients and derivatives of the Hessian wrt the smoothing parameters. For input derivative array packing conventions see trind.generator.

**Usage**

```r
gamlss.gH(X, jj, l1, l2, l3 = 0, i2, l4 = 0, i4, d1b = 0, d2b = 0, deriv = 0, fh = NULL, D = NULL, sandwich = FALSE)
```

**Arguments**

- **X**: matrix containing the model matrices of all the linear predictors.
- **jj**: list of index vectors such that `X[, jj[i]]` is the model matrix of the i-th linear predictor.
- **l1**: array of 1st order derivatives of each element of the log-likelihood wrt each parameter.
- **l2**: array of 2nd order derivatives of each element of the log-likelihood wrt each parameter.
- **i2**: two-dimensional index array, such that `l2[, i2[i,j]]` contains the partial wrt. params indexed by i,j with no restriction on the index values (except that they are in 1,...,ncol(l1)).
- **l3**: array of 3rd order derivatives of each element of the log-likelihood wrt each parameter.
- **i3**: third-dimensional index array, such that `l3[, i3[i,j,k]]` contains the partial w.r.t. params indexed by i,j,k.
- **l4**: array of 4th order derivatives of each element of the log-likelihood wrt each parameter.
- **i4**: third-dimensional index array, such that `l4[, i4[i,j,k,l]]` contains the partial w.r.t. params indexed by i,j,k,l.
- **d1b**: first derivatives of the regression coefficients wrt the smoothing parameters.
- **d2b**: second derivatives of the regression coefficients wrt the smoothing parameters.
- **deriv**: if deriv==0 only first and second order derivatives will be calculated. If deriv==1 the function return also the diagonal of the first derivative of the Hessian, if deriv==2 it return the full 3rd order derivative and if deriv==3 it provides also 4th order derivatives.
- **fh**: eigen-decomposition or Cholesky factor of the penalized Hessian.
- **D**: diagonal matrix, used to provide some scaling.
- **sandwich**: set to TRUE to return sandwich estimator 'filling', as opposed to the Hessian, in l2.
Value

A list containing lb - the grad vector w.r.t. coefs; lbb - the Hessian matrix w.r.t. coefs; d1H - either a list of the derivatives of the Hessian w.r.t. the smoothing parameters, or a single matrix whose columns are the leading diagonals of these derivative matrices; trHid2H - the trace of the inverse Hessian multiplied by the second derivative of the Hessian w.r.t. all combinations of smoothing parameters.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

See Also

trind.generator

gamm

*Generalized Additive Mixed Models*

Description

Fits the specified generalized additive mixed model (GAMM) to data, by a call to lme in the normal errors identity link case, or by a call to gammPQL (a modification of glmmPQL from the MASS library) otherwise. In the latter case estimates are only approximately MLEs. The routine is typically slower than gam, and not quite as numerically robust.

To use lme4 in place of nlme as the underlying fitting engine, see gamm4 from package gamm4.

Smoothes are specified as in a call to gam as part of the fixed effects model formula, but the wiggly components of the smooth are treated as random effects. The random effects structures and correlation structures available for lme are used to specify other random effects and correlations.

It is assumed that the random effects and correlation structures are employed primarily to model residual correlation in the data and that the prime interest is in inference about the terms in the fixed effects model formula including the smooths. For this reason the routine calculates a posterior covariance matrix for the coefficients of all the terms in the fixed effects formula, including the smooths.

To use this function effectively it helps to be quite familiar with the use of gam and lme.

Usage

gamm(formula, random=NULL, correlation=NULL, family=gaussian(), data=list(), weights=NULL, subset=NULL, na.action, knots=NULL, control=list(niterEM=0, optimMethod="L-BFGS-B", returnObject=TRUE), niterPQL=20, verbosePQL=TRUE, method="ML", drop.unused.levels=TRUE, mustart=NULL, etastart=NULL, ...)

Arguments

formula A GAM formula (see also formula.gam and gam.models). This is like the formula for a glm except that smooth terms (s, te etc.) can be added to the right hand side of the formula. Note that ids for smooths and fixed smoothing parameters are not supported. Any offset should be specified in the formula.
random

The (optional) random effects structure as specified in a call to \texttt{lme}: only the list form is allowed, to facilitate manipulation of the random effects structure within \texttt{gamm} in order to deal with smooth terms. See example below.

correlation

An optional \texttt{corStruct} object (see \texttt{corClasses}) as used to define correlation structures in \texttt{lme}. Any grouping factors in the formula for this object are assumed to be nested within any random effect grouping factors, without the need to make this explicit in the formula (this is slightly different to the behaviour of \texttt{lme}). This is a GEE approach to correlation in the generalized case. See examples below.

family

A family as used in a call to \texttt{glm} or \texttt{gam}. The default gaussian with identity link causes \texttt{gamm} to fit by a direct call to \texttt{lme} provided there is no offset term, otherwise \texttt{gammPQL} is used.

data

A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from \texttt{environment(formula)}, typically the environment from which \texttt{gamm} is called.

weights

In the generalized case, weights with the same meaning as \texttt{glm} weights. An \texttt{lme} type weights argument may only be used in the identity link gaussian case, with no offset (see documentation for \texttt{lme} for details of how to use such an argument).

subset

an optional vector specifying a subset of observations to be used in the fitting process.

na.action

a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.

knots

this is an optional list containing user specified knot values to be used for basis construction. Different terms can use different numbers of knots, unless they share a covariate.

control

A list of fit control parameters for \texttt{lme} to replace the defaults returned by \texttt{lmeControl}. Note the setting for the number of EM iterations used by \texttt{lme}: smooths are set up using custom \texttt{pdMat} classes, which are currently not supported by the EM iteration code. If you supply a list of control values, it is advisable to include \texttt{niterEM=0}, as well, and only increase from 0 if you want to perturb the starting values used in model fitting (usually to worse values!). The \texttt{optimMethod} option is only used if your version of R does not have the \texttt{nlmib} optimizer function.

\texttt{niterPQL}

Maximum number of PQL iterations (if any).

\texttt{verbosePQL}

Should PQL report its progress as it goes along?

\texttt{method}

Which of "ML" or "REML" to use in the Gaussian additive mixed model case when \texttt{lme} is called directly. Ignored in the generalized case (or if the model has an offset), in which case \texttt{gammPQL} is used.

\texttt{drop.unused.levels}

by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.

\texttt{mustart}

starting values for mean if PQL used.

\texttt{etastart}

starting values for linear predictor if PQL used (over-rides \texttt{mustart} if supplied).

\texttt{...}

further arguments for passing on e.g. to \texttt{lme}
Details

The Bayesian model of spline smoothing introduced by Wahba (1983) and Silverman (1985) opens up the possibility of estimating the degree of smoothness of terms in a generalized additive model as variances of the wiggly components of the smooth terms treated as random effects. Several authors have recognised this (see Wang 1998; Ruppert, Wand and Carroll, 2003) and in the normal errors, identity link case estimation can be performed using general linear mixed effects modelling software such as lme. In the generalized case only approximate inference is so far available, for example using the Penalized Quasi-Likelihood approach of Breslow and Clayton (1993) as implemented in glmmPQL by Venables and Ripley (2002). One advantage of this approach is that it allows correlated errors to be dealt with via random effects or the correlation structures available in the nlme library (using correlation structures beyond the strictly additive case amounts to using a GEE approach to fitting).

Some details of how GAMs are represented as mixed models and estimated using lme or gammPQL in gamm can be found in Wood (2004, 2006a,b). In addition gamm obtains a posterior covariance matrix for the parameters of all the fixed effects and the smooth terms. The approach is similar to that described in Lin & Zhang (1999) - the covariance matrix of the data (or pseudodata in the generalized case) implied by the weights, correlation and random effects structure is obtained, based on the estimates of the parameters of these terms and this is used to obtain the posterior covariance matrix of the fixed and smooth effects.

The bases used to represent smooth terms are the same as those used in gam, although adaptive smoothing bases are not available. Prediction from the returned gam object is straightforward using predict.gam, but this will set the random effects to zero. If you want to predict with random effects set to their predicted values then you can adapt the prediction code given in the examples below.

In the event of lme convergence failures, consider modifying options(mgcv.vc.logrange): reducing it helps to remove indefiniteness in the likelihood, if that is the problem, but too large a reduction can force over or undersmoothing. See notExp2 for more information on this option. Failing that, you can try increasing the niterEM option in control: this will perturb the starting values used in fitting, but usually to values with lower likelihood! Note that this version of gamm works best with R 2.2.0 or above and nlme, 3.1-62 and above, since these use an improved optimizer.

Value

Returns a list with two items:

- **gam**: an object of class gam, less information relating to GCV/UBRE model selection. At present this contains enough information to use predict, summary and print methods and vis.gam, but not to use e.g. the anova method function to compare models. This is based on the working model when using gammPQL.

- **lme**: the fitted model object returned by lme or gammPQL. Note that the model formulae and grouping structures may appear to be rather bizarre, because of the manner in which the GAMM is split up and the calls to lme and gammPQL are constructed.

WARNINGS

gamm has a somewhat different argument list to gam, gam arguments such as gamma supplied to gamm will just be ignored.

gamm performs poorly with binary data, since it uses PQL. It is better to use gam with s(...,bs="re") terms, or gamm4.
gamm assumes that you know what you are doing! For example, unlike glmPQL from MASS it will return the complete lme object from the working model at convergence of the PQL iteration, including the 'log likelihood', even though this is not the likelihood of the fitted GAMM.

The routine will be very slow and memory intensive if correlation structures are used for the very large groups of data. e.g. attempting to run the spatial example in the examples section with many 1000's of data is definitely not recommended: often the correlations should only apply within clusters that can be defined by a grouping factor, and provided these clusters do not get too huge then fitting is usually possible.

Models must contain at least one random effect: either a smooth with non-zero smoothing parameter, or a random effect specified in argument random.

gamm is not as numerically stable as gam: an lme call will occasionally fail. See details section for suggestions, or try the 'gamm4' package.

gamm is usually much slower than gam, and on some platforms you may need to increase the memory available to R in order to use it with large data sets (see memory.limit).

Note that the weights returned in the fitted GAM object are dummy, and not those used by the PQL iteration: this makes partial residual plots look odd.

Note that the gam object part of the returned object is not complete in the sense of having all the elements defined in gamObject and does not inherit from glm: hence e.g. multi-model anova calls will not work. It is also based on the working model when PQL is used.

The parameterization used for the smoothing parameters in gamm, bounds them above and below by an effective infinity and effective zero. See notExp2 for details of how to change this.

Linked smoothing parameters and adaptive smoothing are not supported.

Author(s)

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References


Wahba, G. (1983) Bayesian confidence intervals for the cross validated smoothing spline. JRSSB 45:133-150


https://www.maths.ed.ac.uk/~swood34/

See Also

magic for an alternative for correlated data, te, s, predict.gam, plot.gam, summary.gam, negbin, vis.gam, pdTens, gamm4 (https://cran.r-project.org/package=gamm4)

Examples

library(mgcv)
## simple examples using gamm as alternative to gam
set.seed(0)
dat <- gamSim(1,n=200,scale=2)
b <- gamm(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b$gam,pages=1)
summary(b$lme) # details of underlying lme fit
summary(b$gam) # gam style summary of fitted model
anova(b$gam)
gam.check(b$gam) # simple checking plots

b <- gamm(y~te(x0,x1)+s(x2)+s(x3),data=dat)
op <- par(mfrow=c(2,2))
plot(b$gam)
par(op)
rm(dat)

## Add a factor to the linear predictor, to be modelled as random
dat <- gamSim(6,n=200,scale=.2,dist="poisson")
b2 <- gamm(y~s(x0)+s(x1)+s(x2),family=poisson,
data=dat,random=list(fac~1))
plot(b2$gam,pages=1)
fac <- dat$fac
rm(dat)
vis.gam(b2$gam)

## In the generalized case the 'gam' object is based on the working
## model used in the PQL fitting. Residuals for this are not
## that useful on their own as the following illustrates...

gam.check(b2$gam)

## But more useful residuals are easy to produce on a model
## by model basis. For example...

fv <- exp(fitted(b2$lme)) ## predicted values (including re)
rsd <- (b2$gam$y - fv)/sqrt(fv) ## Pearson residuals (Poisson case)
op <- par(mfrow=c(1,2))
qqnorm(rsd);plot(fv^.5,rsd)
par(op)

## now an example with autocorrelated errors....
n <- 200; sig <- 2
x <- 0:(n-1)/(n-1)
f <- 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
e <- rnorm(n,0,sig)
for (i in 2:n) e[i] <- 0.6*e[i-1] + e[i]
y <- f + e

op <- par(mfrow=c(2,2))

## Fit model with AR1 residuals
b <- gamm(y~s(x,k=20),correlation=corAR1())
plot(b$gam); lines(x,f-mean(f),col=2)

## Raw residuals still show correlation, of course...
acf(residuals(b$gam),main="raw residual ACF")

## But standardized are now fine...
acf(residuals(b$lme,type="normalized"),main="standardized residual ACF")

## compare with model without AR component...
b <- gam(y~s(x,k=20))
plot(b);lines(x,f-mean(f),col=2)

## more complicated autocorrelation example - AR errors
## only within groups defined by `fac'
e <- rnorm(n,0,sig)
for (i in 2:n) e[i] <- 0.6*e[i-1]*(fac[i-1]==fac[i]) + e[i]
y <- f + e
b <- gamm(y~s(x,k=20),correlation=corAR1(form=~1|fac))
plot(b$gam); lines(x,f-mean(f),col=2)
par(op)

## more complex situation with nested random effects and within
## group correlation
set.seed(0)
n.g <- 10
n <- n.g*10*4

## simulate smooth part...
dat <- gamSim(1,n=n,scale=2)
f <- dat$f

## simulate nested random effects....
fa <- as.factor(rep(1:10,rep(n.g,10)))
ra <- rep(rnorm(10),rep(n.g,10))
fb <- as.factor(rep(rep(1:4,rep(n.g,4)),10))
rb <- rep(rnorm(4),rep(n.g,4))
for (i in 1:9) rb <- c(rb,rep(rnorm(4),rep(n.g,4)))

## simulate auto-correlated errors within groups
e<-array(0,0)
for (i in 1:40) {
  eg <- rnorm(n.g, 0, sig)
  for (j in 2:n.g) eg[j] <- eg[j-1]*0.6+ eg[j]
e<-c(e,eg)
}
dat$y <- f + ra + rb + e
dat$fa <- fa;dat$fb <- fb

## fit model ....
b <- gamm(y~s(x0,bs="cr") + s(x1,bs="cr") + s(x2,bs="cr") +
          s(x3,bs="cr"),data=dat,random=list(fa=~1,fb=~1),
correlation=corAR1())
plot(b$gam,pages=1)
summary(b$gam)
vis.gam(b$gam)

## Prediction from gam object, optionally adding
## in random effects.

## Extract random effects and make names more convenient...
refa <- ranef(b$lme,level=5)
rownames(refa) <- substr(rownames(refa),start=9,stop=20)
refb <- ranef(b$lme,level=6)
rownames(refb) <- substr(rownames(refb),start=9,stop=20)

## make a prediction, with random effects zero...
p0 <- predict(b$gam,data.frame(x0=.3,x1=.6,x2=.98,x3=.77))

## add in effect for fa = "2" and fb="2/4"...
p <- p0 + refa["2",1] + refb["2/4",1]

## and a "spatial" example...
library(nlme);set.seed(1);n <- 100
dat <- gamSim(2,n=n, scale=0) ## standard example
attach(dat)
old.par<-par(mfrow=c(2,2))
contour(truth$x,truth$z,truth$f) ## true function
f <- data$f ## true expected response

## Now simulate correlated errors...
cstr <- corGaus(.1,form = ~x+z)
cstr <- Initialize(cstr,data.frame(x=data$x,z=data$z))
V <- corMatrix(cstr) ## correlation matrix for data
Cv <- chol(V)
e <- t(Cv) %*% rnorm(n)*0.05 # correlated errors

## next add correlated simulated errors to expected values
data$y <- f + e ## ... to produce response
b<- gamm(y~s(x,z,k=50),correlation=corGaus(.1,form=~x+z),
data=data)
plot(b$gam) # gamm fit accounting for correlation
# overfits when correlation ignored.....
b1 <- gamm(y~s(x,z,k=50),data=data);plot(b1$gam)
b2 <- gamm(y~s(x,z,k=50),data=data);plot(b2)
par(old.par)

### gammals

**gammals**

**Gamma location-scale model family**

**Description**

The `gammals` family implements gamma location scale additive models in which the log of the mean and the log of the scale parameter (see details) can depend on additive smooth predictors. Useable only with `gam`, the linear predictors are specified via a list of formulae.

**Usage**

```r

gammals(link=list("identity","log"),b=-7)
```
Arguments

link  two item list specifying the link for the mean and the standard deviation. See
details for meaning which may not be intuitive.

b  The minimum log scale parameter.

Details

Used with gam to fit gamma location - scale models parameterized in terms of the log mean and the
log scale parameter (the response variance is the squared mean multiplied by the scale parameter).
Note that identity links mean that the linear predictors give the log mean and log scale directly.
By default the log link for the scale parameter simply forces the log scale parameter to have a
lower limit given by argument b: if \( \eta \) is the linear predictor for the log scale parameter, \( \phi \), then
\[
\log \phi = b + \log(1 + e^{\eta}).
\]

gam is called with a list containing 2 formulae, the first specifies the response on the left hand side
and the structure of the linear predictor for the log mean on the right hand side. The second is one
sided, specifying the linear predictor for the log scale on the right hand side.

The fitted values for this family will be a two column matrix. The first column is the mean (on
original, not log, scale), and the second column is the log scale. Predictions using predict.gam
will also produce 2 column matrices for type "link" and "response". The first column is on the
original data scale when type="response" and on the log mean scale of the linear predictor when
type="link". The second column when type="response" is again the log scale parameter, but is
on the linear predictor when type="link".

The null deviance reported for this family computed by setting the fitted values to the mean re-
sponse, but using the model estimated scale.

Value

An object inheriting from class general.family.

References

Wood, S.N., N. Pya and B. Saefken (2016), Smoothing parameter and model selection for gen-
01621459.2016.1180986

Examples

library(mgcv)
## simulate some data
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
        (10 * x)^3 * (1 - x)^10
f3 <- function(x) 0 * x
n <- 400; set.seed(9)
x0 <- runif(n); x1 <- runif(n);
x2 <- runif(n); x3 <- runif(n);
mu <- exp((f0(x0)+f2(x2))/5)
th <- exp(f1(x1))/2-2
y <- rgamma(n, shape=1/th, scale=mu*th)
b1 <- gam(list(y~s(x0)+s(x2),-s(x1)+s(x3)),family=gammals)
plot(b1, pages=1)
summary(b1)
gam.check(b1)
plot(mu,fitted(b1)[,1]);abline(0,1,col=2)
plot(log(th),fitted(b1)[,2]);abline(0,1,col=2)

---

gamObject

Fitted gam object

Description

A fitted GAM object returned by function `gam` and of class "gam" inheriting from classes "glm" and "lm". Method functions `anova`, `logLik`, `influence`, `plot`, `predict`, `print`, `residuals` and `summary` exist for this class.

All compulsory elements of "glm" and "lm" objects are present, but the fitting method for a GAM is different to a linear model or GLM, so that the elements relating to the QR decomposition of the model matrix are absent.

Value

A gam object has the following elements:

- `aic`: AIC of the fitted model: bear in mind that the degrees of freedom used to calculate this are the effective degrees of freedom of the model, and the likelihood is evaluated at the maximum of the penalized likelihood in most cases, not at the MLE.
- `assign`: Array whose elements indicate which model term (listed in `pterms`) each parameter relates to: applies only to non-smooth terms.
- `boundary`: `boundary` did parameters end up at boundary of parameter space?
- `call`: the matched call (allows `update` to be used with `gam` objects, for example).
- `cmX`: column means of the model matrix (with elements corresponding to smooths set to zero) — useful for componentwise CI calculation.
- `coefficients`: the coefficients of the fitted model. Parametric coefficients are first, followed by coefficients for each spline term in turn.
- `control`: the `gam` control list used in the fit.
- `converged`: indicates whether or not the iterative fitting method converged.
- `data`: the original supplied data argument (for class "glm" compatibility). Only included if `gam` control argument element `keepData` is set to `TRUE` (default is `FALSE`).
- `db.drho`: matrix of first derivatives of model coefficients w.r.t. log smoothing parameters.
- `deviance`: model deviance (not penalized deviance).
- `df.null`: null degrees of freedom.
- `df.residual`: effective residual degrees of freedom of the model.
- `edf`: estimated degrees of freedom for each model parameter. Penalization means that many of these are less than 1.
- `edf1`: similar, but using alternative estimate of EDF. Useful for testing.
edf2  if estimation is by ML or REML then an edf that accounts for smoothing parameter uncertainty can be computed, this is edf1. edf1 is a heuristic upper bound for edf2.

family  family object specifying distribution and link used.
fitted.values  fitted model predictions of expected value for each datum.
formula  the model formula.
full.sp  full array of smoothing parameters multiplying penalties (excluding any contribution from min.sp argument to gam). May be larger than sp if some terms share smoothing parameters, and/or some smoothing parameter values were supplied in the sp argument of gam.
F  Degrees of freedom matrix. This may be removed at some point, and should probably not be used.
gcv.ubre  The minimized smoothing parameter selection score: GCV, UBRE(AIC), GACV, negative log marginal likelihood or negative log restricted likelihood.
hat  array of elements from the leading diagonal of the 'hat' (or 'influence') matrix. Same length as response data vector.
iter  number of iterations of P-IRLS taken to get convergence.
linear.predictors  fitted model prediction of link function of expected value for each datum.
method  One of "GCV" or "UBRE", "REML", "P-REML", "ML", "P-ML", "PQL", "lme.ML" or "lme.REML", depending on the fitting criterion used.
mgcv.conv  A list of convergence diagnostics relating to the "magic" parts of smoothing parameter estimation - this will not be very meaningful for pure "outer" estimation of smoothing parameters. The items are: full.rank, The apparent rank of the problem given the model matrix and constraints; rank, The numerical rank of the problem; fully.converged, TRUE is multiple GCV/UBRE converged by meeting convergence criteria and FALSE if method stopped with a steepest descent step failure; hess.pos.def Was the hessian of the GCV/UBRE score positive definite at smoothing parameter estimation convergence?: iter How many iterations were required to find the smoothing parameters? score.calls, and how many times did the GCV/UBRE score have to be evaluated?: rms.grad, root mean square of the gradient of the GCV/UBRE score at convergence.
min.edf  Minimum possible degrees of freedom for whole model.
model  model frame containing all variables needed in original model fit.
na.action  The na.action used in fitting.
nsdf  number of parametric, non-smooth, model terms including the intercept.
null.deviance  deviance for single parameter model.
offset  model offset.
optimizer  optimizer argument to gam, or "magic" if it's a pure additive model.
outer.info  If 'outer' iteration has been used to fit the model (see gam argument optimizer) then this is present and contains whatever was returned by the optimization routine used (currently nlm or optim).
paraPen  If the paraPen argument to gam was used then this provides information on the parametric penalties. NULL otherwise.
pred.formula  one sided formula containing variables needed for prediction, used by predict.gam
prior.weights  prior weights on observations.
ptersms  terms object for strictly parametric part of model.
R  Factor R from QR decomposition of weighted model matrix, unpivoted to be in same column order as model matrix (so need not be upper triangular).
rank  apparent rank of fitted model.
reml.scale  The scale (RE)ML scale parameter estimate, if (P-)(RE)ML used for smoothness estimation.
residuals  the working residuals for the fitted model.
rV  If present, rV%*%t(rV)*sig2 gives the estimated Bayesian covariance matrix.
scale  when present, the scale (as sig2)
scale.estimated  TRUE if the scale parameter was estimated, FALSE otherwise.
sig2  estimated or supplied variance/scale parameter.
smooth  list of smooth objects, containing the basis information for each term in the model formula in the order in which they appear. These smooth objects are what gets returned by the smooth.construct objects.
sp  estimated smoothing parameters for the model. These are the underlying smoothing parameters, subject to optimization. For the full set of smoothing parameters multiplying the penalties see full.sp. Divide the scale parameter by the smoothing parameters to get, variance components, but note that this is not valid for smooths that have used rescaling to improve conditioning.
terms  terms object of model model frame.
var.summary  A named list of summary information on the predictor variables. If a parametric variable is a matrix, then the summary is a one row matrix, containing the observed data value closest to the column median, for each matrix column. If the variable is a factor then summary is the modal factor level, returned as a factor, with levels corresponding to those of the data. For numerics and matrix arguments of smooths, the summary is the mean, nearest observed value to median and maximum, as a numeric vector. Used by vis.gam, in particular.
Ve  frequentist estimated covariance matrix for the parameter estimators. Particularly useful for testing whether terms are zero. Not so useful for CI’s as smooths are usually biased.
Vp  estimated covariance matrix for the parameters. This is a Bayesian posterior covariance matrix that results from adopting a particular Bayesian model of the smoothing process. Particularly useful for creating credible/confidence intervals.
Vc  Under ML or REML smoothing parameter estimation it is possible to correct the covariance matrix Vp for smoothing parameter uncertainty. This is the corrected version.
weights  final weights used in IRLS iteration.
y  response data.

WARNINGS

This model object is different to that described in Chambers and Hastie (1993) in order to allow smoothing parameter estimation etc.

Author(s)

Simon N. Wood <simon.wood@r-project.org>
References
A Key Reference on this implementation:
Key Reference on GAMs generally:

See Also
\texttt{gam}

---

\texttt{gamSim} \hspace{1cm} \textit{Simulate example data for GAMs}

Description
Function used to simulate data sets to illustrate the use of \texttt{gam} and \texttt{gamm}. Mostly used in help files to keep down the length of the example code sections.

Usage
\texttt{gamSim(eg=1,n=400,dist="normal",scale=2,verbose=TRUE)}

Arguments
\begin{itemize}
  \item \texttt{eg} \hspace{1cm} numeric value specifying the example required.
  \item \texttt{n} \hspace{1cm} number of data to simulate.
  \item \texttt{dist} \hspace{1cm} character string which may be used to specify the distribution of the response.
  \item \texttt{scale} \hspace{1cm} Used to set noise level.
  \item \texttt{verbose} \hspace{1cm} Should information about simulation type be printed?
\end{itemize}

Details
See the source code for exactly what is simulated in each case.
\begin{enumerate}
  \item Gu and Wahba 4 univariate term example.
  \item A smooth function of 2 variables.
  \item Example with continuous by variable.
  \item Example with factor by variable.
  \item An additive example plus a factor variable.
  \item Additive + random effect.
  \item As 1 but with correlated covariates.
\end{enumerate}

Value
Depends on \texttt{eg}, but usually a dataframe, which may also contain some information on the underlying truth. Sometimes a list with more items, including a data frame for model fitting. See source code or helpfile examples where the function is used for further information.
The `gaulss` family implements Gaussian location-scale additive models in which the mean and the logb of the standard deviation (see details) can depend on additive smooth predictors. Useable only with `gam`, the linear predictors are specified via a list of formulae.

### Description

The `gaulss` family implements Gaussian location scale additive models in which the mean and the logb of the standard deviation (see details) can depend on additive smooth predictors. Useable only with `gam`, the linear predictors are specified via a list of formulae.

### Usage

```r
gaulss(link=list("identity","logb"),b=0.01)
```

### Arguments

- **link**: two item list specifying the link for the mean and the standard deviation. See details.
- **b**: The minimum standard deviation, for the "logb" link.

### Details

Used with `gam` to fit Gaussian location-scale models. `gam` is called with a list containing 2 formulae, the first specifies the response on the left hand side and the structure of the linear predictor for the mean on the right hand side. The second is one sided, specifying the linear predictor for the standard deviation on the right hand side.

Link functions "identity", "inverse", "log" and "sqrt" are available for the mean. For the standard deviation only the "logb" link is implemented: \( \eta = \log(\sigma - b) \) and \( \sigma = b + \exp(\eta) \). This link is designed to avoid singularities in the likelihood caused by the standard deviation tending to zero. Note that internally the family is parameterized in terms of the \( \tau = \sigma^{-1} \), i.e. the standard deviation of the precision, so the link and inverse link are coded to reflect this, however the relationships between the linear predictor and the standard deviation are as given above.

The fitted values for this family will be a two column matrix. The first column is the mean, and the second column is the inverse of the standard deviation. Predictions using `predict.gam` will also produce 2 column matrices for type "link" and "response". The second column when type="response" is again on the reciprocal standard deviation scale (i.e. the square root precision scale). The second column when type="link" is \( \log(\sigma - b) \). Also `plot.gam` will plot smooths relating to \( \sigma \) on the \( \log(\sigma - b) \) scale (so high values correspond to high standard deviation and low values to low standard deviation). Similarly the smoothing penalties are applied on the (log) standard deviation scale, not the log precision scale.
get.var

The null deviance reported for this family is the sum of squares of the difference between the response and the mean response divided by the standard deviation of the response according to the model. The deviance is the sum of squares of residuals divided by model standard deviations.

Value

An object inheriting from class general.family.

References


Examples

library(mgcv);library(MASS)
b <- gam(list(accel~s(times,k=20,bs="ad"),~s(times)),
data=mcycle,family=gaulss())
summary(b)
plot(b,pages=1,scale=0)

get.var Get named variable or evaluate expression from list or data.frame

Description

This routine takes a text string and a data frame or list. It first sees if the string is the name of a variable in the data frame/ list. If it is then the value of this variable is returned. Otherwise the routine tries to evaluate the expression within the data.frame/list (but nowhere else) and if successful returns the result. If neither step works then NULL is returned. The routine is useful for processing gam formulae. If the variable is a matrix then it is coerced to a numeric vector, by default.

Usage

get.var(txt,data,vecMat=TRUE)

Arguments

txt a text string which is either the name of a variable in data or when parsed is an expression that can be evaluated in data. It can also be neither in which case the function returns NULL.
data A data frame or list.
vecMat Should matrices be coerced to numeric vectors?

Value

The evaluated variable or NULL. May be coerced to a numeric vector if it’s a matrix.

Author(s)

Simon N. Wood <simon.wood@r-project.org>
gevlss

Generalized Extreme Value location-scale model family

Description

The gevlss family implements Generalized Extreme Value location scale additive models in which the location, scale and shape parameters depend on additive smooth predictors. Usable only with gam, the linear predictors are specified via a list of formulae.

Usage

gevlss(link=list("identity","identity","logit"))

Arguments

link three item list specifying the link for the location scale and shape parameters. See details.

Details

Used with gam to fit Generalized Extreme Value location scale and shape models. gam is called with a list containing 3 formulae: the first specifies the response on the left hand side and the structure of the linear predictor for the location parameter on the right hand side. The second is one sided, specifying the linear predictor for the log scale parameter on the right hand side. The third is one sided specifying the linear predictor for the shape parameter.

Link functions "identity" and "log" are available for the location (mu) parameter. There is no choice of link for the log scale parameter ($\rho = \log \sigma$). The shape parameter (xi) defaults to a modified logit link restricting its range to (-1..5), the upper limit is required to ensure finite variance, while the lower limit ensures consistency of the MLE (Smith, 1985).

The fitted values for this family will be a three column matrix. The first column is the location parameter, the second column is the log scale parameter, the third column is the shape parameter.

This family does not produce a null deviance. Note that the distribution for $\xi = 0$ is approximated by setting $\xi$ to a small number.
The derivative system code for this family is mostly auto-generated, and the family is still somewhat experimental.

The GEV distribution is rather challenging numerically, and for small datasets or poorly fitting models improved numerical robustness may be obtained by using the extended Fellner-Schall method of Wood and Fasiolo (2017) for smoothing parameter estimation. See examples.

Value

An object inheriting from class `general.family`.

References


Examples

```r
library(mgcv)
Fi.gev <- function(z,mu,sigma,xi) {
## GEV inverse cdf.
xi[abs(xi)<1e-8] <- 1e-8 ## approximate xi=0, by small xi
x <- mu + ((-log(z))^-xi-1)*sigma/xi
}

## simulate test data...
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * 
(10 * x)^3 * (1 - x)^10
set.seed(1)
n <- 500
x0 <- runif(n);x1 <- runif(n);x2 <- runif(n)
mu <- f2(x2)
 rho <- f0(x0)
 xi <- (f1(x1)-4)/9
 y <- Fi.gev(runif(n),mu,exp(rho),xi)
dat <- data.frame(y,x0,x1,x2);pairs(dat)

## fit model....
b <- gam(list(y~s(x2),~s(x0),~s(x1)),family=gevlss,data=dat)

## same fit using the extended Fellner-Schall method which
## can provide improved numerical robustness...
b <- gam(list(y~s(x2),~s(x0),~s(x1)),family=gevlss,data=dat, 
     optimizer="efs")

## plot and look at residuals...
plot(b,pages=1, scale=0)
summary(b)
```
par(mfrow=c(2,2))
mu <- fitted(b)[,1]; rho <- fitted(b)[,2]
xi <- fitted(b)[,3]
## Get the predicted expected response...
fv <- mu + exp(rho)*(gamma(1-xi)-1)/xi
rsd <- residuals(b)
plot(fv,rsd);qqnorm(rsd)
plot(fv,residuals(b,"pearson"))
plot(fv,residuals(b,"response"))

---

**gfam**

*Grouped families*

**Description**

Family for use with `gam` or `bam` allowing a univariate response vector to be made up of variables from several different distributions. The response variable is supplied as a 2 column matrix, where the first column contains the response observations and the second column indexes the distribution (family) from which it comes. `gfam` takes a list of families as its single argument.

Useful for modelling data from different sources that are linked by a model sharing some components. Smooth model components that are not shared are usually handled with by variables (see `gam.models`).

**Usage**

`gfam(fl)`

**Arguments**

- `fl` A list of families. These can be any families inheriting from `family` or `extended.family` usable with `gam`, provided that they do not usually require a matrix response variable.

**Details**

Each component function of `gfam` uses the families supplied in the list `fl` to obtain the required quantities for that family’s subset of data, and combines the results appropriately. For example it provides the total deviance (twice negative log-likelihood) of the model, along with its derivatives, by computing the family specific deviance and derivatives from each family applied to its subset of data, and summing them. Other quantities are computed in the same way.

Regular exponential families do not compute the same quantities as extended families, so `gfam` converts what these families produce to `extended.family` form internally.

Scale parameters obviously have to be handled separately for each family, and treated as parameters to be estimated, just like other `extended.family` non-location distribution parameters. Again this is handled internally. This requirement is part of the reason that an `extended.family` is always produced, even if all elements of `fl` are standard exponential families. In consequence smoothing parameter estimation is always by REML or NCV.

Note that the null deviance is currently computed by assuming a single parameter model for each family, rather than just one parameter, which may slightly lower explained deviances. Note also
that residual checking should probably be done by disaggregating the residuals by family. For this reason functions are not provided to facilitate residual checking with qq.gam.

Prediction on the response scale requires that a family index vector is supplied, with the name of the response, as part of the new prediction data. However, families such as ocat which usually produce matrix predictions for prediction type "response", will not be able to do so when part of gfam.
gfam relies on the methods in Wood, Pya and Saefken (2016).

Value

An object of class extended.family.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


Examples

library(mgcv)
## a mixed family simulator function to play with...
sim.gfam <- function(dist,n=400) {
  ## dist can be norm, pois, gamma, binom, nbinom, tw, ocat (R assumed 4)
  ## links used are identitiy, log or logit.
  dat <- gamSim(1,n=n,verbose=FALSE)
  nf <- length(dist) ## how many families
  fin <- c(1:nf,sample(1:nf,n-nf,replace=TRUE)) ## family index
  dat[,6:10] <- dat[,6:10]/5 ## a scale that works for all links used
  y <- dat$y;
  for (i in 1:nf) {
    ii <- which(fin==i) ## index of current family
    ni <- length(ii);fi <- dat$fi[ii]
    if (dist[i]=="norm") {
      y[ii] <- fi + rnorm(ni)*.5
    } else if (dist[i]=="pois") {
      y[ii] <- rpois(ni,exp(fi))
    } else if (dist[i]=="gamma") {
      scale <- .5
      y[ii] <- rgamma(ni,shape=1/scale,scale=exp(fi)*scale)
    } else if (dist[i]=="binom") {
      y[ii] <- rbinom(ni,1,binomial()$linkinv(fi))
    } else if (dist[i]=="nbinom") {
      y[ii] <- rnbinom(ni,size=3,mu=exp(fi))
    } else if (dist[i]=="tw") {
      y[ii] <- rTweedie(exp(fi),p=1.5,phi=1.5)
    } else if (dist[i]=="ocat") {
      alpha <- c(-Inf,1,2,2.5,Inf)
      R <- length(alpha)-1
      yi <- fi
      u <- runif(ni)
      u <- yi + log(u/(1-u))

      y[ii] <- fi + qgamma(u,shape=1,rate=1/scale)
    }
for (j in 1:R) {
    yi[u > alpha[j] & u <= alpha[j+1]] <- j
    y[iii] <- yi
}
dat$y <- cbind(y,fin)
dat
} ## sim.gfam

## some examples
dat <- sim.gfam(c("binom","tw","norm"))
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),
    family=gfam(list(binomial,tw,gaussian)),data=dat)
predict(b,data.frame(y=1:3,x0=c(.5,.5,.5),x1=c(.3,.2,.3),
    x2=c(.2,.5,.8),x3=c(.1,.5,.9)),type="response",se=TRUE)
summary(b)
plot(b,pages=1)

## set up model so that only the binomial observations depend
## on x0...
dat$id1 <- as.numeric(dat$y[,2]==1)
b1 <- gam(y=s(x0,by=id1)+s(x1)+s(x2)+s(x3),
    family=gfam(list(binomial,tw,gaussian)),data=dat)
plot(b1,pages=1) ## note the CI width increase

ginla

GAM Integrated Nested Laplace Approximation Newton Enhanced

Description

Apply Integrated Nested Laplace Approximation (INLA, Rue et al. 2009) to models estimable
by `gam` or `bam`, using the INLA variant described in Wood (2019). Produces marginal posterior
densities for each coefficient, selected coefficients or linear transformations of the coefficient vector.

Usage

```
ginla(G,A=NULL,nk=16,nb=100,J=1,interactive=FALSE,int=0,approx=0)
```

Arguments

- **G**: A pre-fit gam object, as produced by `gam(.,fit=FALSE)` or `bam(.,discrete=TRUE,fit=FALSE)`.
- **A**: Either a matrix of transforms of the coefficients that are of interest, or an array
  of indices of the parameters of interest. If NULL then distributions are produced
  for all coefficients.
- **nk**: Number of values of each coefficient at which to evaluate its log marginal posterior
density. These points are then spline interpolated.
- **nb**: Number of points at which to evaluate posterior density of coefficients for returning as a gridded function.
ginla

J

How many determinant updating steps to take in the log determinant approximation step. Not recommended to increase this.

interactive

If this is \( \geq 0 \) or TRUE then every approximate posterior is plotted in red, overlaid on the simple Gaussian approximate posterior. If 2 then waits for user to press return between each plot. Useful for judging whether anything is gained by using INLA approach.

int

0 to skip integration and just use the posterior modal smoothing parameter. \( > 0 \) for integration using the CCD approach proposed in Rue et al. (2009).

approx

0 for full approximation; 1 to update Hessian, but use approximate modes; 2 as 1 and assume constant Hessian. See details.

Details

Let \( \beta, \theta \) and \( y \) denote the model coefficients, hyperparameters/smoothing parameters and response data, respectively. In principle, INLA employs Laplace approximations for \( \pi(\beta_i|\theta, y) \) and \( \pi(\theta|y) \) and then obtains the marginal posterior distribution \( \pi(\beta_i|y) \) by intergrating the approximations to \( \pi(\beta_i|\theta, y)\pi(\theta|y) \) w.r.t. \( \theta \) (marginals for the hyperparameters can also be produced). In practice the Laplace approximation for \( \pi(\beta_i|\theta, y) \) is too expensive to compute for each \( \beta_i \) and must itself be approximated. To this end, there are two quantities that have to be computed: the posterior mode \( \beta^*|\beta_i \) and the determinant of the Hessian of the joint log density \( \log \pi(\beta, \theta, y) \) w.r.t. \( \beta \) at the mode. Rue et al. (2009) originally approximated the posterior conditional mode by the conditional mode implied by a simple Gaussian approximation to the posterior \( \pi(\beta|y) \). They then approximated the log determinant of the Hessian as a function of \( \beta_i \) using a first order Taylor expansion, which is cheap to compute for the sparse model representaiton that they use, but not when using the dense low rank basis expansions used by \texttt{gam}. They also offer a more expensive alternative approximation based on computing the log determinant with respect only to those elements of \( \beta \) with sufficiently high correlation with \( \beta_i \) according to the simple Gaussian posterior approximation: efficiency again seems to rest on sparsity. Wood (2018) suggests computing the required posterior modes exactly, and basing the log determinant approximation on a BFGS update of the Hessian at the unconditional model. The latter is efficient with or without sparsity, whereas the former is a “for free” improvement. Both steps are efficient because it is cheap to obtain the Cholesky factor of \( H[-i,-i] \) from that of \( H \) - see \texttt{choldrop}. This is the approach taken by this routine.

The approx argument allows two further approximations to speed up computations. For \texttt{approx==1} the exact posterior conditional modes are not used, but instead the conditional modes implied by the simple Gaussian posterior approximation. For \texttt{approx==2} the same approximation is used for the modes and the Hessian is assumed constant. The latter is quite fast as no log joint density gradient evaluations are required.

Note that for many models the INLA estimates are very close to the usual Gaussian approximation to the posterior, the interactive argument is useful for investigating this issue.

\texttt{bam} models are only supported with the \texttt{discrete=TRUE} option. The \texttt{discrete=FALSE} approach would be too inefficient. AR1 models are not supported (related arguments are simply ignored).

Value

A list with elements \texttt{beta} and \texttt{density}, both of which are matrices. Each row relates to one coefficient (or linear coefficient combination) of interest. Both matrices have \texttt{nb} columns. If \texttt{int!=0} then a further element \texttt{reml} gives the integration weights used in the CCD integration, with the central point weight given first.
WARNINGS

This routine is still somewhat experimental, so details are liable to change. Also currently not all steps are optimally efficient.
The routine is written for relatively expert users.
ginla is not designed to deal with rank deficient models.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


Examples

```r
require(mgcv); require(MASS)
## example using a scale location model for the motorcycle data. A simple plotting function...
## routine is produced first...
plot.inla <- function(x,inla,k=1,levels=c(.025,.1,.5,.9,.975),
lcol = c(2,4,4,4,2),lwd = c(1,1,2,1,1),lty=c(1,1,1,1,1),
xlab="x",ylab="y",cex.lab=1.5) {
## a simple effect plotter, when distributions of function values of 1D smooths have been computed
require(splines)
p <- length(x)
betaq <- matrix(0,length(levels),p) ## storage for beta quantiles
for (i in 1:p) { ## work through x and betas
  j <- i + k - 1
  p <- cumsum(inla$density[j,]*(inla$beta[j,2]-inla$beta[j,1])
## getting quantiles of function values...
  betaq[,i] <- approx(p,y=inla$beta[j,],levels)$y }
xg <- seq(min(x),max(x),length=200)
ylim <- range(betaq)
ylim <- 1.1*(ylim-mean(ylim))+mean(ylim)
for (j in 1:length(levels)) { ## plot the quantiles
  din <- interpSpline(x,betaq[j,])
  if (j==1) {
    plot(xg,predict(din,xg)$y,ylim=ylim,type="l",col=lcol[j],
       xlab=xlab,ylab=ylab,lwd=lwd[j],lty=lty[j],cex.lab=1.5)
  } else lines(xg,predict(din,xg)$y,col=lcol[j],lwd=lwd[j],lty=lty[j])
}
## plot.inla

## set up the model with a `gam' call...
G <- gam(list(accel~s(times,k=20,bs="ad"),~s(times)),
data=mcycle,family=gaulss(),fit=FALSE)
b <- gam(G=G,method="REML") ## regular GAM fit for comparison
```
Now use `ginla` to get posteriors of estimated effect values at evenly spaced times. Create A matrix for this...

```r
rat <- range(mcycle$times)
pd0 <- data.frame(times=seq(rat[1],rat[2],length=20))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X0[,21:30] <- 0
pd1 <- data.frame(times=seq(rat[1],rat[2],length=10))
X1 <- predict(b,newdata=pd1,type="lpmatrix")
X1[,1:20] <- 0
A <- rbind(X0,X1) ## A maps coefs to required function values

## call ginla. Set int to 1 for integrated version.
## Set interactive = 1 or 2 to plot marginal posterior distributions
## (red) and simple Gaussian approximation (black).

inla <- ginla(G,A,int=0)

par(mfrow=c(1,2),mar=c(5,5,1,1))
fv <- predict(b,se=TRUE) ## usual Gaussian approximation, for comparison

## plot inla mean smooth effect...
plot.inla(pd0$times,inla,k=1,xlab="time",ylab=expression(f[1](time)))
## overlay simple Gaussian equivalent (in grey) ...
points(mcycle$times,mcycle$accel,col="grey")
lines(mcycle$times,fv$fit[,1],col="grey",lwd=2)
lines(mcycle$times,fv$fit[,1]+2*fv$se.fit[,1],col="grey",lty=2,lwd=2)
lines(mcycle$times,fv$fit[,1]-2*fv$se.fit[,1],col="grey",lty=2,lwd=2)

## same for log sd smooth...
plot.inla(pd1$times,inla,k=21,xlab="time",ylab=expression(f[2](time)))
lines(mcycle$times,fv$fit[,2],col="grey",lwd=2)
lines(mcycle$times,fv$fit[,2]+2*fv$se.fit[,2],col="grey",lty=2,lwd=2)
lines(mcycle$times,fv$fit[,2]-2*fv$se.fit[,2],col="grey",lty=2,lwd=2)

## ... notice some real differences for the log sd smooth, especially
## at the lower and upper ends of the time interval.
```

---

**gumbls**  
*Gumbel location-scale model family*

**Description**

The `gumbls` family implements Gumbel location scale additive models in which the location and scale parameters (see details) can depend on additive smooth predictors. Useable only with `gam`, the linear predictors are specified via a list of formulae.

**Usage**

```r
gumbls(link=list("identity","log"),b=-7)
```
Arguments

- **link**: two item list specifying the link for the location \( \mu \) and log scale parameter \( \beta \). See details for meaning, which may not be intuitive.

- **b**: The minimum log scale parameter.

Details

Let \( z = (y - \mu)e^{-\beta} \), then the log Gumbel density is \( l = -\beta - z - e^{-z} \). The expected value of a Gumbel r.v. is \( \mu + \gamma e^{\beta} \) where \( \gamma \) is Euler's constant (about 0.57721566). The corresponding variance is \( \pi^2 e^{2\beta} / 6 \).

`gumbls` is used with `gam` to fit Gumbel location-scale models parameterized in terms of location parameter \( \mu \) and the log scale parameter \( \beta \). Note that identity link for the scale parameter means that the corresponding linear predictor gives \( \beta \) directly. By default the log link for the scale parameter simply forces the log scale parameter to have a lower limit given by argument \( b \): if \( \eta \) is the linear predictor for the log scale parameter, \( \beta \), then \( \beta = b + \log(1 + e^\eta) \).

`gam` is called with a list containing 2 formulae, the first specifies the response on the left hand side and the structure of the linear predictor for location parameter, \( \mu \), on the right hand side. The second is one sided, specifying the linear predictor for the log scale, \( \beta \), on the right hand side.

The fitted values for this family will be a two column matrix. The first column is the mean, and the second column is the log scale parameter, \( \beta \). Predictions using `predict.gam` will also produce 2 column matrices for type "link" and "response". The first column is on the original data scale when type="response" and on the log mean scale of the linear predictor when type="link". The second column when type="response" is again the log scale parameter, but is on the linear predictor when type="link".

Value

An object inheriting from class `general.family`.

References


Examples

```r
library(mgcv)
## simulate some data
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * (10 * x)^3 * (1 - x)^10
n <- 400; set.seed(9)
x0 <- runif(n); x1 <- runif(n);
x2 <- runif(n); x3 <- runif(n);
mu <- f0(x0)+f1(x1)
beta <- exp(f2(x2)/5)
y <- mu - beta*log(-log(runif(n))) # Gumbel quantile function
b <- gam(list(y~s(x0)+s(x1),~s(x2)+s(x3)),family=gumbls)
plot(b,pages=1,scale=0)
summary(b)
```

identifiability

Identifiability constraints

Description

Smooth terms are generally only identifiable up to an additive constant. In consequence sum-to-zero identifiability constraints are imposed on most smooth terms. The exceptions are terms with by variables which cause the smooth to be identifiable without constraint (that doesn’t include factor by variables), and random effect terms. Alternatively smooths can be set up to pass through zero at a user specified point.

Details

By default each smooth term is subject to the sum-to-zero constraint

$$\sum_i f(x_i) = 0.$$  

The constraint is imposed by reparameterization. The sum-to-zero constraint causes the term to be orthogonal to the intercept: alternative constraints lead to wider confidence bands for the constrained smooth terms.

No constraint is used for random effect terms, since the penalty (random effect covariance matrix) anyway ensures identifiability in this case. Also if a by variable means that the smooth is anyway identifiable, then no extra constraint is imposed. Constraints are imposed for factor by variables, so that the main effect of the factor must usually be explicitly added to the model (the example below is an exception).

Occasionally it is desirable to substitute the constraint that a particular smooth curve should pass through zero at a particular point: the pc argument to s, te, ti and t2 allows this: if specified then such constraints are always applied.

Author(s)

Simon N. Wood (s.wood@r-project.org)

Examples

```r
## Example of three groups, each with a different smooth dependence on x
## but each starting at the same value...
require(mgcv)
set.seed(53)
n <- 100;x <- runif(3*n);z <- runif(3*n)
fac <- factor(rep(c("a","b","c"),each=100))
y <- c(sin(x[1:100]*4),exp(3*x[101:200])/10-.1,exp(-10*(x[201:300]-.5))/(1+exp(-10*(x[201:300]-.5)))-0.9933071) + z*(1-z)*5 + rnorm(100)*.4
## 'pc' used to constrain smooths to 0 at x=0...
b <- gam(y~s(x,by=fac,pc=0)+s(z))
plot(b,pages=1)
```
Which of a set of points lie within a polygon defined region

Description

Tests whether each of a set of points lie within a region defined by one or more (possibly nested) polygons. Points count as ‘inside’ if they are interior to an odd number of polygons.

Usage

in.out(bnd,x)

Arguments

bnd  A two column matrix, the rows of which define the vertices of polygons defining the boundary of a region. Different polygons should be separated by an NA row, and the polygons are assumed closed. Alternatively can be a lists where bnd[[i]][[1]], bnd[[i]][[2]] defines the ith boundary loop.

x  A two column matrix. Each row is a point to test for inclusion in the region defined by bnd. Can also be a 2-vector, defining a single point.

Details

The algorithm works by counting boundary crossings (using compiled C code).

Value

A logical vector of length nrow(x). TRUE if the corresponding row of x is inside the boundary and FALSE otherwise.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

Examples

library(mgcv)
data(columb.polys)
bnd <- columb.polys[[2]]
plot(bnd,type="n")
polygon(bnd)
x <- seq(7.9,8.7,length=20)
y <- seq(13.7,14.3,length=20)
gr <- as.matrix(expand.grid(x,y))
inside <- in.out(bnd,gr)
points(gr,col=as.numeric(inside)+1)
**influence.gam**

*Extract the diagonal of the influence/hat matrix for a GAM*

**Description**

Extracts the leading diagonal of the influence matrix (hat matrix) of a fitted `gam` object.

**Usage**

```r
## S3 method for class 'gam'
influence(model, ...)
```

**Arguments**

- `model`: fitted model objects of class `gam` as produced by `gam()`.
- `...`: un-used in this case

**Details**

Simply extracts hat array from fitted model. (More may follow!)

**Value**

An array (see above).

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

- `gam`

---

**initial.sp**

*Starting values for multiple smoothing parameter estimation*

**Description**

Finds initial smoothing parameter guesses for multiple smoothing parameter estimation. The idea is to find values such that the estimated degrees of freedom per penalized parameter should be well away from 0 and 1 for each penalized parameter, thus ensuring that the values are in a region of parameter space where the smoothing parameter estimation criterion is varying substantially with smoothing parameter value.

**Usage**

```r
initial.sp(X, S, off, expensive = FALSE, XX = FALSE)
```
Arguments

\( X \) is the model matrix.

\( S \) is a list of penalty matrices. \( S[[i]] \) is the ith penalty matrix, but note that it is not stored as a full matrix, but rather as the smallest square matrix including all the non-zero elements of the penalty matrix. Element 1,1 of \( S[[i]] \) occupies element \( \text{off}[i], \text{off}[i] \) of the ith penalty matrix. Each \( S[[i]] \) must be positive semi-definite.

\( \text{off} \) is an array indicating the first parameter in the parameter vector that is penalized by the penalty involving \( S[[i]] \).

\( \text{expensive} \) if TRUE then the overall amount of smoothing is adjusted so that the average degrees of freedom per penalized parameter is exactly 0.5: this is numerically costly.

\( XX \) if TRUE then \( X \) contains \( X^T X \), rather than \( X \).

Details

Basically uses a crude approximation to the estimated degrees of freedom per model coefficient, to try and find smoothing parameters which bound these e.d.f.'s away from 0 and 1.

Usually only called by \texttt{magic} and \texttt{gam}.

Value

An array of initial smoothing parameter estimates.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

\texttt{magic}, \texttt{gam.outer}, \texttt{gam},

\texttt{inSide} \hspace{1cm} \texttt{Are points inside boundary?}

Description

Assesses whether points are inside a boundary. The boundary must enclose the domain, but may include islands.

Usage

\texttt{inSide(bnd,x,y)}

Arguments

\texttt{bnd} This should have two equal length columns with names matching whatever is supplied in \texttt{x} and \texttt{y}. This may contain several sections of boundary separated by \texttt{NA}. Alternatively \texttt{bnd} may be a list, each element of which contains 2 columns named as above. See below for details.

\texttt{x} \hspace{1cm} \texttt{X co-ordinates of points to be tested.}

\texttt{y} \hspace{1cm} \texttt{Y co-ordinates of points to be tested.}
Details

Segments of boundary are separated by NAs, or are in separate list elements. The boundary co-
ordinates are taken to define nodes which are joined by straight line segments in order to create the
boundary. Each segment is assumed to define a closed loop, and the last point in a segment will be
assumed to be joined to the first. Loops must not intersect (no test is made for this).

The method used is to count how many times a line, in the y-direction from a point, crosses a
boundary segment. An odd number of crossings defines an interior point. Hence in geographic
applications it would be usual to have an outer boundary loop, possibly with some inner ‘islands’
completely enclosed in the outer loop.

The routine calls compiled C code and operates by an exhaustive search for each point in x, y.

Value

The function returns a logical array of the same dimension as x and y. TRUE indicates that the

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

Examples

```
require(mgcv)
m <- 300; n <- 150
xm <- seq(-1,4,length=m);yn<-seq(-1,1,length=n)
x <- rep(xm,n);y<-rep(yn,rep(m,n))
Er <- matrix(fs.test(x,y),m,n)
bd <- fs.boundary()
in.bnd <- inSide(bnd,x,y)
plot(x,y,col=as.numeric(in.bnd)+1,pch=".")
lines(bnd$x,bnd$y,col=3)
points(x,y,col=as.numeric(in.bnd)+1,pch=".")
## check boundary details ...
plot(x,y,col=as.numeric(in.bnd)+1,pch=".",ylim=c(-1,0),xlim=c(3,3.5))
lines(bnd$x,bnd$y,col=3)
points(x,y,col=as.numeric(in.bnd)+1,pch=".")
```

Description

This is an internal function of package mgcv. It is a service routine for gam which splits off the
strictly parametric part of the model formula, returning it as a formula, and interprets the smooth
parts of the model formula.

Not normally called directly.
Usage
interpret.gam(gf, extra.special = NULL)

Arguments
gf A GAM formula as supplied to \texttt{gam} or \texttt{gamm}, or a list of such formulae, as supplied for some \texttt{gam} families.
extra.special Name of any extra special in formula in addition to \texttt{s}, \texttt{te}, \texttt{ti} and \texttt{t2}.

Value
An object of class \texttt{split.gam.formula} with the following items:
pf A model formula for the strictly parametric part of the model.
pfok TRUE if there is a pf formula.
smooth.spec A list of class \texttt{xx.smooth.spec} objects where \texttt{xx} depends on the basis specified for the term. (These can be passed to smooth constructor method functions to actually set up penalties and bases.)
full.formula An expanded version of the model formula in which the options are fully expanded, and the options do not depend on variables which might not be available later.
fake.formula A formula suitable for use in evaluating a model frame.
response Name of the response variable.

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References
https://www.maths.ed.ac.uk/~swood34/

See Also
\texttt{gam} \texttt{gamm}

jagam
Just Another Gibbs Additive Modeller: JAGS support for mgcv.

Description
Facilities to auto-generate model specification code and associated data to simulate with GAMs in JAGS (or BUGS). This is useful for inference about models with complex random effects structure best coded in JAGS. It is a very inefficient approach to making inferences about standard GAMs. The idea is that \texttt{jagam} generates template JAGS code, and associated data, for the smooth part of the model. This template is then directly edited to include other stochastic components. After simulation with the resulting model, facilities are provided for plotting and prediction with the model smooth components.
Usage

```r
jagam(formula, family=gaussian, data=list(), file, weights=NULL, na.action,
offset=NULL, knots=NULL, sp=NULL, drop.unused.levels=TRUE,
control=gam.control(), centred=TRUE, sp.prior = "gamma", diagonalize=FALSE)

sim2jam(sam, pregam, edf.type=2, burnin=0)
```

Arguments

- **formula**: A GAM formula (see `formula.gam` and also `gam.models`). This is exactly like the formula for a GLM except that smooth terms, `s`, `te`, `ti` and `t2` can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).

- **family**: This is a family object specifying the distribution and link function to use. See `glm` and `family` for more details. Currently only gaussian, poisson, binomial and Gamma families are supported, but the user can easily modify the assumed distribution in the JAGS code.

- **data**: A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from `environment(formula)`: typically the environment from which `jagam` is called.

- **file**: Name of the file to which JAGS model specification code should be written. See `setwd` for setting and querying the current working directory.

- **weights**: prior weights on the data.

- **na.action**: a function which indicates what should happen when the data contain ‘NA’s. The default is set by the ‘na.action’ setting of ‘options’, and is ‘na.fail’ if that is unset. The “factory-fresh” default is ‘na.omit’.

- **offset**: Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in `formula`: this conforms to the behaviour of `lm` and `glm`.

- **control**: A list of fit control parameters to replace defaults returned by `gam.control`. Any control parameters not supplied stay at their default values. little effect on `jagam`.

- **knots**: this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the k value supplied (note that the number of knots is not always just k). See `tprs` for what happens in the "tp"/"ts" case. Different terms can use different numbers of knots, unless they share a covariate.

- **sp**: A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula (without forgetting null space penalties). Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then `length(sp)` must correspond to the number of underlying smoothing parameters.

- **drop.unused.levels**: by default unused levels are dropped from factors before fitting. For some smooths involving factor variables you might want to turn this off. Only do so if you know what you are doing.
centred  Should centring constraints be applied to the smooths, as is usual with GAMS? Only set this to FALSE if you know exactly what you are doing. If FALSE there is a (usually global) intercept for each smooth.

sp.prior  "gamma" or "log.uniform" prior for the smoothing parameters? Do check that the default parameters are appropriate for your model in the JAGS code.

diagonalize  Should smooths be re-parameterized to have i.i.d. Gaussian priors (where possible)? For Gaussian data this allows efficient conjugate samplers to be used, and it can also work well with GLMs if the JAGS "glm" module is loaded, but otherwise it is often better to update smoothers blockwise, and not do this.

sam  jags sample object, containing at least fields b (coefficients) and rho (log smoothing parameters). May also contain field mu containing monitored expected response.

pregam  standard mgcv GAM setup data, as returned in jagam return list.

edf.type  Since EDF is not uniquely defined and may be affected by the stochastic structure added to the JAGS model file, 3 options are offered. See details.

burnin  the amount of burn in to discard from the simulation chains. Limited to .9 of the chain length.

Details

Smoothes are easily incorporated into JAGS models using multivariate normal priors on the smooth coefficients. The smoothing parameters and smoothing penalty matrices directly specify the prior multivariate normal precision matrix. Normally a smoothing penalty does not correspond to a full rank precision matrix, implying an improper prior inappropriate for Gibbs sampling. To rectify this problem the null space penalties suggested in Marra and Wood (2011) are added to the usual penalties.

In an additive modelling context it is usual to centre the smooths, to avoid the identifiability issues associated with having an intercept for each smooth term (in addition to a global intercept). Under Gibbs sampling with JAGS it is technically possible to omit this centring, since we anyway force propriety on the priors, and this propriety implies formal model identifiability. However, in most situations this formal identifiability is rather artificial and does not imply statistically meaningful identifiability. Rather it serves only to massively inflate confidence intervals, since the multiple intercept terms are not identifiable from the data, but only from the prior. By default then, jagam imposes standard GAM identifiability constraints on all smooths. The centred argument does allow you to turn this off, but it is not recommended. If you do set centred=FALSE then chain convergence and mixing checks should be particularly stringent.

The final technical issue for model setup is the setting of initial conditions for the coefficients and smoothing parameters. The approach taken is to take the default initial smoothing parameter values used elsewhere by mgcv, and to take a single PIRLS fitting step with these smoothing parameters in order to obtain starting values for the smooth coefficients. In the setting of fully conjugate updating the initial values of the coefficients are not critical, and good results are obtained without supplying them. But in the usual setting in which slice sampling is required for at least some of the updates then very poor results can sometimes be obtained without initial values, as the sampler simply fails to find the region of the posterior mode.

The sim2jam function takes the partial gam object (pregam) from jagam along with simulation output in standard rjags form and creates a reduced version of a gam object, suitable for plotting and prediction of the model’s smooth components. sim2gam computes effective degrees of freedom for each smooth, but it should be noted that there are several possibilities for doing this in the context of a model with a complex random effects structure. The simplest approach (edf.type=0) is to compute the degrees of freedom that the smooth would have had if it had been part of an unweighted
Gaussian additive model. One might choose to use this option if the model has been modified so
that the response distribution and/or link are not those that were specified to \texttt{jagam}. The second
option is (\texttt{edf.type=1}) uses the edf that would have been computed by \texttt{gam} had it produced these
estimates - in the context in which the JAGS model modifications have all been about modifying the
random effects structure, this is equivalent to simply setting all the random effects to zero for the
effective degrees of freedom calculation. The default option (\texttt{edf.type=2}) is to base the EDF on
the sample covariance matrix, $V_p$, of the model coefficients. If the simulation output (\texttt{sim}) includes
a \texttt{mu} field, then this will be used to form the weight matrix $W$ in $X^T W X = \text{t}(X)^* t(W) * X$, where the
EDF is computed from $\text{rowSums}(V_p * X W X) * \text{scale}$. If \texttt{mu} is not supplied then it is estimated from
the the model matrix $X$ and the mean of the simulated coefficients, but the resulting $W$ may not be
strictly compatible with the $V_p$ matrix in this case. In the situation in which the fitted model is very
different in structure from the regression model of the template produced by \texttt{jagam} then the default
option may make no sense, and indeed it may be best to use option 0.

Value
For \texttt{jagam} a three item list containing

- \texttt{pregam} standard \texttt{mgcv} GAM setup data.
- \texttt{jags.data} list of arguments to be supplied to JAGS containing information referenced in
  model specification.
- \texttt{jags.ini} initialization data for smooth coefficients and smoothing parameters.

For \texttt{sim2jam} an object of class "\texttt{jam}": a partial version of an \texttt{mgcv} \texttt{gamObject}, suitable for plotting
and predicting.

WARNINGS
Gibb’s sampling is a very slow inferential method for standard GAMs. It is only likely to be
worthwhile when complex random effects structures are required above what is possible with direct
GAMM methods.

Check that the parameters of the priors on the parameters are fit for your purpose.

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References
Marra, G. and S.N. Wood (2011) Practical variable selection for generalized additive models. Com-
putational Statistics & Data Analysis 55(7): 2372-2387
Here is a key early reference to smoothing using BUGS (although the approach and smooths used
are a bit different to \texttt{jagam})
Crainiceanu, C. M. D Ruppert, & M.P. Wand (2005) Bayesian Analysis for Penalized Spline Re-

See Also
\texttt{gam, gamm, bam}
## Examples

```r
## the following illustrates a typical workflow. To run the
## 'Not run' code you need rjags (and JAGS) to be installed.
require(mgcv)

set.seed(2) ## simulate some data...
  n <- 400
data <- gamSim(1,n=n,dist="normal",scale=2)
## regular gam fit for comparison...
b0 <- gam(y~s(x0)+s(x1) + s(x2)+s(x3),data=dat,method="REML")

## Set directory and file name for file containing jags code.
## In real use you would *never* use tempdir() for this. It is
## only done here to keep CRAN happy, and avoid any chance of
## an accidental overwrite. Instead you would use
## setwd() to set an appropriate working directory in which
## to write the file, and just set the file name to what you
## want to call it (e.g. "test.jags" here).

jags.file <- paste(tempdir(),"/test.jags",sep="")

## Set up JAGS code and data. In this one might want to diagonalize
## to use conjugate samplers. Usually call 'setwd' first, to set
## directory in which model file ("test.jags") will be written.

jd <- jagam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,file=jags.file,
            sp.prior="gamma",diagonalize=TRUE)

## In normal use the model in "test.jags" would now be edited to add
## the non-standard stochastic elements that require use of JAGS....

## Not run:
require(rjags)
load.module("glm") ## improved samplers for GLMs often worth loading
jm <- jags.model(jags.file,data=jd$jags.data,inits=jd$jags.ini,n.chains=1)
list.samplers(jm)
sam <- jags.samples(jm,c("b","rho","scale"),n.iter=10000,thin=10)
jam <- sim2jam(sam,jd$pregam)
plot(jam,pages=1)

pd <- data.frame(x0=c(.5,.6),x1=c(.4,.2),x2=c(.8,.4),x3=c(.1,.1))
fv <- predict(jam,newdata=pd)
## and some minimal checking...
require(coda)
effectiveSize(as.mcmc.list(sam$b))

## End(Not run)

## a gamma example...
set.seed(1); n <- 400

data <- gamSim(1,n=n,dist="normal",scale=2)
scale <- .5; Ey <- exp(data$f/2)
data$y <- rgamma(n,shape=1/scale,rate=Ey*scale)
jd <- jagam(y~s(x0)+te(x1,x2)+s(x3),data=data,family=Gamma(link=log),
            file=jags.file,sp.prior="log.uniform")
```

## In normal use the model in "test.jags" would now be edited to add
## the non-standard stochastic elements that require use of JAGS....

## Not run:
require(rjags)
## following sets random seed, but note that under JAGS 3.4 many
## models are still not fully repeatable (JAGS 4 should fix this)
jd$jags.ini$.RNG.name <- "base::Mersenne-Twister" ## setting RNG
jd$jags.ini$.RNG.seed <- 6 ## how to set RNG seed
jm <- jags.model(jags.file, data=jd$jags.data, inits=jd$jags.ini, n.chains=1)
list.samplers(jm)
sam <- jags.samples(jm,c("b","rho","scale","mu"),n.iter=10000,thin=10)
jam <- sim2jam(sam,jd$pregam)
plot(jam, pages=1)
jam
pd <- data.frame(x0=c(0.5,.6), x1=c(0.4,.2), x2=c(0.8,.4), x3=c(.1,.1))
fv <- predict(jam, newdata=pd)

## End(Not run)

---

**k.check**

*Checking smooth basis dimension*

**Description**

Takes a fitted gam object produced by `gam()` and runs diagnostic tests of whether the basis dimension choices are adequate.

**Usage**

```r
k.check(b, subsample=5000, n.rep=400)
```

**Arguments**

- **b** a fitted `gam` object as produced by `gam()`.
- **subsample** above this number of data, testing uses a random sub-sample of data of this size.
- **n.rep** how many re-shuffles to do to get p-value for k testing.

**Details**

The test of whether the basis dimension for a smooth is adequate (Wood, 2017, section 5.9) is based on computing an estimate of the residual variance based on differencing residuals that are near neighbours according to the (numeric) covariates of the smooth. This estimate divided by the residual variance is the k-index reported. The further below 1 this is, the more likely it is that there is missed pattern left in the residuals. The p-value is computed by simulation: the residuals are randomly re-shuffled n.rep times to obtain the null distribution of the differencing variance estimator, if there is no pattern in the residuals. For models fitted to more than subsample data, the tests are based of subsample randomly sampled data. Low p-values may indicate that the basis dimension, k, has been set too low, especially if the reported edf is close to k. The maximum possible EDF for the term. Note the disconcerting fact that if the test statistic itself is based on random resampling and the null is true, then the associated p-values will of course vary widely.
from one replicate to the next. Currently smooths of factor variables are not supported and will give
an NA p-value.

Doubling a suspect k and re-fitting is sensible: if the reported edf increases substantially then you
may have been missing something in the first fit. Of course p-values can be low for reasons other
than a too low k. See choose.k for fuller discussion.

Value

A matrix containing the output of the tests described above.

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References

and Hall/CRC Press.

https://www.maths.ed.ac.uk/~swood34/

See Also

choose.k, gam, gam.check

Examples

library(mgcv)
set.seed(0)
dat <- gamSim(1,n=200)
b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)
k.check(b)

1detS

Getting log generalized determinant of penalty matrices

Description

INTERNAL function calculating the log generalized determinant of penalty matrix S stored block-
wise in an Sl list (which is the output of Sl.setup).

Usage

1detS(Sl, rho, fixed, np, root = FALSE, repara = TRUE,
nt = 1,deriv=2,sparse=FALSE)
ldTweedie

Arguments

- **Sl**: the output of `Sl.setup`.
- **rho**: the log smoothing parameters.
- **fixed**: an array indicating whether the smoothing parameters are fixed (or free).
- **np**: number of coefficients.
- **root**: indicates whether or not to return the matrix square root, $E$, of the total penalty $S_{tot}$.
- **repara**: if TRUE multi-term blocks will be re-parameterized using `gam.reparam`, and a re-parameterization object supplied in the returned object.
- **nt**: number of parallel threads to use.
- **deriv**: order of derivative to use
- **sparse**: should $E$ be sparse?

Value

A list containing:

- **ldetS**: the log-determinant of $S$.
- **ldetS1**: the gradient of the log-determinant of $S$.
- **ldetS2**: the Hessian of the log-determinant of $S$.
- **Sl**: with modified rS terms, if needed and rho added to each block
- **rp**: a re-parameterization list.
- **rp**: $E$ a total penalty square root such that $t(E) %*% E = S_{tot}$ (if root==TRUE).

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

Description

A function to evaluate the log of the Tweedie density for variance powers between 1 and 2, inclusive. Also evaluates first and second derivatives of log density w.r.t. its scale parameter, phi, and p, or w.r.t rho=log(phi) and theta where $p = (a+b*exp(theta))/(1+exp(theta))$.

Usage

```r
ldTweedie(y,mu=y,p=1.5,phi=1,rho=NA,theta=NA,a=1.001,b=1.999,all.derivs=FALSE)
```
Arguments

- **y**
  values at which to evaluate density.

- **mu**
  corresponding means (either of same length as y or a single value).

- **p**
  the variance of y is proportional to its mean to the power p. p must be between 1 and 2. 1 is Poisson like (exactly Poisson if phi=1), 2 is gamma.

- **phi**
  The scale parameter. Variance of y is phi*mu^p.

- **rho**
  optional log scale parameter. Over-rides phi if theta also supplied.

- **theta**
  parameter such that p = (a+b*exp(theta))/(1+exp(theta)). Over-rides p if rho also supplied.

- **a**
  lower limit parameter (>1) used in definition of p from theta.

- **b**
  upper limit parameter (<2) used in definition of p from theta.

- **all.derivs**
  if TRUE then derivatives w.r.t. mu are also returned. Only available with rho and phi parameterization.

Details

A Tweedie random variable with 1<p<2 is a sum of N gamma random variables where N has a Poisson distribution. The p=1 case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For 1<p<2 the distribution is supported on the positive reals with a point mass at zero. p=2 is a gamma distribution. As p gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at p=1.

ldTweedie is based on the series evaluation method of Dunn and Smyth (2005). Without the restriction on p the calculation of Tweedie densities is less straightforward. If you really need this case then the tweedie package is the place to start.

The rho, theta parameterization is useful for optimization of p and phi, in order to keep p bounded well away from 1 and 2, and phi positive. The derivatives near p=1 tend to infinity.

Note that if p and phi (or theta and rho) both contain only a single unique value, then the underlying code is able to use buffering to avoid repeated calls to expensive log gamma, di-gamma and tri-gamma functions (mu can still be a vector of different values). This is much faster than is possible when these parameters are vectors with different values.

Value

A matrix with 6 columns, or 10 if all.derivs=TRUE. The first is the log density of y (log probability if p=1). The second and third are the first and second derivatives of the log density w.r.t. phi. 4th and 5th columns are first and second derivative w.r.t. p, final column is second derivative w.r.t. phi and p.

If rho and theta were supplied then derivatives are w.r.t. these. In this case, and if all.derivs=TRUE then the 7th column is the derivative w.r.t. mu, the 8th is the 2nd derivative w.r.t. mu, the 9th is the mixed derivative w.r.t. theta and mu and the 10th is the mixed derivative w.r.t. rho and mu.

Author(s)

Simon N. Wood <simon.wood@r-project.org>
References


Examples

```r
library(mgcv)
## convergence to Poisson illustrated
## notice how p>1.1 is OK
y <- seq(1e-10,10,length=1000)
p <- c(1.0001,1.001,1.01,1.1,1.2,1.5,1.8,2)
phi <- .5
fy <- exp(ldTweedie(y,mu=2,p=p[1],phi=phi[,1])[,1])
plot(y,fy,type="l",ylim=c(0,3),main="Tweedie density as p changes")
for (i in 2:length(p)) {
  fy <- exp(ldTweedie(y,mu=2,p=p[i],phi=phi[,1])[,1])
  lines(y,fy,col=i)
}
```

linear.functional.terms

Linear functionals of a smooth in GAMs

Description

`gam` allows the response variable to depend on linear functionals of smooth terms. Specifically dependancies of the form

\[ g(\mu_i) = \ldots + \sum_j L_{ij} f(x_{ij}) + \ldots \]

are allowed, where the \( x_{ij} \) are covariate values and the \( L_{ij} \) are fixed weights. i.e. the response can depend on the weighted sum of the same smooth evaluated at different covariate values. This allows, for example, for the response to depend on the derivatives or integrals of a smooth (approximated by finite differencing or quadrature, respectively). It also allows dependence on predictor functions (sometimes called ‘signal regression’).

The mechanism by which this is achieved is to supply matrices of covariate values to the model smooth terms specified by `s` or `te` terms in the model formula. Each column of the covariate matrix gives rise to a corresponding column of predictions from the smooth. Let the resulting matrix of evaluated smooth values be \( F \) (\( F \) will have the same dimension as the covariate matrices). In the absense of a by variable then these columns are simply summed and added to the linear predictor. i.e. the contribution of the term to the linear predictor is `rowSums(F)`. If a by variable is present then it must be a matrix, \( L \), say, of the same dimension as \( F \) (and the covariate matrices), and it contains the weights \( L_{ij} \) in the summation given above. So in this case the contribution to the linear predictor is `rowSums(L*F)`.
Note that if a \( L_1 \) (i.e. rowSums(L)) is a constant vector, or there is no by variable then the smooth will automatically be centred in order to ensure identifiability. Otherwise it will not be. Note also that for centred smooths it can be worth replacing the constant term in the model with rowSums(L) in order to ensure that predictions are automatically on the right scale.

`predict.gam` can accept matrix predictors for prediction with such terms, in which case its `newdata` argument will need to be a list. However when predicting from the model it is not necessary to provide matrix covariate and by variable values. For example to simply examine the underlying smooth function one would use vectors of covariate values and vector by variables, with the by variable and equivalent of \( L_1 \), above, set to vectors of ones.

The mechanism is usable with random effect smooths which take factor arguments, by using a trick to create a 2D array of factors. Simply create a factor vector containing the columns of the factor matrix stacked end to end (column major order). Then reset the dimensions of this vector to create the appropriate 2D array: the first dimension should be the number of response data and the second the number of columns of the required factor matrix. You can not use `matrix` or `data.matrix` to set up the required matrix of factor levels. See example below.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**Examples**

```r
### matrix argument `linear operator` smoothing
library(mgcv)
set.seed(0)

###############################
## simple summation example...#
###############################

n<-400
sig<-2
x <- runif(n, 0, .9)
f2 <- function(x) 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
x1 <- x + .1

f <- f2(x) + f2(x1)  # response is sum of f at two adjacent x values
y <- f + rnorm(n)*sig

X <- matrix(c(x,x1),n,2)  # matrix covariate contains both x values
b <- gam(y~s(X))

plot(b)  # reconstruction of f
plot(f,fitted(b))

## example of prediction with summation convention...
predict(b,list(X=X[1:3,]))

## example of prediction that simply evaluates smooth (no summation)...
predict(b,data.frame(X=c(.2,.3,.7)))

###############################################################
## Simple random effect model example.
## model: y[i] = f(x[i]) + b[k[i]] - b[j[i]] + e[i]
## k[i] and j[i] index levels of i.i.d. random effects, b.
```
```r
set.seed(7)
n <- 200
x <- runif(n) ## a continuous covariate

## set up a 'factor matrix'...
fac <- factor(sample(letters,n*2,replace=TRUE))
dim(fac) <- c(n,2)

## simulate data from such a model...
nb <- length(levels(fac))
b <- rnorm(nb)
y <- 20*(x-.3)^4 + b[fac[,1]] - b[fac[,2]] + rnorm(n)*.5
L <- matrix(-1,n,2);L[,1] <- 1 ## the differencing 'by' variable

mod <- gam(y ~ s(x) + s(fac,by=L,bs="re"),method="REML")
gam.vcomp(mod)
plot(mod,page=1)

## example of prediction using matrices...
dat <- list(L=L[1:20,],fac=fac[1:20,],x=x[1:20],y=y[1:20])
predict(mod,newdata=dat)
```

## Multivariate integral example. Function `test1` will be integrated
(by midpoint quadrature) over 100 equal area sub-squares covering #
the unit square. Noise is added to the resulting simulated data. #
'`test1`' is estimated from the resulting data using two alternative#
smooths.

```r
test1 <- function(x,z,sx=0.3,sz=0.4)
{ (pi**sx*sz)*(1.2*exp(-(x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
0.8*exp(-(x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
}

## create quadrature (integration) grid, in useful order
ig <- 5 ## integration grid within square
mx <- mz <- (1:ig-.5)/ig
ix <- rep(mx,ig);iz <- rep(mz,rep(ig,ig))
og <- 10 ## observarion grid
mx <- mz <- (1:og-1)/og
ox <- rep(mx,og);ox <- rep(ox,rep(ig^2,og^2))
oz <- rep(mz,rep(og,og));oz <- rep(oz,rep(ig^2,og^2))

x <- ox + ix/og;z <- oz + iz/og ## full grid, subsquare by subsquare

## create matrix covariates...
X <- matrix(x,og^2,ig^2,byrow=TRUE)
Z <- matrix(z,og^2,ig^2,byrow=TRUE)

## create simulated test data...
dA <- 1/(og*ig)^2  ## quadrature square area
```
F <- test1(X,Z)  ## evaluate on grid
f <- rowSums(F)*dA  ## integrate by midpoint quadrature
y <- f + rnorm(og^2)*5e-4  ## add noise
  ## ... so each y is a noisy observation of the integral of `test1'
  ## over a 0.1 by 0.1 sub-square from the unit square

  ## Now fit model to simulated data...
L <- X*0 + dA
  ## ... let F be the matrix of the smooth evaluated at the x,z values
  ## in matrices X and Z. rowSums(L+F) gives the model predicted
  ## integrals of `test1' corresponding to the observed `y'
L1 <- rowSums(L)  ## smooths are centred --- need to add in LX*L1
  ## fit models to reconstruct `test1'....
b <- gam(y~s(X,Z,by=L)+L1-1)  ## (L1 and const are confounded here)
b1 <- gam(y~te(X,Z,by=L)+L1-1)  ## tensor product alternative
  ## plot results...
old.par<-par(mfrow=c(2,2)); x<-runif(n); z<-runif(n);
xz<-seq(0,1,length=30); z<-seq(0,1,length=30)
pr<-data.frame(x=rep(xs,30), z=rep(zs,rep(30,30)))
truth<-matrix(test1(pr$x,pr$z),30,30)
contour(xs,zs,truth)
plot(b)
vis.gam(b,view=c("X","Z"),cond=list(L1=1,L=1),plot.type="contour")
vis.gam(b1,view=c("X","Z"),cond=list(L1=1,L=1),plot.type="contour")

rf <- function(x=seq(0,1,length=100)) {
  ## generates random functions...
  m <- ceiling(runif(1)*5)  ## number of components
  f <- x*0;
  mu <- runif(m,min(x),max(x)); sig <- (runif(m)+.5)*(max(x)-min(x))/10
  for (i in 1:m) f <- f + dnorm(x,mu[i],sig[i])
  f
}
x <- seq(0,1,length=100)  ## evaluation points
  ## example functional predictors...
par(mfrow=c(3,3)); for (i in 1:9) plot(x,rf(x),type="l",xlab="x")
  ## simulate 200 functions and store in rows of L...
L <- matrix(NA,200,100)
for (i in 1:200) L[i,] <- rf()  ## simulate the functional predictors
f2 <- function(x) {  ## the coefficient function
  (0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10)/10}
f <- f2(x) ## the true coefficient function

y <- L%*%f + rnorm(200)*20 ## simulated response data

## Now fit the model E(y) = L%*%f(x) where f is a smooth function.
## The summation convention is used to evaluate smooth at each value
## in matrix X to get matrix F, say. Then rowSum(L*F) gives E(y).

## create matrix of eval points for each function. Note that
## `smoothCon` is smart and will recognize the duplication...
X <- matrix(x,200,100,byrow=TRUE)

b <- gam(y~s(X,by=L,k=20))
par(mfrow=c(1,1))
plot(b,shade=TRUE);lines(x,f,col=2)

---

**logLik.gam**

*AIC and Log likelihood for a fitted GAM*

**Description**

Function to extract the log-likelihood for a fitted `gam` model (note that the models are usually fitted by penalized likelihood maximization). Used by `AIC`. See details for more information on AIC computation.

**Usage**

```r
## S3 method for class 'gam'
logLik(object,...)
```

**Arguments**

- `object`  fitted model objects of class `gam` as produced by `gam()`.
- `...`  un-used in this case

**Details**

Modification of `logLik.glm` which corrects the degrees of freedom for use with `gam` objects.

The function is provided so that `AIC` functions correctly with `gam` objects, and uses the appropriate degrees of freedom (accounting for penalization). See e.g. Wood, Pya and Saefken (2016) for a derivation of an appropriate AIC.

For `gaussian` family models the MLE of the scale parameter is used. For other families with a scale parameter the estimated scale parameter is used. This is usually not exactly the MLE, and is not the simple deviance based estimator used with `glm` models. This is because the simple deviance based estimator can be badly biased in some cases, for example when a Tweedie distribution is employed with low count data.

There are two possible AIC’s that might be considered for use with GAMs. Marginal AIC is based on the marginal likelihood of the GAM, that is the likelihood based on treating penalized (e.g.
spline) coefficients as random and integrating them out. The degrees of freedom is then the number of smoothing/variance parameters + the number of fixed effects. The problem with Marginal AIC is that marginal likelihood underestimates variance components/oversmooths, so that the approach favours simpler models excessively (substituting REML does not work, because REML is not comparable between models with different unpenalized/fixed components). Conditional AIC uses the likelihood of all the model coefficients, evaluated at the penalized MLE. The degrees of freedom to use then is the effective degrees of freedom for the model. However, Greven and Kneib (2010) show that the neglect of smoothing parameter uncertainty can lead to this conditional AIC being excessively likely to select larger models. Wood, Pya and Saefken (2016) propose a simple correction to the effective degrees of freedom to fix this problem. mgcv applies this correction whenever possible: that is when using ML or REML smoothing parameter selection with gam or bam. The correction is not computable when using the Extended Fellner Schall or BFGS optimizer (since the correction requires an estimate of the covariance matrix of the log smoothing parameters).

Value

Standard logLik object: see logLik.

Author(s)

Simon N. Wood <simon.wood@r-project.org> based directly on logLik.glm

References


See Also

AIC

ls.size

Size of list elements

Description

Produces a named array giving the size, in bytes, of the elements of a list.

Usage

ls.size(x)

Arguments

x A list.
Value

A numeric vector giving the size in bytes of each element of the list \textit{x}. The elements of the array have the same names as the elements of the list. If \textit{x} is not a list then its size in bytes is returned, un-named.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

Examples

library(mgcv)
b <- list(M=matrix(runif(100),10,10),quote=
"The world is ruled by idiots because only an idiot would want to rule the world.",
fam=binomial())
ls.size(b)
is a list of penalty matrices. $S[[i]]$ is the $i$th penalty matrix, but note that it is not stored as a full matrix, but rather as the smallest square matrix including all the non-zero elements of the penalty matrix. Element 1,1 of $S[[i]]$ occupies element off[i], off[i] of the $i$th penalty matrix. Each $S[[i]]$ must be positive semi-definite. Set to list() if there are no smoothing parameters to be estimated.

off is an array indicating the first parameter in the parameter vector that is penalized by the penalty involving $S[[i]]$.

L is a matrix mapping $\log(sp)$ to the log smoothing parameters that actually multiply the penalties defined by the elements of S. Taken as the identity, if NULL. See above under sp.

lsp0 If L is not NULL this is a vector of constants in the linear transformation from $\log(sp)$ to the actual log smoothing parameters. So the logs of the smoothing parameters multiplying the $S[[i]]$ are given by $L \times \log(sp) + lsp0$. Taken as 0 if NULL.

rank is an array specifying the ranks of the penalties. This is useful, but not essential, for forming square roots of the penalty matrices.

H is the optional offset penalty - i.e. a penalty with a smoothing parameter fixed at 1. This is useful for allowing regularization of the estimation process, fixed smoothing penalties etc.

C is the optional matrix specifying any linear equality constraints on the fitting problem. If $b$ is the parameter vector then the parameters are forced to satisfy $Cb = 0$.

w the regression weights. If this is a matrix then it is taken as being the square root of the inverse of the covariance matrix of $y$, specifically $V^{-1} = w'w$. If $w$ is an array then it is taken as the diagonal of this matrix, or simply the weight for each element of $y$. See below for an example using this.

gamma is an inflation factor for the model degrees of freedom in the GCV or UBRE score.

scale is the scale parameter for use with UBRE.

gcv should be set to TRUE if GCV is to be used, FALSE for UBRE.

It is sometimes useful to apply a ridge penalty to the fitting problem, penalizing the parameters in the constrained space directly. Setting this parameter to a value greater than zero will cause such a penalty to be used, with the magnitude given by the parameter value.

control is a list of iteration control constants with the following elements:

tol The tolerance to use in judging convergence.

step.half If a trial step fails then the method tries halving it up to a maximum of step.half times.

rank.tol is a constant used to test for numerical rank deficiency of the problem. Basically any singular value less than rank.tol multiplied by the largest singular value of the problem is set to zero.

extra.rss is a constant to be added to the residual sum of squares (squared norm) term in the calculation of the GCV, UBRE and scale parameter estimate. In conjunction with n.score, this is useful for certain methods for dealing with very large data sets.
number to use as the number of data in GCV/UBRE score calculation: usually the actual number of data, but there are methods for dealing with very large datasets that change this.

`nthreads` magic can make use of multiple threads if this is set to >1.

**Details**

The method is a computationally efficient means of applying GCV or UBRE (often approximately AIC) to the problem of smoothing parameter selection in generalized ridge regression problems of the form:

\[
\min_{\theta} \|W(Xb - y)\|^2 + b'Hb + \sum_{i=1}^{m} \theta_i b'S_i b
\]

possibly subject to constraints \(Cb = 0\). \(X\) is a design matrix, \(b\) a parameter vector, \(y\) a data vector, \(W\) a weight matrix, \(S_i\) a positive semi-definite matrix of coefficients defining the \(i\)th penalty with associated smoothing parameter \(\theta_i\), \(H\) is the positive semi-definite offset penalty matrix and \(C\) a matrix of coefficients defining any linear equality constraints on the problem. \(X\) need not be of full column rank.

The \(\theta_i\) are chosen to minimize either the GCV score:

\[
V_g = n\|W(y - Ay)\|^2 / [tr(I - \gamma A)]^2
\]

or the UBRE score:

\[
V_u = \|W(y - Ay)\|^2 / n - 2\phi tr(I - \gamma A) / n + \phi
\]

where \(\gamma\) is gamma the inflation factor for degrees of freedom (usually set to 1) and \(\phi\) is scale, the scale parameter. \(A\) is the hat matrix (influence matrix) for the fitting problem (i.e the matrix mapping data to fitted values). Dependence of the scores on the smoothing parameters is through \(A\).

The method operates by Newton or steepest descent updates of the logs of the \(\theta_i\). A key aspect of the method is stable and economical calculation of the first and second derivatives of the scores w.r.t. the log smoothing parameters. Because the GCV/UBRE scores are flat w.r.t. very large or very small \(\theta_i\), it’s important to get good starting parameters, and to be careful not to step into a flat region of the smoothing parameter space. For this reason the algorithm rescales any Newton step that would result in a \(log(\theta_i)\) change of more than 5. Newton steps are only used if the Hessian of the GCV/UBRE is positive definite, otherwise steepest descent is used. Similarly steepest descent is used if the Newton step has to be contracted too far (indicating that the quadratic model underlying Newton is poor). All initial steepest descent steps are scaled so that their largest component is 1. However a step is calculated, it is never expanded if it is successful (to avoid flat portions of the objective), but steps are successively halved if they do not decrease the GCV/UBRE score, until they do, or the direction is deemed to have failed. (Given the smoothing parameters the optimal \(b\) parameters are easily found.)

The method is coded in C with matrix factorizations performed using LINPACK and LAPACK routines.

**Value**

The function returns a list with the following items:

\(b\) The best fit parameters given the estimated smoothing parameters.
the estimated (GCV) or supplied (UBRE) scale parameter.

score the minimized GCV or UBRE score.

sp an array of the estimated smoothing parameters.

sp.full an array of the smoothing parameters that actually multiply the elements of $S$ (same as sp if L was NULL). This is $\exp(L\%*%\log(sp))$.

rV a factored form of the parameter covariance matrix. The (Bayesian) covariance matrix of the parameters b is given by $rV%*%t(rV)*scale$.

gcv.info is a list of information about the performance of the method with the following elements:

full.rank The apparent rank of the problem: number of parameters less number of equality constraints.

rank The estimated actual rank of the problem (at the final iteration of the method).

fully.converged is TRUE if the method converged by satisfying the convergence criteria, and FALSE if it converged by failing to decrease the score along the search direction.

hess.pos.def is TRUE if the hessian of the UBRE or GCV score was positive definite at convergence.

iter is the number of Newton/Steepest descent iterations taken.

score.calls is the number of times that the GCV/UBRE score had to be evaluated.

rms.grad is the root mean square of the gradient of the UBRE/GCV score w.r.t. the smoothing parameters.

$R$ The factor $R$ from the QR decomposition of the weighted model matrix. This is un-pivoted so that column order corresponds to $X$. So it may not be upper triangular.

Note that some further useful quantities can be obtained using magic.post.proc.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


https://www.maths.ed.ac.uk/~swood34/

See Also

magic.post.proc, gam

Examples

## Use 'magic' for a standard additive model fit ...
library(mgcv)
set.seed(1);n <- 200;sig <- 1
dat <- gamSim(1,n=n,scale=sig)
k <- 30
## set up additive model
G <- gam(y~s(x0,k=k)+s(x1,k=k)+s(x2,k=k)+s(x3,k=k),fit=FALSE,data=dat)
## fit using magic (and gam default tolerance)
mgfit <- magic(G$y,G$X,G$sp,G$S,G$off,rank=G$rank,
    control=list(tol=1e-7,step.half=15))
## and fit using gam as consistency check
b <- gam(G=G)
mgfit$b$sp # compare smoothing parameter estimates
edf <- magic.post.proc(G$X,mgfit,G$w)$edf # get e.d.f. per param
range(edf-b$edf) # compare

## p>n example... fit model to first 100 data only, so more
## params than data...
mgfit <- magic(G$y[1:100],G$X[1:100,],G$sp,G$S,G$off,rank=G$rank)
edf <- magic.post.proc(G$X[1:100,],mgfit,G$w[1:100])$edf

## constrain first two smooths to have identical smoothing parameters
L <- diag(3);L <- rbind(L[1,],L)
mgfit <- magic(G$y,G$X,rep(-1,3),G$S,G$off,L=L,rank=G$rank,C=G$C)

## Now a correlated data example ...

## simulate truth
set.seed(1);n<-400;sig<-2
x <- 0:(n-1)/(n-1)
f <- 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
## produce scaled covariance matrix for AR1 errors...
V <- corMatrix(Initialize(corAR1(.6),data.frame(x=x)))
Cv <- chol(V) # t(Cv)%*%Cv=V
## Simulate AR1 errors ...
e <- t(Cv)%*%rnorm(n,0,sig) # so cov(e) = V * sig^2
## Observe truth + AR1 errors
y <- f + e

## GAM ignoring correlation
par(mfrow=c(1,2))
b <- gam(y~s(x,k=20))
plot(b);lines(x,f-mean(f),col=2);title("Ignoring correlation")

## Fit smooth, taking account of *known* correlation...
w <- solve(t(Cv)) # V^-1 = w
## Use 'gam' to set up model for fitting...
G <- gam(y~s(x,k=20),fit=FALSE)
## fit using magic, with weight *matrix*
mgfit <- magic(G$y,G$X,rep(-1,3),G$S,G$off,rank=G$rank,C=G$C,w=w)

## Modify previous gam object using new fit, for plotting...
mg.stuff <- magic.post.proc(G$X,mgfit,w)
b$edf <- mg.stuff$edf;b$Vp <- mg.stuff$Vb
b$coefficients <- mgfit$b
plot(b);lines(x,f-mean(f),col=2);title("Known correlation")

---

**magic.post.proc**

**Auxiliary information from magic fit**

**Description**

Obtains Bayesian parameter covariance matrix, frequentist parameter estimator covariance matrix, estimated degrees of freedom for each parameter and leading diagonal of influence/hat matrix, for
a penalized regression estimated by magic.

Usage

`magic.post.proc(X, object, w=NULL)`

Arguments

- `X`: the model matrix.
- `object`: is the list returned by `magic` after fitting the model with model matrix `X`.
- `w`: is the weight vector used in fitting, or the weight matrix used in fitting (i.e. supplied to `magic`, if one was.). If `w` is a vector then its elements are typically proportional to reciprocal variances (but could even be negative). If `w` is a matrix then `t(w)%*%w` should typically give the inverse of the covariance matrix of the response data supplied to `magic`.

Details

`object` contains `rV` (V, say), and `scale` (ϕ, say) which can be used to obtain the require quantities as follows. The Bayesian covariance matrix of the parameters is `VV'ϕ`. The vector of estimated degrees of freedom for each parameter is the leading diagonal of `VV'X'WX` where `W` is either the weight matrix `w` or the matrix `diag(w)`. The hat/influence matrix is given by `WXVV'X'W'`.

The frequentist parameter estimator covariance matrix is `VV'X'WXVV'ϕ`: it is sometimes useful for testing terms for equality to zero.

Value

A list with three items:

- `Vb`: the Bayesian covariance matrix of the model parameters.
- `Ve`: the frequentist covariance matrix for the parameter estimators.
- `hat`: the leading diagonal of the hat (influence) matrix.
- `edf`: the array giving the estimated degrees of freedom associated with each parameter.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

`magic`
Description

This page provides answers to some of the questions that get asked most often about mgcv

FAQ list

1. **How can I compare gamm models?** In the identity link normal errors case, then AIC and hypothesis testing based methods are fine. Otherwise it is best to work out a strategy based on the summary.gam Alternatively, simple random effects can be fitted with gam, which makes comparison straightforward. Package gamm4 is an alternative, which allows AIC type model selection for generalized models.

2. **How do I get the equation of an estimated smooth?** This slightly misses the point of semi-parametric modelling: the idea is that we estimate the form of the function from data without assuming that it has a particular simple functional form. Of course for practical computation the functions do have underlying mathematical representations, but they are not very helpful, when written down. If you do need the functional forms then see chapter 5 of Wood (2017). However for most purposes it is better to use predict.gam to evaluate the function for whatever argument values you need. If derivatives are required then the simplest approach is to use finite differencing (which also allows SEs etc to be calculated).

3. **Some of my smooths are estimated to be straight lines and their confidence intervals vanish at some point in the middle. What is wrong?** Nothing. Smooths are subject to sum-to-zero identifiability constraints. If a smooth is estimated to be a straight line then it consequently has one degree of freedom, and there is no choice about where it passes through zero — so the CI must vanish at that point.

4. **How do I test whether a smooth is significantly different from a straight line.** See tprs and the example therein.

5. **An example from an mgcv helpfile gives an error - is this a bug?** It might be, but first please check that the version of mgcv you have loaded into R corresponds to the version from which the helpfile came. Many such problems are caused by trying to run code only supported in a later mgcv version in an earlier version. Another possibility is that you have an object loaded whose name clashes with an mgcv function (for example you are trying to use the mgcv multinom function, but have another object called multinom loaded.)

6. **Some code from Wood (2006) causes an error: why?** The book was written using mgcv version 1.3. To allow for REML estimation of smoothing parameters in versions 1.5, some changes had to be made to the syntax. In particular the function gam.method no longer exists. The smoothness selection method (GCV, REML etc) is now controlled by the method argument to gam while the optimizer is selected using the optimizer argument. See gam for details.

7. **Why is a model object saved under a previous mgcv version not usable with the current mgcv version?** I’m sorry about this issue, I know it’s really annoying. Here’s my defence. Each mgcv version is run through an extensive test suite before release, to ensure that it gives the same results as before, unless there are good statistical reasons why not (e.g. improvements to p-value approximation, fixing of an error). However it is sometimes necessary to modify the internal structure of model objects in a way that makes an old style object unusable with a newer version. For example, bug fixes or new R features sometimes require changes in the way that things are computed which in turn require modification of the object structure. Similarly
improvements, such as the ability to compute smoothing parameters by RE/ML require object level changes. The only fix to this problem is to access the old object using the original mgcv version (available on CRAN), or to recompute the fit using the current mgcv version.

8. **When using gamm or gamm4, the reported AIC is different for the gam object and the lme or lmer object. Why is this?** There are several reasons for this. The most important is that the models being used are actually different in the two representations. When treating the GAM as a mixed model, you are implicitly assuming that if you gathered a replicate dataset, the smooths in your model would look completely different to the smooths from the original model, except for having the same degree of smoothness. Technically you would expect the smooths to be drawn afresh from their distribution under the random effects model. When viewing the gam from the usual penalized regression perspective, you would expect smooths to look broadly similar under replication of the data. i.e. you are really using Bayesian model for the smooths, rather than a random effects model (it’s just that the frequentist random effects and Bayesian computations happen to coincide for computing the estimates). As a result of the different assumptions about the data generating process, AIC model comparisons can give rather different answers depending on the model adopted. Which you use should depend on which model you really think is appropriate. In addition the computations of the AICs are different. The mixed model AIC uses the marginal likelihood and the corresponding number of model parameters. The gam model uses the penalized likelihood and the effective degrees of freedom.

9. **What does ’mgcv’ stand for? ’Mixed GAM Computation Vehicle’, is my current best effort (let me know if you can do better). Originally it stood for ’Multiple GCV’, which has long since ceased to be usefully descriptive, (and I can’t really change ’mgcv’ now without causing disruption). On a bad inbox day ’Mad GAM Computing Vulture’.

10. **My new method is failing to beat mgcv, what can I do?** If speed is the problem, then make sure that you use the slowest basis possible ("tp") with a large sample size, and experiment with different optimizers to find one that is slow for your problem. For prediction error/MSE, then leaving the smoothing basis dimensions at their arbitrary defaults, when these are inappropriate for the problem setting, is a good way of reducing performance. Similarly, using p-splines in place of derivative penalty based splines will often shave a little more from the performance here. Unlike REML/ML, prediction error based smoothness selection criteria such as Mallows Cp and GCV often produce a small proportion of severe overfits, so careful choice of smoothness selection method can help further. In particular GCV etc. usually result in worse confidence interval and p-value performance than ML or REML. If all this fails, try using a really odd simulation setup for which mgcv is clearly not suited: for example poor performance is almost guaranteed for small noisy datasets with large numbers of predictors.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


mgcv.package

Mixed GAM Computation Vehicle with GCV/AIC/REML/NCV smoothness estimation and GAMMs by REML/PQL

Description

mgcv provides functions for generalized additive modelling (gam and bam) and generalized additive mixed modelling (gamm, and random.effects). The term GAM is taken to include any model dependent on unknown smooth functions of predictors and estimated by quadratically penalized (possibly quasi-) likelihood maximization. Available distributions are covered in family.mgcv and available smooths in smooth.terms.

Particular features of the package are facilities for automatic smoothness selection (Wood, 2004, 2011), and the provision of a variety of smooths of more than one variable. User defined smooths can be added. A Bayesian approach to confidence/credible interval calculation is provided. Linear functionals of smooths, penalization of parametric model terms and linkage of smoothing parameters are all supported. Lower level routines for generalized ridge regression and penalized linearly constrained least squares are also available. In addition to the main modelling functions, jagam provided facilities to ease the set up of models for use with JAGS, while ginla provides marginal inference via a version of Integrated Nested Laplace Approximation.

Details

mgcv provides generalized additive modelling functions gam, predict.gam and plot.gam, which are very similar in use to the S functions of the same name designed by Trevor Hastie (with some extensions). However the underlying representation and estimation of the models is based on a penalized regression spline approach, with automatic smoothness selection. A number of other functions such as summary.gam and anova.gam are also provided, for extracting information from a fitted gamObject.

Use of gam is much like use of glm, except that within a gam model formula, isotropic smooths of any number of predictors can be specified using s terms, while scale invariant smooths of any number of predictors can be specified using te, ti or t2 terms. smooth.terms provides an overview of the built in smooth classes, and random.effects should be refered to for an overview of random effects terms (see also mrf for Markov random fields). Estimation is by penalized likelihood or quasi-likelihood maximization, with smoothness selection by GCV, GACV, gAIC/UBRE, NCV or (RE)ML.

See gam, gam.models, linear.functional.terms and gam.selection for some discussion of model specification and selection. For detailed control of fitting see gam.convergence, gam arguments method and optimizer and gam.control. For checking and visualization see gam.check, choose.k, vis.gam and plot.gam. While a number of types of smoother are built into the package, it is also extendable with user defined smooths, see smooth.construct, for example.

A Bayesian approach to smooth modelling is used to derive standard errors on predictions, and hence credible intervals (see Marra and Wood, 2012). The Bayesian covariance matrix for the model coefficients is returned in Vp of the gamObject. See predict.gam for examples of how this can be used to obtain credible regions for any quantity derived from the fitted model, either directly, or by direct simulation from the posterior distribution of the model coefficients. Approximate p-values can also be obtained for testing individual smooth terms for equality to the zero function, using similar ideas (see Wood, 2013a,b). Frequentist approximations can be used for hypothesis testing based model comparison. See anova.gam and summary.gam for more on hypothesis testing.

For large datasets (that is large n) see bam which is a version of gam with a much reduced memory footprint. bam(...) offers the very efficient methods of Wood et al. (2017) and Li and Wood (2020).
The package also provides a generalized additive mixed modelling function, \texttt{gamm}, based on a PQL approach and \texttt{lme} from the \texttt{nlme} library (for an \texttt{lme4} based version, see package \texttt{gamm4}). \texttt{gamm} is particularly useful for modelling correlated data (i.e. where a simple independence model for the residual variation is inappropriate). In addition, low level routine \texttt{magic} can fit models to data with a known correlation structure.

Some underlying GAM fitting methods are available as low level fitting functions: see \texttt{magic}. But there is little functionality that can not be more conveniently accessed via \texttt{gam}. Penalized weighted least squares with linear equality and inequality constraints is provided by \texttt{pcls}.

For a complete list of functions type \texttt{library\(\text{\texttt{\{\texttt{help=mgcv}\}}}\)\). See also \texttt{mgcv.FAQ}.

Author(s)

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References

These provide details for the underlying mgcv methods, and fuller references to the large literature on which the methods are based.


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Examples

### see examples for gam, bam and gamm

---

**Description**

`mgcv` can make some use of multiple cores or a cluster.

`bam` can use an openMP based parallelization approach alongside discretisation of covariates to achieve substantial speed ups. This is selected using the `discrete=TRUE` option to `bam`, with the number of threads controlled via the `nthreads` argument. This is the approach that scales best. See example below.

Alternatively, function `bam` can use the facilities provided in the `parallel` package. See examples below. Note that most multi-core machines are memory bandwidth limited, so parallel speed up tends to be rather variable.

Function `gam` can use parallel threads on a (shared memory) multi-core machine via openMP (where this is supported). To do this, set the desired number of threads by setting `nthreads` to the number of cores to use, in the `control` argument of `gam`. Note that, for the most part, only the dominant $O(np^2)$ steps are parallelized ($n$ is number of data, $p$ number of parameters). For additive Gaussian models estimated by GCV, the speed up can be disappointing as these employ an $O(p^3)$ SVD step that can also have substantial cost in practice. `magic` can also use multiple cores, but the same comments apply as for the GCV Gaussian additive model.

When using `NCV` with `gam` worthwhile performance improvements are available by setting `ncv.threads` in `gam.control`.

If `control$nthreads` is set to more than the number of cores detected, then only the number of detected cores is used. Note that using virtual cores usually gives very little speed up, and can even slow computations slightly. For example, many Intel processors reporting 4 cores actually have 2 physical cores, each with 2 virtual cores, so using 2 threads gives a marked increase in speed, while using 4 threads makes little extra difference.

Note that on Intel and similar processors the maximum performance is usually achieved by disabling Hyper-Threading in BIOS, and then setting the number of threads to the number of physical cores used. This prevents the operating system scheduler from sending 2 floating point intensive threads to the same physical core, where they have to share a floating point unit (and cache) and therefore slow each other down. The scheduler tends to do this under the manager - worker multi-threading approach used in `mgcv`, since the manager thread looks very busy up to the point at which the workers are set to work, and at the point of scheduling the scheduler has no way of knowing that the manager thread actually has nothing more to do until the workers are finished. If you are working on a many cored platform where you can not disable hyper-threading then it may be worth setting the number of threads to one less than the number of physical cores, to reduce the frequency of such scheduling problems.

`mgcv`'s work splitting always makes the simple assumption that all your cores are equal, and you are not sharing them with other floating point intensive threads.

In addition to hyper-threading several features may lead to apparently poor scaling. The first is that many CPUs have a Turbo mode, whereby a few cores can be run at higher frequency, provided the overall power used by the CPU does not exceed design limits, however it is not possible for all cores on the CPU to run at this frequency. So as you add threads eventually the CPU frequency has to be reduced below the Turbo frequency, with the result that you don’t get the expected speed up.
from adding cores. Secondly, most modern CPUs have their frequency set dynamically according to load. You may need to set the system power management policy to favour high performance in order to maximize the chance that all threads run at the speed you were hoping for (you can turn off dynamic power control in BIOS, but then you turn off the possibility of Turbo also).

Because the computational burden in mgcv is all in the linear algebra, then parallel computation may provide reduced or no benefit with a tuned BLAS. This is particularly the case if you are using a multi threaded BLAS, but a BLAS that is tuned to make efficient use of a particular cache size may also experience loss of performance if threads have to share the cache.

Author(s)

Simon Wood <simon.wood@r-project.org>

References

https://hpc-tutorials.llnl.gov/openmp/

Examples

```r
## illustration of multi-threading with gam...
require(mgcv);set.seed(9)
dat <- gamSim(1,n=2000,dist="poisson",scale=.1)
k <- 12;bs <- "cr";ctrl <- list(nthreads=2)
system.time(b1<-gam(y~s(x0,bs=bs)+s(x1,bs=bs)+s(x2,bs=bs,k=k)
,family=poisson,data=dat,method="REML"))[3]

system.time(b2<-gam(y~s(x0,bs=bs)+s(x1,bs=bs)+s(x2,bs=bs,k=k),
family=poisson,data=dat,method="REML",control=ctrl))[3]

## Poisson example on a cluster with 'bam'.
## Note that there is some overhead in initializing the
## computation on the cluster, associated with loading
## the Matrix package on each node. Sample sizes are low
## here to keep example quick -- for such a small model
## little or no advantage is likely to be seen.
k <- 13;set.seed(9)
dat <- gamSim(1,n=6000,dist="poisson",scale=.1)

require(parallel)
nc <- 2  ## cluster size, set for example portability
if (detectCores()>1) { ## no point otherwise
  cl <- makeCluster(nc)
  ## could also use makeForkCluster, but read warnings first!
} else cl <- NULL

system.time(b3 <- bam(y ~ s(x0,bs=bs,k=7)+s(x1,bs=bs,k=7)+s(x2,bs=bs,k=k)
 ,data=dat,family=poisson(),chunk.size=5000,cluster=cl))

fv <- predict(b3,cluster=cl) ## parallel prediction
if (!is.null(cl)) stopCluster(cl)
b3

## Alternative, better scaling example, using the discrete option with bam...
```
mini.roots

Obtain square roots of penalty matrices

**Description**

INTERNAL function to obtain square roots, $B[i]$, of the penalty matrices $S[i]$’s having as few columns as possible.

**Usage**

mini.roots(S, off, np, rank = NULL)

**Arguments**

- **S**: a list of penalty matrices, in packed form.
- **off**: a vector where the i-th element is the offset for the i-th matrix. The elements in columns 1:off[i] of $B[[i]]$ will be equal to zero.
- **np**: total number of parameters.
- **rank**: here rank[i] is optional supplied rank of $S[[i]]$. Set rank[i] < 1, or rank=NULL to estimate.

**Value**

A list of matrix square roots such that $S[[i]]=B[[i]]%*%t(B[[i]])$.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>.

missing.data

Missing data in GAMs

**Description**

If there are missing values in the response or covariates of a GAM then the default is simply to use only the ‘complete cases’. If there are many missing covariates, this can get rather wasteful. One possibility is then to use imputation. Another is to substitute a simple random effects model in which the by variable mechanism is used to set $s(x)$ to zero for any missing $x$, while a Gaussian random effect is then substituted for the ‘missing’ $s(x)$. See the example for details of how this works, and `gam.models` for the necessary background on by variables.

**Author(s)**

Simon Wood <simon.wood@r-project.org>
## The example takes a couple of minutes to run...

```r
require(mgcv)
par(mfrow=c(4,4),mar=c(4,4,1,1))
for (sim in c(1,7)) { ## cycle over uncorrelated and correlated covariates
  n <- 350; set.seed(2)
  ## simulate data but randomly drop 300 covariate measurements
  ## leaving only 50 complete cases...
  dat <- gamSim(sim,n=n,scale=3) ## 1 or 7
  drop <- sample(1:n,300) ## to
  for (i in 2:5) dat[drop[i-1:75+(i-2)*75],i] <- NA
  ## process data.frame producing binary indicators of missingness,
  ## mx0, mx1 etc. For each missing value create a level of a factor
  ## idx0, idx1, etc. So idx0 has as many levels as x0 has missing
  ## values. Replace the NA's in each variable by the mean of the
  ## non missing for that variable...
  dname <- names(dat)[2:5]
  dat1 <- dat
  for (i in 1:4) {
    by.name <- paste("m",dname[i],sep="")
    dat1[[by.name]] <- is.na(dat1[[dname[i]]])
    dat1[[dname[i]]][dat1[[by.name]]] <- mean(dat1[[dname[i]]],na.rm=TRUE)
    lev <- rep(1,n); lev[dat1[[by.name]]] <- 1:sum(dat1[[by.name]])
    id.name <- paste("id",dname[i],sep="")
    dat1[[id.name]] <- factor(lev)
    dat1[[by.name]] <- as.numeric(dat1[[by.name]])
  }
  ## Fit a gam, in which any missing value contributes zero
  ## to the linear predictor from its smooth, but each
  ## missing has its own random effect, with the random effect
  ## variances being specific to the variable. e.g.
  ## for s(x0,by=ordered(!mx0)), declaring the 'by' as an ordered
  ## factor ensures that the smooth is centred, but multiplied
  ## by zero when mx0 is one (indicating a missing x0). This means
  ## that any value (within range) can be put in place of the
  ## NA for x0.  s(idx0,bs="re",by=mx0) produces a separate Gaussian
  ## random effect for each missing value of x0 (in place of s(x0),
  ## effectively). The 'by' variable simply sets the random effect to
  ## zero when x0 is non-missing, so that we can set idx0 to any
  ## existing level for these cases.
  b <- bam(y~s(x0,by=ordered(!mx0))+s(x1,by=ordered(!mx1))+
    s(x2,by=ordered(!mx2))+s(x3,by=ordered(!mx3))+
    s(idx0,bs="re",by=mx0)+s(idx1,bs="re",by=mx1)+
    s(idx2,bs="re",by=mx2)+s(idx3,bs="re",by=mx3)
  ,data=dat1,discrete=TRUE)
  for (i in 1:4) plot(b,select=i) ## plot the smooth effects from b
```

See Also

gam.vcomp, gam.models, s, smooth.construct.re.smooth.spec.gam

Examples

```r
## Examples
```
## fit the model to the 'complete case' data...

```r
b2 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML")
plot(b2) ## plot the complete case results
```

### model.matrix.gam

Extract model matrix from GAM fit

**Description**

Obtains the model matrix from a fitted `gam` object.

**Usage**

```r
## S3 method for class 'gam'
model.matrix(object, ...)  
```

**Arguments**

- `object`: fitted model object of class `gam` as produced by `gam()`.
- `...`: other arguments, passed to `predict.gam`.

**Details**

Calls `predict.gam` with no `newdata` argument and `type="lpmatrix"` in order to obtain the model matrix of object.

**Value**

A model matrix.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**See Also**

`gam`

**Examples**

```r
require(mgcv)
n <- 15
x <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=6),knots=list(x=seq(0,1,length=6)))
model.matrix(mod)
```
Description

Finds linear constraints sufficient for monotonicity (and optionally upper and/or lower boundedness) of a cubic regression spline. The basis representation assumed is that given by the `gam", cr" basis: that is the spline has a set of knots, which have fixed x values, but the y values of which constitute the parameters of the spline.

Usage

```r
mono.con(x, up=TRUE, lower=NA, upper=NA)
```

Arguments

- `x` The array of knot locations.
- `up` If TRUE then the constraints imply increase, if FALSE then decrease.
- `lower` This specifies the lower bound on the spline unless it is NA in which case no lower bound is imposed.
- `upper` This specifies the upper bound on the spline unless it is NA in which case no upper bound is imposed.

Details

Consider the natural cubic spline passing through the points \{x\_i, p\_i : i = 1 \ldots n\}. Then it is possible to find a relatively small set of linear constraints on p sufficient to ensure monotonicity (and bounds if required): A p \geq b. Details are given in Wood (1994).

Value

A list containing constraint matrix A and constraint vector b.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

See Also

`magic`, `pcls`

Examples

```r
## see ?pcls
```
Description

Find a square root of a positive semi-definite matrix, having as few columns as possible. Uses either pivoted choleski decomposition or singular value decomposition to do this.

Usage

mroot(A, rank=NULL, method="chol")

Arguments

A  The positive semi-definite matrix, a square root of which is to be found.
rank  if the rank of the matrix A is known then it should be supplied. NULL or <1 imply that it should be estimated.
method  "chol" to use pivoted choleski decompositon, which is fast but tends to overestimate rank. "svd" to use singular value decomposition, which is slow, but is the most accurate way to estimate rank.

Details

The function uses SVD, or a pivoted Choleski routine. It is primarily of use for turning penalized regression problems into ordinary regression problems.

Value

A matrix, B with as many columns as the rank of A, and such that A = BB'.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

require(mgcv)
set.seed(0)
a <- matrix(runif(24),6,4)
A <- a%*%t(a)  ## A is +ve semi-definite, rank 4
B <- mroot(A)  ## default pivoted choleski method
tol <- 100*.Machine$double.eps
chol.err <- max(abs(A-B%*%t(B))):chol.err
if (chol.err>tol) warning("mroot (chol) suspect")
B <- mroot(A,method="svd")  ## svd method
svd.err <- max(abs(A-B%*%t(B))):svd.err
if (svd.err>tol) warning("mroot (svd) suspect")
Description

Family for use with `gam`, implementing regression for categorical response data. Categories must be coded 0 to K, where K is a positive integer. `gam` should be called with a list of K formulae, one for each category except category zero (extra formulae for shared terms may also be supplied: see `formula.gam`). The first formula also specifies the response variable.

Usage

```r
multinom(K=1)
```

Arguments

- **K**
  
  There are K+1 categories and K linear predictors.

Details

The model has K linear predictors, \( \eta_j \), each dependent on smooth functions of predictor variables, in the usual way. If response variable, \( y \), contains the class labels 0,...,K then the likelihood for \( y>0 \) is \( \exp(\eta_y)/(1 + \sum_j \exp(\eta_j)) \). If \( y=0 \) the likelihood is \( 1/(1 + \sum_j \exp(\eta_j)) \). In the two class case this is just a binary logistic regression model. The implementation uses the approach to GAMLSS models described in Wood, Pya and Saefken (2016).

The residuals returned for this model are simply the square root of -2 times the deviance for each observation, with a positive sign if the observed \( y \) is the most probable class for this observation, and a negative sign otherwise.

Use `predict` with `type="response"` to get the predicted probabilities in each category.

Note that the model is not completely invariant to category relabelling, even if all linear predictors have the same form. Realistically this model is unlikely to be suitable for problems with large numbers of categories. Missing categories are not supported.

Value

An object of class `general.family`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>, with a variance bug fix from Max Goplerud.

References


See Also

`ocat`
Examples

```r
library(mgcv)
set.seed(6)
## simulate some data from a three class model
n <- 1000
f1 <- function(x) sin(3*pi*x)*exp(-x)
f2 <- function(x) x^3
f3 <- function(x) .5*exp(-x^2)-.2
f4 <- function(x) 1
x1 <- runif(n);x2 <- runif(n)
eta1 <- 2*(f1(x1) + f2(x2))-.5
eta2 <- 2*(f3(x1) + f4(x2))-1
p <- exp(cbind(0,eta1,eta2))
p <- p/rowSums(p) ## prob. of each category
cp <- t(apply(p,1,cumsum)) ## cumulative prob.
## simulate multinomial response with these probabilities
## see also ?rmultinom
y <- apply(cp,1,function(x) min(which(x>runif(1))))-1
## plot simulated data...
plot(x1,x2,col=y+3)

## now fit the model...
b <- gam(list(y~s(x1)+s(x2),~s(x1)+s(x2)),family=multinom(K=2))
plot(b,pages=1)
gam.check(b)

## now a simple classification plot...
expand.grid(x1=seq(0,1,length=40),x2=seq(0,1,length=40)) -> gr
pp <- predict(b,newdata=gr,type="response")
pc <- apply(pp,1,function(x) which(max(x)==x)[1])-1
plot(gr,col=pc+3,pch=19)

## example sharing a smoother between linear predictors
## ?formula.gam gives more details.
b <- gam(list(y~s(x1),~s(x1),1+2~s(x2)-1),family=multinom(K=2))
plot(b,pages=1)
```

mvn

**Multivariate normal additive models**

**Description**

Family for use with `gam` implementing smooth multivariate Gaussian regression. The means for each dimension are given by a separate linear predictor, which may contain smooth components. Extra linear predictors may also be specified giving terms which are shared between components (see `formula.gam`). The Choleski factor of the response precision matrix is estimated as part of fitting.

**Usage**

```r
mvn(d=2)
```
Arguments

\[ d \] The dimension of the response (>1).

Details

The response is \( d \) dimensional multivariate normal, where the covariance matrix is estimated, and the means for each dimension have separate linear predictors. Model specification is via a list of gamlike formulae - one for each dimension. See example.

Currently the family ignores any prior weights, and is implemented using first derivative information sufficient for BFGS estimation of smoothing parameters. "response" residuals give raw residuals, while "deviance" residuals are standardized to be approximately independent standard normal if all is well.

Value

An object of class `general.family`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

`gaussian`

Examples

```r
library(mgcv)
## simulate some data...
V <- matrix(c(2,1,1,2),2,2)
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * 
(10 * x)^3 * (1 - x)^10
n <- 300
x0 <- runif(n);x1 <- runif(n);
x2 <- runif(n);x3 <- runif(n)
y <- matrix(0,n,2)
for (i in 1:n) {
  mu <- c(f0(x0[i])+f1(x1[i]),f2(x2[i]))
  y[i,] <- rmvn(1,mu,V)
}
dat <- data.frame(y0=y[,1],y1=y[,2],x0=x0,x1=x1,x2=x2,x3=x3)
## fit model...
b <- gam(list(y0~s(x0)+s(x1),y1~s(x2)+s(x3)),family=mvn(d=2),data=dat)
b
summary(b)
```
NCV estimates smoothing parameters by optimizing the average ability of a model to predict subsets of data when subsets of data are omitted from fitting. Usually the predicted subset is a subset of the omitted subset. If both subsets are the same single datapoint, and the average is over all datapoints, then NCV is leave-one-out cross validation. QNCV is a quadratic approximation to NCV, guaranteed finite for any family link combination.

In detail, suppose that a model is estimated by minimizing a penalized loss

$$
\sum_i D(y_i, \theta_i) + \sum_j \lambda_j \beta^T S_j \beta
$$

where $D$ is a loss (such as a negative log likelihood), dependent on response $y_i$ and parameter vector $\theta_i$, which in turn depends on covariates via one or more smooth linear predictors with coefficients $\beta$. The quadratic penalty terms penalize model complexity: $S_j$ is a known matrix and $\lambda_j$ an unknown smoothing parameter. Given smoothing parameters the penalized loss is readily minimized to estimate $\beta$.

The smoothing parameters also have to be estimated. To this end, choose $k = 1, \ldots, m$ subsets $\alpha(k) \subset \{1, \ldots, n\}$ and $\delta(k) \subset \{1, \ldots, n\}$. Usually $\delta(k)$ is a subset of (or equal to) $\alpha(k)$. Let $\hat{\theta}_i^{\alpha(k)}$ denote the estimate of $\theta_i$ when the points indexed by $\alpha(k)$ are omitted from fitting. Then the NCV criterion

$$
V = \sum_{k=1}^m \sum_{i \in \alpha(k)} D(y_i, \hat{\theta}_i^{\alpha(k)})
$$

is minimized w.r.t. the smoothing parameters, $\lambda_j$. If $m = n$ and $\alpha(k) = \delta(k) = k$ then ordinary leave-one-out cross validation is recovered. This formulation covers many of the variants of cross validation reviewed in Arlot and Celisse (2010), for example.

Except for a quadratic loss, $V$ can not be computed exactly, but it can be computed to $O(n^{-2})$ accuracy (fixed basis size), by taking single Newton optimization steps from the full data $\beta$ estimates to the equivalent when each $\alpha(k)$ is dropped. This is what mgcv does. The Newton steps require update of the full model Hessian to the equivalent when each datum is dropped. This can be achieved at $O(p^2)$ cost, where $p$ is the dimension of $\beta$. Hence, for example, the ordinary cross validation criterion is computable at the $O(np^2)$ cost of estimating the model given smoothing parameters.

The NCV score computed in this way is optimized using a BFGS quasi-Newton method, adapted to the case in which smoothing parameters tending to infinity may cause indefiniteness.

**Spatial and temporal short range autocorrelation**

A routine applied problem is that smoothing parameters tend to be underestimated in the presence of un-modelled short range autocorrelation, as the smooths try to fit the local excursions in the data caused by the local autocorrelation. Cross validation will tend to 'fit the noise' when there is autocorrelation, since a model that fits the noise in the data correlated with an omitted datum, will also tend to closely fit the noise in the omitted datum, because of the correlation. That is autocorrelation works against the avoidance of overfit that cross validation seeks to achieve.
For short range autocorrelation the problems can be avoided, or at least mitigated, by predicting each datum when all the data in its ‘local’ neighbourhood are omitted. The neighbourhoods being constructed in order that un-modelled correlation is minimized between the point of interest and points outside its neighbourhood. That is we set \( m = n \), \( \delta(k) = k \) and \( \alpha(k) = \text{nei}(k) \), where \( \text{nei}(k) \) are the indices of the neighbours of point \( k \). This approach has been known for a long time (e.g. Chu and Marron, 1991; Robert et al. 2017), but was previously rather too expensive for regular use for smoothing parameter estimation.

Specifying the neighbourhoods

The neighbourhood subsets \( \alpha(k) \) and \( \delta(k) \) have to be supplied to \texttt{gam}, and the \texttt{nei} argument does this. It is a list with the following arguments.

- \( k \) is the vector of indices to be dropped for each neighbourhood.
- \( m \) gives the end of each neighbourhood. So \( \text{nei}$k[(\text{nei}$m[j-1]+1):\text{nei}$m[j]] \) gives the points dropped for the neighbourhood \( j \): that is \( \alpha(j) \).
- \( i \) is the vector of indices of points to predict.
- \( \text{mi} \) gives the corresponding endpoints \( \text{mi} \). So \( \text{nei}i[(\text{nei}mi[j-1]+1):\text{nei}mi[j]] \) indexes the points to predict for neighbourhood \( j \): that is \( \delta(j) \).
- \texttt{jackknife} is an optional element. If supplied and \texttt{TRUE} then variance estimates are based on the raw Jackknife estimate, if \texttt{FALSE} then on the standard Bayesian results. If not supplied (usual) then an estimator accounting for the neighbourhood structure is used, that largely accounts for any correlation present within neighbourhoods. \texttt{jackknife} is ignored if NCV is being calculated for a model where another method is used for smoothing parameter selection.

If \( \text{nei}==\text{NULL} \) (or \( k \) or \( m \) are missing) then leave-one-out cross validation is used. If \( \text{nei} \) is supplied but NCV is not selected as the smoothing parameter estimation method, then it is simply computed (but not optimized).

Numerical issues

If a model is specified in which some coefficient values, \( \beta \), have non-finite likelihood then the NCV criterion computed with single Newton steps could also be non-finite. A simple fix replaces the NCV criterion with a quadratic approximation to the criterion around the full data fit. The quadratic approximation is always finite. This ‘QNCV’ is essential for some families, such as \texttt{gevlss}.

Although the leading order cost of NCV is the same as REML or GCV, the actual cost is higher because the dominant operations costs are in matrix-vector, rather than matrix-matrix, operations, so BLAS speed ups are small. However multi-core computing is worthwhile for NCV. See the option \texttt{ncv.threads} in \texttt{gam.control}.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Examples

```r
require(mgcv)
nei.cor <- function(h,n) { ## construct nei structure
  nei <- list(mi=1:n,i=1:n)
  nei$m <- cumsum(c((h+1):(2*h+1),rep(2*h+1,n-2*h-2),(2*h+1):(h+1))
  k0 <- rep(0,0); if (h>0) for (i in 1:h) k0 <- c(k0,1:(h+i))
  k1 <- n-k0[length(k0):1]+1
  nei$k <- c(k0,1:(2*h+1)+rep(0:(n-2*h-1),each=2*h+1),k1)
  nei
}
set.seed(1)
n <- 500; sig <- .6
x <- 0:(n-1)/(n-1)
f <- sin(4*pi*x)*exp(-x*2)*5/2
e <- rnorm(n,0,sig)
for (i in 2:n) e[i] <- 0.6*e[i-1] + e[i]
y <- f + e ## autocorrelated data
nei <- nei.cor(4,n) ## construct neighbourhoods to mitigate
b0 <- gam(y~s(x,k=40)) ## GCV based fit
gc <- gam.control(ncv.threads=2)
b1 <- gam(y~s(x,k=40),method="NCV",nei=nei,control=gc)
## use "QNCV", which is identical here...
b2 <- gam(y~s(x,k=40),method="QNCV",nei=nei,control=gc)
## plot GCV and NCV based fits...
f <- f - mean(f)
par(mfrow=c(1,2))
plot(b0,rug=FALSE,scheme=1);lines(x,f,col=2)
plot(b1,rug=FALSE,scheme=1);lines(x,f,col=2)
```

negbin

GAM negative binomial families

Description

The `negbin` family is designed to be able to use the `negbin` family (a modification of MASS library `negative.binomial` family by Venables and Ripley), or the `nb` function designed for integrated estimation of parameter `theta`. The parameter such that $\text{var}(y) = \mu + \mu^2/\theta$, where $\mu = \text{E}(y)$.

Two approaches to estimating `theta` are available (with `gam` only):

- With `negbin` then if ‘performance iteration’ is used for smoothing parameter estimation (see `gam`), then smoothing parameters are chosen by GCV and `theta` is chosen in order to ensure that the Pearson estimate of the scale parameter is as close as possible to 1, the value that the scale parameter should have.
- If ‘outer iteration’ is used for smoothing parameter selection with the `nb` family then `theta` is estimated alongside the smoothing parameters by ML or REML.

To use the first option, set the optimizer argument of `gam` to “perf” (it can sometimes fail to converge).

Usage

```r
negbin(theta = stop("theta' must be specified"), link = "log")
nb(theta = NULL, link = "log")
```
Arguments

theta
Either i) a single value known value of theta or ii) two values of theta specifying the endpoints of an interval over which to search for theta (this is an option only for negbin, and is deprecated). For nb then a positive supplied theta is treated as a fixed known parameter, otherwise it is estimated (the absolute value of a negative theta is taken as a starting value).

link
The link function: one of "log", "identity" or "sqrt"

Details

nb allows estimation of the theta parameter alongside the model smoothing parameters, but is only usable with gam or bam (not gamm).

For negbin, if a single value of theta is supplied then it is always taken as the known fixed value and this is useable with bam and gamm. If theta is two numbers (theta[2]>theta[1]) then they are taken as specifying the range of values over which to search for the optimal theta. This option is deprecated and should only be used with performance iteration estimation (see gam argument optimizer), in which case the method of estimation is to choose \( \hat{\theta} \) so that the GCV (Pearson) estimate of the scale parameter is one (since the scale parameter is one for the negative binomial). In this case \( \theta \) estimation is nested within the IRLS loop used for GAM fitting. After each call to fit an iteratively weighted additive model to the IRLS pseudodata, the \( \theta \) estimate is updated. This is done by conditioning on all components of the current GCV/Pearson estimator of the scale parameter except \( \theta \) and then searching for the \( \hat{\theta} \) which equates this conditional estimator to one. The search is a simple bisection search after an initial crude line search to bracket one. The search will terminate at the upper boundary of the search region is a Poisson fit would have yielded an estimated scale parameter <1.

Value

For negbin an object inheriting from class family, with additional elements

- dvar the function giving the first derivative of the variance function w.r.t. mu.
- d2var the function giving the second derivative of the variance function w.r.t. mu.
- getTheta A function for retrieving the value(s) of theta. This also useful for retrieving the estimate of theta after fitting (see example).

For nb an object inheriting from class extended.family.

WARNINGS

- gamm does not support theta estimation

The negative binomial functions from the MASS library are no longer supported.

Author(s)

Simon N. Wood <simon.wood@r-project.org> modified from Venables and Ripley’s negative.binomial family.

References

Examples

```r
library(mgcv)
set.seed(3)
n <- 400
dat <- gamSim(1,n=n)
g <- exp(dat$f/5)

## negative binomial data...
dat$y <- rnbinom(g,size=3,mu=g)
## known theta fit ...
b0 <- gam(y-s(x0)+s(x1)+s(x2)+s(x3),family=negbin(3),data=dat)
plot(b0,pages=1)
print(b0)

## same with theta estimation...
b <- gam(y-s(x0)+s(x1)+s(x2)+s(x3),family=nb(),data=dat)
plot(b,pages=1)
print(b)
b$family$getTheta(TRUE) ## extract final theta estimate

## another example...
set.seed(1)
f <- dat$f
f <- f - min(f)+5; g <- f^2/10
dat$y <- rnbinom(g,size=3,mu=g)
b2 <- gam(y-s(x0)+s(x1)+s(x2)+s(x3),family=nb(link="sqrt"),
          data=dat,method="REML")
plot(b2,pages=1)
print(b2)
rm(dat)
```

Description

gamm works by transforming a GAMM into something that can be estimated by lme, but this involves creating new variables, the names of which should not clash with the names of other variables on which the model depends. This simple service routine checks a suggested name against a list of those in use, and if necessary modifies it so that there is no clash.

Usage

```r
new.name(proposed,old.names)
```

Arguments

- `proposed` a suggested name
- `old.names` An array of names that must not be duplicated

Value

A name that is not in `old.names`. 
notExp

Description

It is common practice in statistical optimization to use log-parameterizations when a parameter ought to be positive. i.e. if an optimization parameter \( a \) should be non-negative then we use \( a = \exp(b) \) and optimize with respect to the unconstrained parameter \( b \). This often works well, but it does imply a rather limited working range for \( b \): using 8 byte doubles, for example, if \( b \)'s magnitude gets much above 700 then \( a \) overflows or underflows. This can cause problems for numerical optimization methods.

\( \text{notExp} \) is a monotonic function for mapping the real line into the positive real line with much less extreme underflow and overflow behaviour than \( \exp \). It is a piece-wise function, but is continuous to second derivative: see the source code for the exact definition, and the example below to see what it looks like.

\( \text{notLog} \) is the inverse function of \( \text{notExp} \).

The major use of these functions was originally to provide more robust \( \text{pdMat} \) classes for \text{lm}e for use by \text{gamm}. Currently the \text{notExp2} and \text{notLog2} functions are used in their place, as a result of changes to the \text{nlme} optimization routines.

Usage

\( \text{notExp}(x) \)

\( \text{notLog}(x) \)

Arguments

\( x \quad \text{Argument array of real numbers (notExp) or positive real numbers (notLog).} \)

Value

An array of function values evaluated at the supplied argument values.
Author(s)
Simon N. Wood <simon.wood@r-project.org>

References
https://www.maths.ed.ac.uk/~swood34/

See Also
pdTens, pdIdnot, gamm

Examples
## Illustrate the notExp function:
## less steep than exp, but still monotonic.
require(mgcv)
x <- -100:100/10
op <- par(mfrow=c(2,2))
plot(x,notExp(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
x <- x/4
plot(x,notExp(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
par(op)
range(notLog(notExp(x))-x) # show that inverse works!

Description
notLog2 and notExp2 are alternatives to log and exp or notLog and notExp for re-parameterization of variance parameters. They are used by the pdTens and pdIdnot classes which in turn implement smooths for gamm.

The functions are typically used to ensure that smoothing parameters are positive, but the notExp2 is not monotonic: rather it cycles between ‘effective zero’ and ‘effective infinity’ as its argument changes. The notLog2 is the inverse function of the notExp2 only over an interval centered on zero.

Parameterizations using these functions ensure that estimated smoothing parameters remain positive, but also help to ensure that the likelihood is never indefinite: once a working parameter pushes a smoothing parameter below ‘effective zero’ or above ‘effective infinity’ the cyclic nature of the notExp2 causes the likelihood to decrease, where otherwise it might simply have flattened.

This parameterization is really just a numerical trick, in order to get lme to fit gamm models, without failing due to indefiniteness. Note in particular that asymptotic results on the likelihood/REML criterion are not invalidated by the trick, unless parameter estimates end up close to the effective zero or effective infinity: but if this is the case then the asymptotics would also have been invalid for a conventional monotonic parameterization.
This reparameterization was made necessary by some modifications to the underlying optimization method in lme introduced in nlme 3.1-62. It is possible that future releases will return to the notExp parameterization.

Note that you can reset ‘effective zero’ and ‘effective infinity’: see below.

Usage

\[
\text{notExp2}(x, d = .\text{Options}\$\text{mgcv.vc.logrange}, b = 1/d)
\]

\[
\text{notLog2}(x, d = .\text{Options}\$\text{mgcv.vc.logrange}, b = 1/d)
\]

Arguments

- **x**: Argument array of real numbers (notExp) or positive real numbers (notLog).
- **d**: the range of notExp2 runs from \(\exp(-d)\) to \(\exp(d)\). To change the range used by gamm reset mgcv.vc.logrange using options.
- **b**: determines the period of the cycle of notExp2.

Value

An array of function values evaluated at the supplied argument values.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

See Also

pdTens, pdIdnot, gamm

Examples

```r
## Illustrate the notExp2 function:
require(mgcv)
x <- seq(-50, 50, length=1000)
op <- par(mfrow=c(2,2))
plot(x, notExp2(x), type="l")
lines(x, exp(x), col=2)
plot(x, log(notExp2(x)), type="l")
lines(x, log(exp(x)), col=2) # redundancy intended
x <- x/4
plot(x, notExp2(x), type="l")
lines(x, exp(x), col=2)
plot(x, log(notExp2(x)), type="l")
lines(x, log(exp(x)), col=2) # redundancy intended
par(op)
```
null.space.dimension

null.space.dimension  The basis of the space of un-penalized functions for a TPRS

Description

The thin plate spline penalties give zero penalty to some functions. The space of these functions is spanned by a set of polynomial terms. null.space.dimension finds the dimension of this space, $M$, given the number of covariates that the smoother is a function of, $d$, and the order of the smoothing penalty, $m$. If $m$ does not satisfy $2m > d$ then the smallest possible dimension for the null space is found given $d$ and the requirement that the smooth should be visually smooth.

Usage

null.space.dimension(d,m)

Arguments

d  
as a positive integer - the number of variables of which the t.p.s. is a function.
m  
as a non-negative integer giving the order of the penalty functional, or signalling that the default order should be used.

Details

Thin plate splines are only visually smooth if the order of the wiggliness penalty, $m$, satisfies $2m > d + 1$. If $2m < d + 1$ then this routine finds the smallest $m$ giving visual smoothness for the given $d$, otherwise the supplied $m$ is used. The null space dimension is given by:

$$M = (m + d - 1)!/(d!(m - 1)!)$$

which is the value returned.

Value

An integer (array), the null space dimension $M$.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

See Also

tprs

Examples

require(mgcv)
null.space.dimension(2,0)
**GAM ordered categorical family**

**Description**

Family for use with `gam` or `bam`, implementing regression for ordered categorical data. A linear predictor provides the expected value of a latent variable following a logistic distribution. The probability of this latent variable lying between certain cut-points provides the probability of the ordered categorical variable being of the corresponding category. The cut-points are estimated along side the model smoothing parameters (using the same criterion). The observed categories are coded 1, 2, 3, ... up to the number of categories.

**Usage**

```
ocat(theta=NULL,link="identity",R=NULL)
```

**Arguments**

- `theta` cut point parameter vector (dimension R-2). If supplied and all positive, then taken to be the cut point increments (first cut point is fixed at -1). If any are negative then absolute values are taken as starting values for cutpoint increments.
- `link` The link function: only "identity" allowed at present (possibly for ever).
- `R` the number of categories.

**Details**

Such cumulative threshold models are only identifiable up to an intercept, or one of the cut points. Rather than remove the intercept, `ocat` simply sets the first cut point to -1. Use `predict.gam` with type="response" to get the predicted probabilities in each category.

**Value**

An object of class `extended.family`.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**Examples**

```
library(mgcv)
## Simulate some ordered categorical data...
set.seed(3);n<-400
dat <- gamSim(1,n=n)
dat$f <- dat$f - mean(dat$f)
```
alpha <- c(-Inf,-1,0,5,Inf)
R <- length(alpha)-1
y <- dat$f
u <- runif(n)
u <- dat$f + log(u/(1-u))
for (i in 1:R) {
y[u > alpha[i] & u <= alpha[i+1]] <- i
} 
dat$y <- y
## plot the data...
par(mfrow=c(2,2))
with(dat,plot(x0,y));with(dat,plot(x1,y))
with(dat,plot(x2,y));with(dat,plot(x3,y))
## fit ocat model to data...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ocat(R=R),data=dat)
b
plot(b,pages=1)
gam.check(b)
summary(b)
b$family$getTheta(TRUE) ## the estimated cut points
## predict probabilities of being in each category
predict(b,dat[1:2,],type="response",se=TRUE)

one.se.rule

The one standard error rule for smoother models

Description

The ‘one standard error rule’ (see e.g. Hastie, Tibshirani and Friedman, 2009) is a way of producing smoother models than those directly estimated by automatic smoothing parameter selection methods. In the single smoothing parameter case, we select the largest smoothing parameter within one standard error of the optimum of the smoothing parameter selection criterion. This approach can be generalized to multiple smoothing parameters estimated by REML or ML.

Details

Under REML or ML smoothing parameter selection an asymptotic distributional approximation is available for the log smoothing parameters. Let \( \rho \) denote the log smoothing parameters that we want to increase to obtain a smoother model. The large sample distribution of the estimator of \( \rho \) is \( \mathcal{N}(\rho, V) \) where \( V \) is the matrix returned by \texttt{sp.vcov}. Drop any elements of \( \rho \) that are already at ‘effective infinity’, along with the corresponding rows and columns of \( V \). The standard errors of the log smoothing parameters can be obtained from the leading diagonal of \( V \). Let the vector of these be \( d \). Now suppose that we want to increase the estimated log smoothing parameters by an amount \( \alpha d \). We choose \( \alpha \) so that \( \alpha d^T V^{-1} d = \sqrt{2p} \), where \( p \) is the dimension of \( d \) and \( 2p \) the variance of a chi-squared r.v. with \( p \) degrees of freedom.

The idea is that we increase the log smoothing parameters in proportion to their standard deviation, until the RE/ML is increased by 1 standard deviation according to its asymptotic distribution.

Author(s)

Simon N. Wood <simon.wood@r-project.org>
References


See Also

gam

Examples

require(mgcv)
set.seed(2) ## simulate some data...
dat <- gamSim(1,n=400,dist="normal",scale=2)
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML")
b
## only the first 3 smoothing parameters are candidates for
## increasing here...
V <- sp.vcov(b)[1:3,1:3] ## the approx cov matrix of sps
d <- diag(V)^.5
## sp se.
## compute the log smoothing parameter step...
d <- sqrt(2*length(d))/d
sp <- b$sp ## extract original sp estimates
sp[1:3] <- sp[1:3]*exp(d) ## apply the step
## refit with the increased smoothing parameters...
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML",sp=sp)
b;b1 ## compare fits

---

**pcls**

**Penalized Constrained Least Squares Fitting**

Description

Solves least squares problems with quadratic penalties subject to linear equality and inequality constraints using quadratic programming.

Usage

`pcls(M)`

Arguments

- **M**
  - is the single list argument to `pcls`. It should have the following elements:
    - **y** The response data vector.
    - **w** A vector of weights for the data (often proportional to the reciprocal of the variance).
    - **X** The design matrix for the problem, note that `ncol(M$X)` must give the number of model parameters, while `nrow(M$X)` should give the number of data.
    - **C** Matrix containing any linear equality constraints on the problem (e.g. `Cp = c`). If you have no equality constraints initialize this to a zero by zero matrix. Note that there is no need to supply the vector `c`, it is defined implicitly by the initial parameter estimates `p`. 
A list of penalty matrices. $S[[i]]$ is the smallest contiguous matrix including all the non-zero elements of the $i$th penalty matrix. The first parameter it penalizes is given by off[[1]]+1 (starting counting at 1).

**off** Offset values locating the elements of $S$ in the correct location within each penalty coefficient matrix. (Zero offset implies starting in first location)

**sp** An array of smoothing parameter estimates.

**p** An array of feasible initial parameter estimates - these must satisfy the constraints, but should avoid satisfying the inequality constraints as equality constraints.

**Ain** Matrix for the inequality constraints $A_{in} p > b_{in}$.

**bin** vector in the inequality constraints.

### Details

This solves the problem:

$$
\text{minimise } \|W^{1/2}(Xp - y)\|^2 + \sum_{i=1}^{m} \lambda_i p'S_ip
$$

subject to constraints $Cp = c$ and $A_{in} p > b_{in}$, w.r.t. $p$ given the smoothing parameters $\lambda_i$. $X$ is a design matrix, $p$ a parameter vector, $y$ a data vector, $W$ a diagonal weight matrix, $S_i$ a positive semi-definite matrix of coefficients defining the $i$th penalty and $C$ a matrix of coefficients defining the linear equality constraints on the problem. The smoothing parameters are the $\lambda_i$. Note that $X$ must be of full column rank, at least when projected into the null space of any equality constraints. $A_{in}$ is a matrix of coefficients defining the inequality constraints, while $b_{in}$ is a vector involved in defining the inequality constraints.

Quadratic programming is used to perform the solution. The method used is designed for maximum stability with least squares problems: i.e. $X'X$ is not formed explicitly. See Gill et al. 1981.

### Value

The function returns an array containing the estimated parameter vector.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References


https://www.maths.ed.ac.uk/~swood34/

### See Also

magic, mono.con
Examples

```r
require(mgcv)
# first an un-penalized example - fit E(y)=a+bx subject to a>0
set.seed(0)
n <- 100
x <- runif(n); y <- x - 0.2 + rnorm(n)*0.1
M <- list(X=matrix(0,n,2),p=c(0.1,0.5),off=array(0,0),S=list(),
          Ain=matrix(0,1,2),bin=0,C=matrix(0,0,0),sp=array(0,0),y=y,w=y*0+1)
M$X[,1] <- 1; M$X[,2] <- x; M$Ain[1,] <- c(1,0)
pcls(M) -> M$p
plot(x,y); abline(M$p,col=2); abline(coef(lm(y~x)),col=3)

# Penalized example: monotonic penalized regression spline ......

# Generate data from a monotonic truth.
x <- runif(100)*4-1; x <- sort(x);
f <- exp(4*x)/(1+exp(4*x)); y <- f+rnorm(100)*0.1; plot(x,y)

# Show regular spline fit (and save fitted object)
f.ug <- gam(y~s(x,k=10,bs="cr")); lines(x,fitted(f.ug))
# Create Design matrix, constraints etc. for monotonic spline....
sm <- smoothCon(s(x,k=10,bs="cr"),dat,knots=NULL)[[1]]
F <- mono.con(sm$xp); # get constraints
G <- list(X=sm$X,C=matrix(0,0,0),sp=f.ug$sp,p=sm$xp,y=y,w=y*0+1)
G$Ain <- F$A; G$bin <- F$b; G$S <- sm$S; G$off <- 0
p <- pcls(G); # fit spline (using s.p. from unconstrained fit)
fv<-Predict.matrix(sm,data.frame(x=x))%*%p
lines(x,fv,col=2)

# now a tprs example of the same thing....

f.ug <- gam(y~s(x,k=10)); lines(x,fitted(f.ug))
# Create Design matrix, constraints etc. for monotonic spline....
sm <- smoothCon(s(x,k=10,bs="tp"),dat,knots=NULL)[[1]]
xc <- 0:39/39 # points on [0,1]
cn <- length(xc) # number of constraints
xc <- xc+4-1 # points at which to impose constraints
A0 <- Predict.matrix(sm,data.frame(x=xc))
# ... A0%*%p evaluates spline at xc points
A1 <- Predict.matrix(sm,data.frame(x=xc+1e-6))
A <- (A1-A0)/1e-6
# ... approx. constraint matrix (A0%*%p is -ve
# spline gradient at points xc)
G <- list(X=sm$X,C=matrix(0,0,0),sp=f.ug$sp,y=y,w=y*0+1,S=sm$S,off=0)
G$Ain <- A; # constraint matrix
G$bin <- rep(0,cn); # constraint vector
G$p <- rep(0,10); G$p[10] <- 0.1
# ... monotonic start params, got by setting coefs of polynomial part
p <- pcls(G); # fit spline (using s.p. from unconstrained fit)
fv2<-Predict.matrix(sm,data.frame(x=x))%*%p
lines(x,fv2,col=3)
```

```
## monotonic additive model example...

### First simulate data...

```r
set.seed(10)
f1 <- function(x) 5*exp(4*x)/(1+exp(4*x));
f2 <- function(x) {
  ind <- x > .5
  f[ind] <- (x[ind] - .5)^2*10
  f
}
f3 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 +
  10 * (10 * x)^3 * (1 - x)^10
n <- 200
x <- runif(n); z <- runif(n); v <- runif(n)
mu <- f1(x) + f2(z) + f3(v)
y <- mu + rnorm(n)
```

### Preliminary unconstrained gam fit...

```r
G <- gam(y~s(x)+s(z)+s(v,k=20),fit=FALSE)
b <- gam(G)
```

### generate constraints, by finite differencing

```r
eps <- 1e-7
pd0 <- data.frame(x=seq(0,1,length=100),z=rep(.5,100),
v=rep(.5,100))
pd1 <- data.frame(x=seq(0,1,length=100)+eps,z=rep(.5,100),
v=rep(.5,100))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X1 <- predict(b,newdata=pd1,type="lpmatrix")
Xx <- (X1 - X0)/eps # Xx %>% coef(b) must be positive
pd0 <- data.frame(z=seq(0,1,length=100),x=rep(.5,100),
v=rep(.5,100))
pd1 <- data.frame(z=seq(0,1,length=100)+eps,x=rep(.5,100),
v=rep(.5,100))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X1 <- predict(b,newdata=pd1,type="lpmatrix")
Xz <- (X1-X0)/eps
G$Ain <- rbind(Xx,Xz) # inequality constraint matrix
G$bin <- rep(0,nrow(G$Ain))
G$C = matrix(0,0,ncol(G$X))
G$sp <- b$sp
G$p <- coef(b)
G$off <- G$off-1 # to match what pcls is expecting
```

### force initial parameters to meet constraint

```r
p <- pcls(G) # constrained fit
```

### note that standard errors in preceding plot are obtained from
### unconstrained fit

```r
par(mfrow=c(2,3))
plot(b) # original fit
b$coefficients <- p
plot(b) # constrained fit
```
pdIdnot

Overflow proof pdMat class for multiples of the identity matrix

Description

This set of functions is a modification of the pdMat class pdIdent from library nlme. The modification is to replace the log parameterization used in pdMat with a notLog2 parameterization, since the latter avoids indefiniteness in the likelihood and associated convergence problems: the parameters also relate to variances rather than standard deviations, for consistency with the pdTens class. The functions are particularly useful for working with Generalized Additive Mixed Models where variance parameters/smoothing parameters can be very large or very small, so that overflow or underflow can be a problem.

These functions would not normally be called directly, although unlike the pdTens class it is easy to do so.

Usage

pdIdnot(value = numeric(0), form = NULL, nam = NULL, data = sys.frame(sys.parent()))

Arguments

value Initialization values for parameters. Not normally used.
form A one sided formula specifying the random effects structure.
nam a names argument, not normally used with this class.
data data frame in which to evaluate formula.

Details

The following functions are provided: Dim.pdIdnot, coef.pdIdnot, corMatrix.pdIdnot, logDet.pdIdnot, pdConstruct.pdIdnot, pdFactor.pdIdnot, pdMatrix.pdIdnot, solve.pdIdnot, summary.pdIdnot. (e.g. mgcv:::coef.pdIdnot to access.)

Note that while the pdFactor and pdMatrix functions return the inverse of the scaled random effect covariance matrix or its factor, the pdConstruct function is initialised with estimates of the scaled covariance matrix itself.

Value

A class pdIdnot object, or related quantities. See the nlme documentation for further details.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

The nlme source code.
https://www.maths.ed.ac.uk/~swood34/
Functions implementing a pdMat class for tensor product smooths

Description

This set of functions implements an nlme library pdMat class to allow tensor product smooths to be estimated by lme as called by gamm. Tensor product smooths have a penalty matrix made up of a weighted sum of penalty matrices, where the weights are the smoothing parameters. In the mixed model formulation the penalty matrix is the inverse of the covariance matrix for the random effects of a term, and the smoothing parameters (times a half) are variance parameters to be estimated. It’s not possible to transform the problem to make the required random effects covariance matrix look like one of the standard pdMat classes: hence the need for the pdTens class. A notLog2 parameterization ensures that the parameters are positive.

These functions (pdTens, pdConstruct.pdTens, pdFactor.pdTens, pdMatrix.pdTens, coef.pdTens and summary.pdTens) would not normally be called directly.

Usage

pdTens(value = numeric(0), form = NULL, nam = NULL, data = sys.frame(sys.parent()))

Arguments

- value: Initialization values for parameters. Not normally used.
- form: A one sided formula specifying the random effects structure. The formula should have an attribute S which is a list of the penalty matrices the weighted sum of which gives the inverse of the covariance matrix for these random effects.
- nam: a names argument, not normally used with this class.
- data: data frame in which to evaluate formula.

Details

If using this class directly note that it is worthwhile scaling the S matrices to be of ‘moderate size’, for example by dividing each matrix by its largest singular value: this avoids problems with lme defaults (smooth.construct.tensor.smooth.spec does this automatically).

This appears to be the minimum set of functions required to implement a new pdMat class.

Note that while the pdFactor and pdMatrix functions return the inverse of the scaled random effect covariance matrix or its factor, the pdConstruct function is sometimes initialised with estimates of the scaled covariance matrix, and sometimes initialized with its inverse.
Value

A class pdTens object, or its coefficients or the matrix it represents or the factor of that matrix. pdFactor returns the factor as a vector (packed column-wise) (pdMatrix always returns a matrix).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

The nlme source code.
https://www.maths.ed.ac.uk/~swood34/

See Also

t2 gamm

Examples

# see gamm

description

Finds the coefficients penalized by each penalty and adds up their effective degrees of freedom. Very useful for t2 terms, but hard to interpret for terms where the penalties penalize overlapping sets of parameters (e.g. te terms).

Usage

pen.edf(x)

Arguments

x an object inheriting from gam

Details

Useful for models containing t2 terms, since it splits the EDF for the term up into parts due to different components of the smooth. This is useful for figuring out which interaction terms are actually needed in a model.

Value

A vector of EDFs, named with labels identifying which penalty each EDF relates to.
requires(mgcv)
set.seed(20)
dat <- gamSim(1, n=400, scale=2) # simulate data
# following 't2' smooth basically separates smooth
# of x0,x1 into main effects + interaction....

b <- gam(y~t2(x0,x1,bs="tp",m=1,k=7)+s(x2)+s(x3),
data=dat,method="ML")
pen.edf(b)

# label "rr" indicates interaction edf (range space times range space)
# label "nr" (null space for x0 times range space for x1) is main
# effect for x1.
# label "rn" is main effect for x0
# clearly interaction is negligible

# second example with higher order marginals.

b <- gam(y~t2(x0,x1,bs="tp",m=2,k=7,full=TRUE)
+s(x2)+s(x3),data=dat,method="ML")
pen.edf(b)

# In this case the EDF is negligible for all terms in the t2 smooth
# apart from the 'main effects' (r2 and 2r). To understand the labels
# consider the following 2 examples....
# "r1" relates to the interaction of the range space of the first
# marginal smooth and the first basis function of the null
# space of the second marginal smooth
# "2r" relates to the interaction of the second basis function of
# the null space of the first marginal smooth with the range
# space of the second marginal smooth.

place.knots(x,nk)

Automatically place a set of knots evenly through covariate values

Description

Given a univariate array of covariate values, places a set of knots for a regression spline evenly through the covariate values.

Usage

place.knots(x,nk)
Arguments

\texttt{x} \quad \text{array of covariate values (need not be sorted).}
\texttt{nk} \quad \text{integer indicating the required number of knots.}

Details

Places knots evenly throughout a set of covariates. For example, if you had 11 covariate values and wanted 6 knots then a knot would be placed at the first (sorted) covariate value and every second (sorted) value thereafter. With less convenient numbers of data and knots the knots are placed within intervals between data in order to achieve even coverage, where even means having approximately the same number of data between each pair of knots.

Value

An array of knot locations.

Author(s)

Simon N. Wood \textless{}simon.wood@r-project.org\textgreater{}

References

https://www.maths.ed.ac.uk/~swood34/

See Also

smooth.construct.cc.smooth.spec

Examples

require(mgcv)
\texttt{x \leftarrow runif(30)}
\texttt{place.knots(x,7)}
\texttt{rm(x)}

\begin{verbatim}
plot.gam
\end{verbatim}

\textit{Default GAM plotting}

Description

Takes a fitted \texttt{gam} object produced by \texttt{gam()} and plots the component smooth functions that make it up, on the scale of the linear predictor. Optionally produces term plots for parametric model components as well.

Usage

\begin{verbatim}
## S3 method for class 'gam'
plot(x,residuals=FALSE,rug=NULL,se=TRUE/pages=0,select=NULL,seWithMean=FALSE,unconditional=FALSE,by.resids=FALSE,
\end{verbatim}

\begin{verbatim}
scale=-1,n=100,n2=40,n3=3,theta=30,phi=30,jit=FALSE,xlab=NULL,
ylab=NULL,main=NULL,ylim=NULL,xlim=NULL,too.far=0.1,
all.terms=FALSE,shade=FALSE,shade.col="gray80",shift=0,
trans=I,scheme=0,...)
\end{verbatim}
Arguments

- **x**: a fitted `gam` object as produced by `gam()`.
- **residuals**: If `TRUE` then partial residuals are added to plots of 1-D smooths. If `FALSE` then no residuals are added. If this is an array of the correct length then it is used as the array of residuals to be used for producing partial residuals. If `TRUE` then the residuals are the working residuals from the IRLS iteration weighted by the (square root) IRLS weights, in order that they have constant variance if the model is correct. Partial residuals for a smooth term are the residuals that would be obtained by dropping the term concerned from the model, while leaving all other estimates fixed (i.e. the estimates for the term plus the residuals).
- **rug**: When `TRUE` the covariate to which the plot applies is displayed as a rug plot at the foot of each plot of a 1-d smooth, and the locations of the covariates are plotted as points on the contour plot representing a 2-d smooth. The default of `NULL` sets `rug` to `TRUE` when the dataset size is <= 10000 and `FALSE` otherwise.
- **se**: when `TRUE` (default) upper and lower lines are added to the 1-d plots at 2 standard errors above and below the estimate of the smooth being plotted while for 2-d plots, surfaces at +1 and -1 standard errors are contoured and overlayed on the contour plot for the estimate. If a positive number is supplied then this number is multiplied by the standard errors when calculating standard error curves or surfaces. See also shade, below.
- **pages**: (default 0) the number of pages over which to spread the output. For example, if `pages=1` then all terms will be plotted on one page with the layout performed automatically. Set to 0 to have the routine leave all graphics settings as they are.
- **select**: Allows the plot for a single model term to be selected for printing. e.g. if you just want the plot for the second smooth term set `select=2`.
- **scale**: set to -1 (default) to have the same y-axis scale for each plot, and to 0 for a different y axis for each plot. Ignored if `ylim` supplied.
- **n**: number of points used for each 1-d plot - for a nice smooth plot this needs to be several times the estimated degrees of freedom for the smooth. Default value 100.
- **n2**: Square root of number of points used to grid estimates of 2-d functions for contouring.
- **n3**: Square root of number of panels to use when displaying 3 or 4 dimensional functions.
- **theta**: One of the perspective plot angles.
- **phi**: The other perspective plot angle.
- **jit**: Set to `TRUE` if you want rug plots for 1-d terms to be jittered.
- **xlab**: If supplied then this will be used as the x label for all plots.
- **ylab**: If supplied then this will be used as the y label for all plots.
- **main**: Used as title (or z axis label) for plots if supplied.
- **ylim**: If supplied then this pair of numbers are used as the y limits for each plot.
- **xlim**: If supplied then this pair of numbers are used as the x limits for each plot.
- **too.far**: If greater than 0 then this is used to determine when a location is too far from data to be plotted when plotting 2-D smooths. This is useful since smooths tend to go wild away from data. The data are scaled into the unit square before deciding what to exclude, and `too.far` is a distance within the unit square. Setting to zero can make plotting faster for large datasets, but care then needed with interpretation of plots.
all.terms  
if set to TRUE then the partial effects of parametric model components are also plotted, via a call to `termplot`. Only terms of order 1 can be plotted in this way. Also see warnings.

shade  
Set to TRUE to produce shaded regions as confidence bands for smooths (not available for parametric terms, which are plotted using `termplot`).

shade.col  
define the color used for shading confidence bands.

shift  
constant to add to each smooth (on the scale of the linear predictor) before plotting. Can be useful for some diagnostics, or with `trans`.

trans  
monotonic function to apply to each smooth (after any shift), before plotting. Monotonicity is not checked, but default plot limits assume it. `shift` and `trans` are occasionally useful as a means for getting plots on the response scale, when the model consists only of a single smooth.

seWithMean  
if TRUE the component smooths are shown with confidence intervals that include the uncertainty about the overall mean. If FALSE then the uncertainty relates purely to the centred smooth itself. If `seWithMean=2` then the intervals include the uncertainty in the mean of the fixed effects (but not in the mean of any uncentred smooths or random effects). Marra and Wood (2012) suggests that TRUE results in better coverage performance, and this is also suggested by simulation.

unconditional  
if TRUE then the smoothing parameter uncertainty corrected covariance matrix is used to compute uncertainty bands, if available. Otherwise the bands treat the smoothing parameters as fixed.

by.resids  
Should partial residuals be plotted for terms with by variables? Usually the answer is no, they would be meaningless.

scheme  
Integer or integer vector selecting a plotting scheme for each plot. See details.

...  
other graphics parameters to pass on to plotting commands. See details for smooth plot specific options.

Details

Produces default plot showing the smooth components of a fitted GAM, and optionally parametric terms as well, when these can be handled by `termplot`.

For smooth terms `plot.gam` actually calls plot method functions depending on the class of the smooth. Currently `random.effects`, Markov random fields (`mrf`), `Spherical.Spline` and `factor.smooth.interaction` terms have special methods (documented in their help files), the rest use the defaults described below.

For plots of 1-d smooths, the x axis of each plot is labelled with the covariate name, while the y axis is labelled `s(cov, edf)` where `cov` is the covariate name, and `edf` the estimated (or user defined for regression splines) degrees of freedom of the smooth. `scheme == 0` produces a smooth curve with dashed curves indicating 2 standard error bounds. `scheme == 1` illustrates the error bounds using a shaded region.

For `scheme==0`, contour plots are produced for 2-d smooths with the x-axes labelled with the first covariate name and the y axis with the second covariate name. The main title of the plot is something like `s(var1, var2, edf)`, indicating the variables of which the term is a function, and the estimated degrees of freedom for the term. When `se=TRUE`, estimator variability is shown by overlaying contour plots at plus and minus 1 s.e. relative to the main estimate. If `se` is a positive number then contour plots are at plus or minus `se preyed s.e multiplied by the s.e. Contour levels are chosen to try and ensure reasonable separation of the contours of the different plots, but this is not always easy to achieve. Note that these plots can not be modified to the same extent as the other plot.
For 2-d smooths scheme==1 produces a perspective plot, while scheme==2 produces a heatmap, with overlaid contours and scheme==3 a greyscale heatmap (contour.col controls the contour colour).

Smooths of 3 and 4 variables are displayed as tiled heatmaps with overlaid contours. In the 3 variable case the third variable is discretized and a contour plot of the first 2 variables is produced for each discrete value. The panels in the lower and upper rows are labelled with the corresponding third variable value. The lowest value is bottom left, and highest at top right. For 4 variables, two of the variables are coarsely discretized and a square array of image plots is produced for each combination of the discrete values. The first two arguments of the smooth are the ones used for the image/contour plots, unless a tensor product term has 2D marginals, in which case the first 2D marginal is image/contour plotted. n3 controls the number of panels. See also vis.gam.

Fine control of plots for parametric terms can be obtained by calling termplot directly, taking care to use its terms argument.

Note that, if seWithMean=TRUE, the confidence bands include the uncertainty about the overall mean. In other words although each smooth is shown centred, the confidence bands are obtained as if every other term in the model was constrained to have average 0, (average taken over the covariate values), except for the smooth concerned. This seems to correspond more closely to how most users interpret componentwise intervals in practice, and also results in intervals with close to nominal (frequentist) coverage probabilities by an extension of Nychka’s (1988) results presented in Marra and Wood (2012). There are two possible variants of this approach. In the default variant the extra uncertainty is in the mean of all other terms in the model (fixed and random, including uncentred smooths). Alternatively, if seWithMean=2 then only the uncertainty in parametric fixed effects is included in the extra uncertainty (this latter option actually tends to lead to wider intervals when the model contains random effects).

Several smooth plots methods using image will accept an hcolors argument, which can be anything documented in heat.colors (in which case something like hcolors=rainbow(50) is appropriate), or the grey function (in which case something like hcolors=grey(0:50/50) is needed). Another option is contour.col which will set the contour colour for some plots. These options are useful for producing grey scale pictures instead of colour.

Sometimes you may want a small change to a default plot, and the arguments to plot.gam just won’t let you do it. In this case, the quickest option is sometimes to clone the smooth.construct and Predict.matrix methods for the smooth concerned, modifying only the returned smoother class (e.g. to foo.smooth). Then copy the plot method function for the original class (e.g. mgcv:::plot.mgcv.smooth), modify the source code to plot exactly as you want and rename the plot method function (e.g. plot.foo.smooth). You can then use the cloned smooth in models (e.g. s(x,bs="foo")), and it will automatically plot using the modified plotting function.

Value

The functions main purpose is its side effect of generating plots. It also silently returns a list of the data used to produce the plots, which can be used to generate customized plots.

WARNING

Note that the behaviour of this function is not identical to plot.gam() in S-PLUS.

Plotting can be slow for models fitted to large datasets. Set rug=FALSE to improve matters. If it’s still too slow set too.far=0, but then take care not to overinterpret smooths away from supporting data.

Plots of 2-D smooths with standard error contours shown can not easily be customized.
all.terms uses termplot which looks for the original data in the environment of the fitted model object formula. Since gam resets this environment to avoid large saved model objects containing data in hidden environments, this can fail.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Henric Nilsson <henric.nilsson@statisticon.se> donated the code for the shade option.

The design is inspired by the S function of the same name described in Chambers and Hastie (1993) (but is not a clone).

References


See Also

gam, predict.gam, vis.gam

Examples

library(mgcv)
set.seed(0)
## fake some data...
f1 <- function(x) {exp(2 * x)}
f2 <- function(x) {
  0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
}
f3 <- function(x) {x*0}
n<-200
sig2<-4
x0 <- rep(1:4,50)
x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1)
x3 <- runif(n, 0, 1)
e <- rnorm(n, 0, sqrt(sig2))
y <- 2*x0 + f1(x1) + f2(x2) + f3(x3) + e
x0 <- factor(x0)

## fit and plot...
b<-gam(y~x0+s(x1)+s(x2)+s(x3))
plot(b,pages=1,residuals=TRUE,all.terms=TRUE,shade=TRUE,shade.col=2)
plot(b,pages=1,seWithMean=TRUE) ## better coverage intervals

## just parametric term alone...
termplot(b,terms="x0",se=TRUE)
## more use of color...
op <- par(mfrow=c(2,2),bg="blue")
x <- 0:1000/1000
for (i in 1:3)
  plot(b,select=i,rug=FALSE,col="green",
   col.axis="white",col.lab="white",all.terms=TRUE)
  for (j in 1:2) axis(j,col="white",labels=FALSE)
  box(col="white")
  eval(parse(text=paste("fx <- f",i,"(x)",sep="")))
  fx <- fx-mean(fx)
  lines(x,fx,col=2) ## overlay `truth` in red
}
par(op)

## example with 2-d plots, and use of schemes...
b1 <- gam(y~x0+s(x1,x2)+s(x3))
op <- par(mfrow=c(2,2))
plot(b1,all.terms=TRUE)
par(op)

## 3 and 4 D smooths can also be plotted
dat <- gamSim(1,n=400)
b1 <- gam(y~te(x0,x1,x2,d=c(1,2),k=c(5,15))+s(x3),data=dat)

## Now plot. Use cex.lab and cex.axis to control axis label size,
## n3 to control number of panels, n2 to control panel grid size,
## scheme=1 to get greyscale...
plot(b1,pages=1)

---

polys.plot

Plot geographic regions defined as polygons

Description

Produces plots of geographic regions defined by polygons, optionally filling the polygons with a color or grey shade dependent on a covariate.

Usage

polys.plot(pc,z=NULL,scheme="heat",lab="",...)

Arguments

pc
A named list of matrices. Each matrix has two columns. The matrix rows each define the vertex of a boundary polygon. If a boundary is defined by several polygons, then each of these must be separated by an NA row in the matrix. See mrf for an example.
predict.bam

z A vector of values associated with each area (item) of pc. If the vector elements have names then these are used to match elements of z to areas defined in pc. Otherwise pc and z are assumed to be in the same order. If z is NULL then polygons are not filled.
scheme One of "heat" or "grey", indicating how to fill the polygons in accordance with the value of z.
lab label for plot.
... other arguments to pass to plot (currently only if z is NULL).

Details
Any polygon within another polygon counts as a hole in the area. Further nesting is dealt with by treating any point that is interior to an odd number of polygons as being within the area, and all other points as being exterior. The routine is provided to facilitate plotting with models containing mrf smooths.

Value
Simply produces a plot.

Author(s)
Simon Wood <simon.wood@r-project.org>

See Also
mrf and columb.polys.

Examples
## see also ?mrf for use of z
require(mgcv)
data(columb.polys)
polys.plot(columb.polys)

predict.bam Prediction from fitted Big Additive Model model

Description
In most cases essentially a wrapper for predict.gam for prediction from a model fitted by bam. Can compute on a parallel cluster. For models fitted using discrete methods with discrete=TRUE then discrete prediction methods are used instead.

Takes a fitted bam object produced by bam and produces predictions given a new set of values for the model covariates or the original values used for the model fit. Predictions can be accompanied by standard errors, based on the posterior distribution of the model coefficients. The routine can optionally return the matrix by which the model coefficients must be pre-multiplied in order to yield the values of the linear predictor at the supplied covariate values: this is useful for obtaining credible regions for quantities derived from the model (e.g. derivatives of smooths), and for lookup table prediction outside R.
predict.bam

Usage

## S3 method for class 'bam'
predict(object, newdata, type = "link", se.fit = FALSE, terms = NULL,
        exclude = NULL, block.size = 50000, newdata.guaranteed = FALSE,
        na.action = na.pass, cluster = NULL, discrete = TRUE, n.threads = 1,
        gc.level = 0, ...)  

Arguments

object  
a fitted bam object as produced by bam.

newdata  
A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If newdata is provided then it should contain all the variables needed for prediction: a warning is generated if not.

type  
When this has the value "link" (default) the linear predictor (possibly with associated standard errors) is returned. When type="terms" each component of the linear predictor is returned separately (possibly with standard errors): this includes parametric model components, followed by each smooth component, but excludes any offset and any intercept. type="iterms" is the same, except that any standard errors returned for smooth components will include the uncertainty about the intercept/overall mean. When type="response" predictions on the scale of the response are returned (possibly with approximate standard errors). When type="lpmatrix" then a matrix is returned which yields the values of the linear predictor (minus any offset) when postmultiplied by the parameter vector (in this case se.fit is ignored). The latter option is most useful for getting variance estimates for quantities derived from the model: for example integrated quantities, or derivatives of smooths. A linear predictor matrix can also be used to implement approximate prediction outside R (see example code, below).

se.fit  
when this is TRUE (not default) standard error estimates are returned for each prediction.

terms  
if type="terms" or type="iterms" then only results for the terms (smooth or parametric) named in this array will be returned. Otherwise any terms not named in this array will be set to zero. If NULL then all terms are included. "(Intercept)" is the intercept term.

exclude  
if type="terms" or type="iterms" then terms (smooth or parametric) named in this array will not be returned. Otherwise any terms named in this array will be set to zero. If NULL then no terms are excluded. To avoid supplying covariate values for excluded smooth terms, set newdata.guaranteed=TRUE, but note that this skips all checks of newdata.

block.size  
maximum number of predictions to process per call to underlying code: larger is quicker, but more memory intensive.

newdata.guaranteed  
Set to TRUE to turn off all checking of newdata except for sanity of factor levels: this can speed things up for large prediction tasks, but newdata must be complete, with no NA values for predictors required in the model.

na.action  
what to do about NA values in newdata. With the default na.pass, any row of newdata containing NA values for required predictors, gives rise to NA predictions (even if the term concerned has no NA predictors). na.exclude or na.omit result in the dropping of newdata rows, if they contain any NA values for required predictors. If newdata is missing then NA handling is determined from object$na.action.
predict.bam

cluster predict.bam can compute in parallel using `parLapply` from the `parallel` package, if it is supplied with a cluster on which to do this (a cluster here can be some cores of a single machine). See details and example code for `bam`.

discrete if TRUE then discrete prediction methods used with model fitted by discrete methods. FALSE for regular prediction. See details.

n.threads if se.fit=TRUE and discrete prediction is used then parallel computation can be used to speed up se calculation. This specifies number of threads to use.

gc.level increase from 0 to up the level of garbage collection if default does not give enough.

... other arguments.

Details

The standard errors produced by `predict.gam` are based on the Bayesian posterior covariance matrix of the parameters Vp in the fitted `bam` object.

To facilitate plotting with `termplot`, if object possesses an attribute "para.only" and type="terms" then only parametric terms of order 1 are returned (i.e. those that `termplot` can handle).

Note that, in common with other prediction functions, any offset supplied to `bam` as an argument is always ignored when predicting, unlike offsets specified in the `bam` model formula.

See the examples in `predict.gam` for how to use the `lpmatrix` for obtaining credible regions for quantities derived from the model.

When discrete=TRUE the prediction data in `newdata` is discretized in the same way as is done when using discrete fitting methods with `bam`. However the discretization grids are not currently identical to those used during fitting. Instead, discretization is done afresh for the prediction data. This means that if you are predicting for a relatively small set of prediction data, or on a regular grid, then the results may in fact be identical to those obtained without discretization. The disadvantage to this approach is that if you make predictions with a large data frame, and then split it into smaller data frames to make the predictions again, the results may differ slightly, because of slightly different discretization errors.

Value

If type="lpmatrix" then a matrix is returned which will give a vector of linear predictor values (minus any offset) at the supplied covariate values, when applied to the model coefficient vector. Otherwise, if se.fit is TRUE then a 2 item list is returned with items (both arrays) fit and se.fit containing predictions and associated standard error estimates, otherwise an array of predictions is returned. The dimensions of the returned arrays depends on whether type is "terms" or not: if it is then the array is 2 dimensional with each term in the linear predictor separate, otherwise the array is 1 dimensional and contains the linear predictor/predicted values (or corresponding s.e.s). The linear predictor returned termwise will not include the offset or the intercept.

`newdata` can be a data frame, list or model.frame: if it’s a model frame then all variables must be supplied.

WARNING

Predictions are likely to be incorrect if data dependent transformations of the covariates are used within calls to smooths. See examples in `predict.gam`. 
Author(s)

Simon N. Wood <simon.wood@r-project.org>

The design is inspired by the S function of the same name described in Chambers and Hastie (1993) (but is not a clone).

References


See Also

bam, predict.gam

Examples

## for parallel computing see examples for ?bam
## for general useage follow examples in ?predict.gam

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predict.gam

Prediction from fitted GAM model

Description

Takes a fitted gam object produced by gam() and produces predictions given a new set of values for the model covariates or the original values used for the model fit. Predictions can be accompanied by standard errors, based on the posterior distribution of the model coefficients. The routine can optionally return the matrix by which the model coefficients must be pre-multiplied in order to yield the values of the linear predictor at the supplied covariate values: this is useful for obtaining credible regions for quantities derived from the model (e.g. derivatives of smooths), and for lookup table prediction outside R (see example code below).

Usage

## S3 method for class 'gam'
predict(object, newdata, type=",link", se.fit=FALSE, terms=NULL,
exclude=NULL, block.size=NULL, newdata.guaranteed=FALSE,
na.action=na.pass, unconditional=FALSE, iters.type=NULL,...)

Documentation extracted from the R Project at http://www.R-project.org
Arguments

- **object**: a fitted gam object as produced by `gam()`.
- **newdata**: A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If `newdata` is provided then it should contain all the variables needed for prediction: a warning is generated if not. See details for use with `link(linear.functional.terms)`.
- **type**: When this has the value "link" (default) the linear predictor (possibly with associated standard errors) is returned. When `type="terms"` each component of the linear predictor is returned separately (possibly with standard errors): this includes parametric model components, followed by each smooth component, but excludes any offset and any intercept. `type="iterms"` is the same, except that any standard errors returned for smooth components will include the uncertainty about the intercept/overall mean. When `type="response"` predictions on the scale of the response are returned (possibly with approximate standard errors). When `type="lpmatrix"` then a matrix is returned which yields the values of the linear predictor (minus any offset) when post-multiplied by the parameter vector (in this case `se.fit` is ignored). The latter option is most useful for getting variance estimates for quantities derived from the model: for example integrated quantities, or derivatives of smooths. A linear predictor matrix can also be used to implement approximate prediction outside R (see example code below).
- **se.fit**: when this is TRUE (not default) standard error estimates are returned for each prediction.
- **terms**: if `type="terms"` or `type="iterms"` then only results for the terms (smooth or parametric) named in this array will be returned. Otherwise any terms not named in this array will be set to zero. If NULL then all terms are included.
- **exclude**: if `type="terms"` or `type="iterms"` then terms (smooth or parametric) named in this array will not be returned. Otherwise any terms named in this array will be set to zero. If NULL then no terms are excluded. Note that this is the term names as it appears in the model summary, see example. You can avoid providing the covariates for excluded smooth terms by setting `newdata.guaranteed=TRUE`, which will avoid all checks on newdata (covariates for parametric terms can not be skipped).
- **block.size**: maximum number of predictions to process per call to underlying code: larger is quicker, but more memory intensive. Set to < 1 to use total number of predictions as this. If NULL then block size is 1000 if new data supplied, and the number of rows in the model frame otherwise.
- **newdata.guaranteed**: Set to TRUE to turn off all checking of `newdata` except for sanity of factor levels: this can speed things up for large prediction tasks, but `newdata` must be complete, with no NA values for predictors required in the model.
- **na.action**: what to do about NA values in newdata. With the default `na.pass`, any row of newdata containing NA values for required predictors, gives rise to NA predictions (even if the term concerned has no NA predictors). `na.exclude` or `na.omit` result in the dropping of newdata rows, if they contain any NA values for required predictors. If `newdata` is missing then NA handling is determined from `object$na.action`.
- **unconditional**: if TRUE then the smoothing parameter uncertainty corrected covariance matrix is used, when available, otherwise the covariance matrix conditional on the estimated smoothing parameters is used.
predict.gam

iterms.type

if type="iterms" then standard errors can either include the uncertainty in the overall mean (default, with fixed and random effects included) or the uncertainty in the mean of the non-smooth fixed effects only (iterms.type=2).

... other arguments.

Details

The standard errors produced by predict.gam are based on the Bayesian posterior covariance matrix of the parameters \( \theta \) in the fitted gam object.

When predicting from models with `linear.functional.terms` then there are two possibilities. If the summation convention is to be used in prediction, as it was in fitting, then `newdata` should be a list, with named matrix arguments corresponding to any variables that were matrices in fitting. Alternatively one might choose to simply evaluate the constituent smooths at particular values in which case arguments that were matrices can be replaced by vectors (and `newdata` can be a dataframe). See `linear.functional.terms` for example code.

To facilitate plotting with `termplot`, if object possesses an attribute "para.only" and type="terms" then only parametric terms of order 1 are returned (i.e. those that `termplot` can handle).

Note that, in common with other prediction functions, any offset supplied to `gam` as an argument is always ignored when predicting, unlike offsets specified in the `gam` model formula.

See the examples for how to use the `lpmatrix` for obtaining credible regions for quantities derived from the model.

Value

If type="lpmatrix" then a matrix is returned which will give a vector of linear predictor values (minus any offset) at the supplied covariate values, when applied to the model coefficient vector. Otherwise, if `se.fit` is TRUE then a 2 item list is returned with items (both arrays) `fit` and `se.fit` containing predictions and associated standard error estimates, otherwise an array of predictions is returned. The dimensions of the returned arrays depends on whether type is "terms" or not: if it is then the array is 2 dimensional with each term in the linear predictor separate, otherwise the array is 1 dimensional and contains the linear predictor/predicted values (or corresponding s.e.s). The linear predictor returned termwise will not include the offset or the intercept.

`newdata` can be a data frame, list or model.frame: if it’s a model frame then all variables must be supplied.

WARNING

Predictions are likely to be incorrect if data dependent transformations of the covariates are used within calls to smooths. See examples.

Note that the behaviour of this function is not identical to `predict.gam()` in Splus. type="terms" does not exactly match what `predict.lm` does for parametric model components.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

The design is inspired by the S function of the same name described in Chambers and Hastie (1993) (but is not a clone).
References


See Also

gam, gamm, plot.gam

Examples

library(mgcv)

n <- 200
sig <- 2
data <- gamSim(1,n=n,scale=sig)

b <- gam(y~s(x0)+s(I(x1^2))+s(x2)+offset(x3),data=data)

newd <- data.frame(x0=(0:30)/30,x1=(0:30)/30,x2=(0:30)/30,x3=(0:30)/30)
pred <- predict.gam(b,newd)
pred0 <- predict(b,newd,exclude="s(x0)") # prediction excluding a term 
#...and the same, but without needing to provide x0 prediction data...
newd1 <- newd;newd1$x0 <- NULL # remove x0 from `newd1'
pred1 <- predict(b,newd1,exclude="s(x0)",newdata.guaranteed=TRUE)

# custom perspective plot...

m1 <- 20;m2 <- 30; n <- m1*m2
x1 <- seq(.2,.8,length=m1);x2 <- seq(.2,.8,length=m2) # marginal grid points
df <- data.frame(x0=rep(.5,n),x1=rep(x1,m2),x2=rep(x2,each=m1),x3=rep(0,n))
pf <- predict(b,newdata=df,type="terms")
persp(x1,x2,matrix(pf[,2]+pf[,3],m1,m2),theta=-130,col="blue",zlab="")

# difference between "terms" and "iterms"
#nd2 <- data.frame(x0=rep(.25,5),x1=rep(.25,5),x2=rep(.25,5),x3=rep(.25,5))
predict(b,nd2,type="terms",se=TRUE)
predict(b,nd2,type="iterms",se=TRUE)

# now get variance of sum of predictions using lpmatrix
# Xp <- predict(b,newd,type="lpmatrix")

# Xp %*% coef(b) yields vector of predictions

a <- rep(1,31)
Xs <- t(a) %*% Xp # Xs %*% coef(b) gives summary of predictions
var.sum <- Xs %*% b$Vp %*% t(Xs)
Now get the variance of non-linear function of predictions by simulation from posterior distribution of the params

```r
rmvn <- function(n, mu, sig) {  ## MVN random deviates
    L <- mroot(sig); m <- ncol(L);
    t(mu + L%*%matrix(rnorm(m*n), m, n))
}

br <- rmvn(1000, coef(b), b$Vp)  ## 1000 replicate param. vectors
res <- rep(0, 1000)
for (i in 1:1000) {
    pr <- Xp %*% br[i,]  ## replicate predictions
    res[i] <- sum(log(abs(pr)))  ## example non-linear function
}
mean(res); var(res)

## loop is replace-able by following ....
res <- colSums(log(abs(Xp %*% t(br))))
```

The following shows how to use use an "lpmatrix" as a lookup table for approximate prediction. The idea is to create approximate prediction matrix rows by appropriate linear interpolation of an existing prediction matrix. The additivity of a GAM makes this possible.

There is no reason to ever do this in R, but the following code provides a useful template for predicting from a fitted gam *outside* R: all that is needed is the coefficient vector and the prediction matrix. Use larger `Xp`/ smaller `dx` and/or higher order interpolation for higher accuracy.

```r
xn <- c(.341, .122, .476, .981)  ## want prediction at these values
x0 <- 1  ## intercept column
dx <- 1/30  ## covariate spacing in `newd`
for (j in 0:2) {  ## loop through smooth terms
    cols <- 1+j*9 + 1:9  ## relevant cols of Xp
    i <- floor(xn[j+1]*30)  ## find relevant rows of Xp
    w1 <- (xn[j+1]-i*dx)/dx  ## interpolation weights
    ## find approx. predict matrix row portion, by interpolation
    x0 <- c(x0, Xp[i+2, cols]*w1 + Xp[i+1, cols]*(1-w1))
}
dim(x0)<-c(1,28)
fv <- x0%*%coef(b) + xn[4]; fv  ## evaluate and add offset
se <- sqrt(x0%*%b$Vp%*%t(x0)); se  ## get standard error
## compare to normal prediction
predict(b, newdata=data.frame(x0=xn[1], x1=xn[2],
                              x2=xn[3], x3=xn[4]), se=TRUE)
```

# illustration of unsafe scale dependent transforms in smooths....
Predict.matrix

Predict methods for smooth terms in a GAM

Description

Takes smooth objects produced by smooth.construct methods and obtains the matrix mapping the parameters associated with such a smooth to the predicted values of the smooth at a set of new
In practice this method is often called via the wrapper function `PredictMat`.

**Usage**

```
Predict.matrix(object, data)
Predict.matrix2(object, data)
```

**Arguments**

- `object` is a smooth object produced by a `smooth.construct` method function. The object contains all the information required to specify the basis for a term of its class, and this information is used by the appropriate `Predict.matrix` function to produce a prediction matrix for new covariate values. Further details are given in `smooth.construct`.

- `data` A data frame containing the values of the (named) covariates at which the smooth term is to be evaluated. Exact requirements are as for `smooth.construct` and `smooth.construct2`.

**Details**

Smooth terms in a GAM formula are turned into smooth specification objects of class `xx.smooth.spec` during processing of the formula. Each of these objects is converted to a smooth object using an appropriate `smooth.construct` function. The `Predict.matrix` functions are used to obtain the matrix that will map the parameters associated with a smooth term to the predicted values for the term at new covariate values.

Note that new smooth classes can be added by writing a new `smooth.construct` method function and a corresponding `Predict.matrix` method function: see the example code provided for `smooth.construct` for details.

**Value**

A matrix which will map the parameters associated with the smooth to the vector of values of the smooth evaluated at the covariate values given in `object`. If the smooth class is one which generates offsets the corresponding offset is returned as attribute "offset" of the matrix.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**See Also**

`gam, gamm, smooth.construct, PredictMat`

**Examples**

```
# See smooth.construct examples
```
Predict.matrix.cr.smooth

*Predict matrix method functions*

**Description**

The various built in smooth classes for use with `gam` have associate `Predict.matrix` method functions to enable prediction from the fitted model.

**Usage**

```r
## S3 method for class 'cr.smooth'
Predict.matrix(object, data)
## S3 method for class 'cs.smooth'
Predict.matrix(object, data)
## S3 method for class 'cyclic.smooth'
Predict.matrix(object, data)
## S3 method for class 'pspline.smooth'
Predict.matrix(object, data)
## S3 method for class 'tensor.smooth'
Predict.matrix(object, data)
## S3 method for class 'tprs.smooth'
Predict.matrix(object, data)
## S3 method for class 'ts.smooth'
Predict.matrix(object, data)
## S3 method for class 't2.smooth'
Predict.matrix(object, data)
```

**Arguments**

- `object`: a smooth object, usually generated by a `smooth.construct` method having processed a smooth specification object generated by an `s` or `te` term in a `gam` formula.
- `data`: A data frame containing the values of the (named) covariates at which the smooth term is to be evaluated. Exact requirements are as for `smooth.construct` and `smooth.construct2`.

**Details**

The `Predict.matrix` function is not normally called directly, but is rather used internally by `predict.gam` etc. to predict from a fitted `gam` model. See `Predict.matrix` for more details, or the specific smooth.construct pages for details on a particular smooth class.

**Value**

A matrix mapping the coefficients for the smooth term to its values at the supplied data values.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>
Predict.matrix.soap.film

References


Examples

## see smooth.construct

Predict.matrix.soap.film

### Prediction matrix for soap film smooth

Description

Creates a prediction matrix for a soap film smooth object, mapping the coefficients of the smooth to the linear predictor component for the smooth. This is the `Predict.matrix` method function required by `gam`.

Usage

```r
## S3 method for class 'soap.film'
Predict.matrix(object, data)
## S3 method for class 'sw'
Predict.matrix(object, data)
## S3 method for class 'sf'
Predict.matrix(object, data)
```

Arguments

- `object`: A class "soap.film", "sf" or "sw" object.
- `data`: A list list or data frame containing the arguments of the smooth at which predictions are required.

Details

The smooth object will be largely what is returned from `smooth.construct.so.smooth.spec`, although elements X and S are not needed, and need not be present, of course.

Value

A matrix. This may have an "offset" attribute corresponding to the contribution from any known boundary conditions on the smooth.

Author(s)

Simon N. Wood <s.wood@bath.ac.uk>

References

[https://www.maths.ed.ac.uk/~swood34/](https://www.maths.ed.ac.uk/~swood34/)
Predict.matrix.soap.film

See Also

smooth.construct.so.smooth.spec

Examples

## This is a lower level example. The basis and
## penalties are obtained explicitly
## and ‘magic’ is used as the fitting routine...

require(mgcv)
set.seed(66)

## create a boundary...
sb <- list(fs.boundary())

## create some internal knots...
knots <- data.frame(x=rep(seq(-.5,3,by=.5),4),
y=rep(c(-.6,-.3,.3,.6),rep(8,4)))

## Simulate some fitting data, inside boundary...
n<-1000
x <- runif(n)*5-1;y<-runif(n)*2-1
z <- fs.test(x,y,b=1)
ind <- inSide(fsb,x,y) ## remove outsiders
z <- z[ind];x <- x[ind]; y <- y[ind]
n <- length(z)
z <- z + rnorm(n)*.3 ## add noise

## plot boundary with knot and data locations
plot(fsb[[1]]$x,fsb[[1]]$y,type="l");points(knots$x,knots$y,pch=20,col=2)
points(x,y,pch=".",col=3);

## set up the basis and penalties...
sob <- smooth.construct2(s(x,y,bs="so",k=40,xt=list(bnd=fsb,nmax=100)),
data=data.frame(x=x,y=y),knots=knots)

## ... model matrix is element ‘X’ of sob, penalties matrices
## are in list element ‘S’.

## fit using ‘magic’
um <- magic(z,sob$X,sp=c(-1,-1),sob$S,off=c(1,1))
beta <- um$b

## produce plots...
par(mfrow=c(2,2),mar=c(4,4,1,1))
m<-100;n<-50
xm <- seq(-1,3.5,length=m);yn<-seq(-1,1,length=n)
xx <- rep(xm,n);yy<-rep(yn,rep(m,n))

## plot truth...
tru <- matrix(fs.test(xx,yy),m,n) ## truth
image(xm,yn,tru,col=heat.colors(100),xlab="x",ylab="y")
lines(fsb[[1]]$x,fsb[[1]]$y,lwd=3)
contour(xm,yn,tru,levels=seq(-5,5,by=.25),add=TRUE)

## Plot soap, by first predicting on a fine grid...
## First get prediction matrix...
X <- Predict.matrix2(sob, data=list(x=xx, y=yy))

## Now the predictions...
fv <- X%*%beta

## Plot the estimated function...
image(xm, yn, matrix(fv, m, n), col=heat.colors(100), xlab="x", ylab="y")
lines(fsb[[1]]$x, fsb[[1]]$y, lwd=3)
points(x, y, pch=".")
contour(xm, yn, matrix(fv, m, n), levels=seq(-5, 5, by=.25), add=TRUE)

## Plot TPRS...
b <- gam(z~s(x, y, k=100))
fv.gam <- predict(b, newdata=data.frame(x=xx, y=yy))
names(sob$sd$bnd[[1]]) <- c("xx", "yy", "d")
ind <- inSide(sob$sd$bnd, xx, yy)
fv.gam[!ind] <- NA
image(xm, yn, matrix(fv.gam, m, n), col=heat.colors(100), xlab="x", ylab="y")
lines(fsb[[1]]$x, fsb[[1]]$y, lwd=3)
points(x, y, pch=".")
contour(xm, yn, matrix(fv.gam, m, n), levels=seq(-5, 5, by=.25), add=TRUE)

---

**print.gam**

*Print a Generalized Additive Model object.*

### Description

The default print method for a `gam` object.

### Usage

```r
## S3 method for class 'gam'
print(x, ...)
```

### Arguments

- `x, ...`: fitted model objects of class `gam` as produced by `gam()`.

### Details

Prints out the family, model formula, effective degrees of freedom for each smooth term, and optimized value of the smoothness selection criterion used. See `gamObject` (or `names(x)`) for a listing of what the object contains. `summary.gam` provides more detail.

Note that the optimized smoothing parameter selection criterion reported is one of GCV, UBRE(AIC), GACV, negative log marginal likelihood (ML), or negative log restricted likelihood (REML).

If rank deficiency of the model was detected then the apparent rank is reported, along with the length of the coefficient vector (rank in absence of rank deficiency). Rank deficiency occurs when not all coefficients are identifiable given the data. Although the fitting routines (except `gamm`) deal gracefully with rank deficiency, interpretation of rank deficient models may be difficult.
Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

See Also

gam, summary.gam

---

**psum.chisq**

*Evaluate the c.d.f. of a weighted sum of chi-squared deviates*

**Description**

Evaluates the c.d.f. of a weighted sum of chi-squared random variables by the method of Davies (1973, 1980). That is it computes

\[ P(q < \sum_{i=1}^{r} \lambda_i X_i + \sigma_z Z) \]

where \( X_j \) is a chi-squared random variable with \( df[j] \) (integer) degrees of freedom and non-centrality parameter \( nc[j] \), while \( Z \) is a standard normal deviate.

**Usage**

```r
psum.chisq(q, lb, df=rep(1,length(lb)), nc=rep(0,length(lb)), sigz=0,
lower.tail=FALSE, tol=2e-5, nlim=100000, trace=FALSE)
```

**Arguments**

- **q**
  - is the vector of quantile values at which to evaluate.
- **lb**
  - contains \( \lambda_i \), the weight for deviate \( i \). Weights can be positive and/or negative.
- **df**
  - is the integer vector of chi-squared degrees of freedom.
- **nc**
  - is the vector of non-centrality parameters for the chi-squared deviates.
- **sigz**
  - is the multiplier for the standard normal deviate. Non-positive to exclude this term.
- **lower.tail**
  - indicates whether lower or upper tail probabilities are required.
- **tol**
  - is the numerical tolerance to work to.
- **nlim**
  - is the maximum number of integration steps to allow
- **trace**
  - can be set to TRUE to return some trace information and a fault code as attributes.
Details

This calls a C translation of the original Algol60 code from Davies (1980), which numerically inverts the characteristic function of the distribution (see Davies, 1973). Some modifications have been made to remove goto statements and global variables, to use a slightly more efficient sorting of lb and to use R functions for log(1+x). In addition the integral and associated error are accumulated in single terms, rather than each being split into 2, since only their sums are ever used. If q is a vector then psum.chisq calls the algorithm separately for each q[1].

If the Davies algorithm returns an error then an attempt will be made to use the approximation of Liu et al (2009) and a warning will be issued. If that is not possible then an NA is returned. A warning will also be issued if the algorithm detects that round off errors may be significant.

If trace is set to TRUE then the result will have two attributes. "ifault" is 0 for no problem, 1 if the desired accuracy can not be obtained, 2 if round-off error may be significant, 3 is invalid parameters have been supplied or 4 if integration parameters can not be located. "trace" is a 7 element vector: 1. absolute value sum; 2. total number of integration terms; 3. number of integrations; 4. integration interval in main integration; 5. truncation point in initial integration; 6. sd of convergence factor term; 7. number of cycles to locate integration parameters. See Davies (1980) for more details.

Note that for vector q these attributes relate to the final element of q.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


Examples

```r
require(mgcv)
lb <- c(4.1,1.2,1e-3,-1) ## weights
df <- c(2,1,1) ## degrees of freedom
nc <- c(1,1.5,4,1) ## non-centrality parameter
q <- c(1,6,20) ## quantiles to evaluate
psum.chisq(q.lb,df,nc)

## same by simulation...
p sim <- function(q,lb,df=lb*0+1,nc=df*0,ns=10000) {
  r <- length(lb);p <- q
  X <- rowSums(rep(lb,each=ns) *
    matrix(rchisq(r*ns,rep(df,each=ns)),ns,r))
  apply(matrix(q),1,function(q) mean(X>q))
} ## psc.sim
psum.chisq(q.lb,df,nc)
p sim(q,lb,df,nc,100000)
```
**Description**

Takes a fitted gam object produced by `gam()` and produces QQ plots of its residuals (conditional on the fitted model coefficients and scale parameter). If the model distributional assumptions are met then usually these plots should be close to a straight line (although discrete data can yield marked random departures from this line).

**Usage**

```r
qq.gam(object, rep=0, level=.9, s.rep=10,
       type=c("deviance","pearson","response"),
       pch=".", rl.col=2, rep.col="gray80", ...)```

**Arguments**

- **object**: a fitted gam object as produced by `gam()` (or a glm object).
- **rep**: How many replicate datasets to generate to simulate quantiles of the residual distribution. 0 results in an efficient simulation free method for direct calculation, if this is possible for the object family.
- **level**: If simulation is used for the quantiles, then reference intervals can be provided for the QQ-plot, this specifies the level. 0 or less for no intervals, 1 or more to simply plot the QQ plot for each replicate generated.
- **s.rep**: how many times to randomize uniform quantiles to data under direct computation.
- **type**: what sort of residuals should be plotted? See `residuals.gam`.
- **pch**: plot character to use. 19 is good.
- **rl.col**: color for the reference line on the plot.
- **rep.col**: color for reference bands or replicate reference plots.
- **...**: extra graphics parameters to pass to plotting functions.

**Details**

QQ-plots of the the model residuals can be produced in one of two ways. The cheapest method generates reference quantiles by associating a quantile of the uniform distribution with each datum, and feeding these uniform quantiles into the quantile function associated with each datum. The resulting quantiles are then used in place of each datum to generate approximate quantiles of residuals. The residual quantiles are averaged over `s.rep` randomizations of the uniform quantiles to data.

The second method is to use direct simulation. For each replicate, data are simulated from the fitted model, and the corresponding residuals computed. This is repeated `rep` times. Quantiles are readily obtained from the empirical distribution of residuals so obtained. From this method reference bands are also computable.

Even if `rep` is set to zero, the routine will attempt to simulate quantiles if no quantile function is available for the family. If no random deviate generating function family is available (e.g. for the
quasi families), then a normal QQ-plot is produced. The routine conditions on the fitted model coefficients and the scale parameter estimate.

The plots are very similar to those proposed in Ben and Yohai (2004), but are substantially cheaper to produce (the interpretation of residuals for binary data in Ben and Yohai is not recommended).

Note that plots for raw residuals from fits to binary data contain almost no useful information about model fit. Whether the residual is negative or positive is decided by whether the response is zero or one. The magnitude of the residual, given its sign, is determined entirely by the fitted values. In consequence only the most gross violations of the model are detectable from QQ-plots of residuals for binary data. To really check distributional assumptions from residuals for binary data you have to be able to group the data somehow. Binomial models other than binary are ok.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


https://www.maths.ed.ac.uk/~swood34/

See Also

choose.k, gam

Examples

library(mgcv)
## simulate binomial data...
set.seed(0)
n.samp <- 400
dat <- gamSim(1,n=n.samp,dist="binary",scale=.33)
p <- binomial()$linkinv(dat$f) ## binomial p
n <- sample(c(1,3),n.samp,replace=TRUE) ## binomial n
dat$y <- rbinom(n,n,p)
dat$n <- n

lr.fit <- gam(y/n-s(x0)+s(x1)+s(x2)+s(x3)
,family=binomial,data=dat,weights=n,method="REML")

par(mfrow=c(2,2))
## normal QQ-plot of deviance residuals
qqnorm(residuals(lr.fit),pch=19,cex=.3)
## Quick QQ-plot of deviance residuals
qq.gam(lr.fit,pch=19,cex=.3)
## Simulation based QQ-plot with reference bands
qq.gam(lr.fit,rep=100,level=.9)
## Simulation based QQ-plot, Pearson resid, all
## simulated reference plots shown...
qq.gam(lr.fit,rep=100,level=1,type="pearson",pch=19,cex=.2)

## Now fit the wrong model and check....
### random.effects

**Random effects in GAMs**

**Description**

The smooth components of GAMs can be viewed as random effects for estimation purposes. This means that more conventional random effects terms can be incorporated into GAMs in two ways. The first method converts all the smooths into fixed and random components suitable for estimation by standard mixed modelling software. Once the GAM is in this form then conventional random effects are easily added, and the whole model is estimated as a general mixed model. `gamm` and `gamm4` from the `gamm4` package operate in this way.

The second method represents the conventional random effects in a GAM in the same way that the smooths are represented — as penalized regression terms. This method can be used with `gam` by making use of `s(...,bs="re")` terms in a model: see `smooth.construct.re.smooth.spec`, for full details. The basic idea is that, e.g., `s(x,z,g,bs="re")` generates an i.i.d. Gaussian random effect with model matrix given by `model.matrix(~x:z:g-1)` — in principle such terms can take any number of arguments. This simple approach is sufficient for implementing a wide range of commonly used random effect structures. For example if `g` is a factor then `s(g,bs="re")` produces a random coefficient for each level of `g`, with the random coefficients all modelled as i.i.d. normal. If `g` is a factor and `x` is numeric, then `s(x,g,bs="re")` produces an i.i.d. normal random slope relating the response to `x` for each level of `g`. If `h` is another factor then `s(h,g,bs="re")` produces another i.i.d. normal random effect relating the response to `h` for each level of `g`. This approach can be extended to illustrate the wide variety of random effects that can be incorporated into GAMs in this way.
produces the usual i.i.d. normal $g$ - $h$ interaction. Note that a rather useful approximate test for zero random effect is also implemented for such terms based on Wood (2013). If the precision matrix is known to within a multiplicative constant, then this can be supplied via the xt argument of $s$. See smooth.construct.re.smooth.spec for details and example. Some models require differences between different levels of the same random effect: these can be implemented as described in linear.functional.terms.

Alternatively, but less straightforwardly, the paraPen argument to gam can be used: see gam.models. If smoothing parameter estimation is by ML or REML (e.g. gam(...,method="REML") then this approach is a completely conventional likelihood based treatment of random effects.

gam can be slow for fitting models with large numbers of random effects, because it does not exploit the sparsity that is often a feature of parametric random effects. It can not be used for models with more coefficients than data. However gam is often faster and more reliable than gamm or gamm4, when the number of random effects is modest.

To facilitate the use of random effects with gam, gam.vcomp is a utility routine for converting smoothing parameters to variance components. It also provides confidence intervals, if smoothness estimation is by ML or REML.

Note that treating random effects as smooths does not remove the usual problems associated with testing variance components for equality to zero: see summary.gam and anova.gam.

Author(s)
Simon Wood <simon.wood@r-project.org>

References

See Also
gam.vcomp, gam.models, smooth.terms, smooth.construct.re.smooth.spec, gamm

Examples
### see also examples for gam.models, gam.vcomp, gamm
### and smooth.construct.re.smooth.spec

### simple comparison of lme and gam
require(mgcv)
require(nlme)
b0 <- lme(travel~1,data=Rail,~1|Rail,method="REML")
b <- gam(travel~s(Rail,bs="re"),data=Rail,method="REML")
intervals(b0)
```r
## simulate example...
dat <- gamSim(1,n=400,scale=2)  ## simulate 4 term additive truth
fac <- sample(1:20,400,replace=TRUE)
b <- rnorm(20)*.5
dat$y <- dat$y + b[fac]
dat$fac <- as.factor(fac)

rm1 <- gam(y ~ s(fac,bs="re") + s(x0) + s(x1) + s(x2) + s(x3), data=dat, method="ML")
gam.vcomp(rm1)

fv0 <- predict(rm1, exclude="s(fac)")  ## predictions setting r.e. to 0
fv1 <- predict(rm1)  ## predictions setting r.e. to predicted values
## prediction setting r.e. to 0 and not having to provide 'fac'...
pd <- dat; pd$fac <- NULL
fv0 <- predict(rm1, pd, exclude="s(fac)", newdata.guaranteed=TRUE)

## Prediction with levels of fac not in fit data.
## The effect of the new factor levels (or any interaction involving them)
## is set to zero.
xx <- seq(0,1,length=10)
pd <- data.frame(x0=xx, x1=xx, x2=xx, x3=xx, fac=c(1:10,21:30))
fv <- predict(rm1, pd)
pd$fac <- NULL
fv0 <- predict(rm1, pd, exclude="s(fac)", newdata.guaranteed=TRUE)
```

---

### residuals.gam

**Generalized Additive Model residuals**

**Description**

Returns residuals for a fitted `gam` model object. Pearson, deviance, working and response residuals are available.

**Usage**

```r
## S3 method for class 'gam'
residuals(object, type = "deviance", ...)
```

**Arguments**

- `object` a `gam` fitted model object.
- `type` the type of residuals wanted. Usually one of "deviance", "pearson", "scaled.pearson", "working", or "response".
- `...` other arguments.
Details

Response residuals are the raw residuals (data minus fitted values). Scaled Pearson residuals are raw residuals divided by the standard deviation of the data according to the model mean variance relationship and estimated scale parameter. Pearson residuals are the same, but multiplied by the square root of the scale parameter (so they are independent of the scale parameter); \( \frac{(y - \mu)}{\sqrt{V(\mu)}} \), where \( y \) is data \( \mu \) is model fitted value and \( V \) is model mean-variance relationship.). Both are provided since not all texts agree on the definition of Pearson residuals. Deviance residuals simply return the deviance residuals defined by the model family. Working residuals are the residuals returned from model fitting at convergence.

Families can supply their own residual function, which is used in place of the standard function if present, (e.g. `cox.ph`).

Value

A vector of residuals.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

See Also

`gam`

---

**rig**  
*Generate inverse Gaussian random deviates*

Description

Generates inverse Gaussian random deviates.

Usage

`rig(n, mean, scale)`

Arguments

- `n`: the number of deviates required. If this has length > 1 then the length is taken as the number of deviates required.
- `mean`: vector of mean values.
- `scale`: vector of scale parameter values (lambda, see below)

Details

If \( x \) is the returned vector, then \( E(x) = \text{mean} \) while \( \text{var}(x) = \text{scale} \times \text{mean}^3 \). For density and distribution functions see the `statmod` package. The algorithm used is Algorithm 5.7 of Gentle (2003), based on Michael et al. (1976). Note that \( \text{scale} \) here is the scale parameter in the GLM sense, which is the reciprocal of the usual ‘lambda’ parameter.
Value

A vector of inverse Gaussian random deviates.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

Examples

```r
require(mgcv)
set.seed(7)
## An inverse.gaussian GAM example, by modify 'gamSim' output...
dat <- gamSim(1,n=400,dist="normal",scale=1)
dat$f <- dat$f/4  ## true linear predictor
ey <- exp(dat$f); scale <- .5  ## mean and GLM scale parameter
## simulate inverse Gaussian response...
big <- gam(y~ s(x0)+ s(x1)+s(x2)+s(x3),family=inverse.gaussian(link=log),
data=dat,method="REML")
plot(big,pages=1)
gam.check(big)
summary(big)
```

rmvn

Generate from or evaluate multivariate normal or t densities.

Description

Generates multivariate normal or t random deviates, and evaluates the corresponding log densities.

Usage

```r
rmvn(n,mu,V)
rmvt(n,mu,V,df)
dmvn(x,mu,V,R=NULL)
dmvt(x,mu,V,df,R=NULL)
```

Arguments

- `n`: number of simulated vectors required.
- `mu`: the mean of the vectors: either a single vector of length \(p = \text{ncol}(V)\) or an \(n\) by \(p\) matrix.
- `V`: A positive semi definite covariance matrix.
- `df`: The degrees of freedom for a t distribution.
- `x`: A vector or matrix to evaluate the log density of.
- `R`: An optional Cholesky factor of \(V\) (not pivoted).
**Rrank**

**Details**

Uses a ‘square root’ of \( V \) to transform standard normal deviates to multivariate normal with the correct covariance matrix.

**Value**

An \( n \) row matrix, with each row being a draw from a multivariate normal or t density with covariance matrix \( V \) and mean vector \( \mu \). Alternatively each row may have a different mean vector if \( \mu \) is a vector.

For density functions, a vector of log densities.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

ldTweedie, Tweedie

**Examples**

```r
library(mgcv)
V <- matrix(c(2,1,1,2),2,2)
mu <- c(1,3)
n <- 1000
z <- rmvn(n,mu,V)
crossprod(sweep(z,2,colMeans(z)))/n ## observed covariance matrix
colMeans(z) ## observed mu
dmvn(z,mu,V)
```

---

**Rrank**

*Find rank of upper triangular matrix*

**Description**

Finds rank of upper triangular matrix \( R \), by estimating condition number of upper rank by rank block, and reducing rank until this is acceptably low. Assumes \( R \) has been computed by a method that uses pivoting, usually pivoted QR or Choleski.

**Usage**

```r
Rrank(R,tol=.Machine$double.eps^.9)
```

**Arguments**

- **R**
  An upper triangular matrix, obtained by pivoted QR or pivoted Choleski.
- **tol**
  the tolerance to use for judging rank.

**Details**

The method is based on Cline et al. (1979) as described in Golub and van Loan (1996).
Author(s)
Simon N. Wood <simon.wood@r-project.org>

References

Examples
```r
set.seed(0)
n <- 10;p <- 5
x <- runif(n*(p-1))
X <- matrix(c(x,x[1:n]),n,p)
qrX <- qr(X,LAPACK=TRUE)
Rrank(qr.R(qrX))
```

rTweedie

Generate Tweedie random deviates

Description
Generates Tweedie random deviates, for powers between 1 and 2.

Usage
```r
rTweedie(mu,p=1.5,phi=1)
```

Arguments
- `mu` vector of expected values for the deviates to be generated. One deviate generated for each element of `mu`.
- `p` the variance of a deviate is proportional to its mean, `mu` to the power `p`. `p` must be between 1 and 2. 1 is Poisson like (exactly Poisson if `phi=1`), 2 is gamma.
- `phi` The scale parameter. Variance of the deviates is given by `phi*mu^p`.

Details
A Tweedie random variable with 1 < p < 2 is a sum of N gamma random variables where N has a Poisson distribution, with mean `mu^((2-p)/(2-p)*phi)`. The Gamma random variables that are summed have shape parameter `(2-p)/(p-1)` and scale parameter `phi*mu^((p-1)*mu^p(p-1))` (note that this scale parameter is different from the scale parameter for a GLM with Gamma errors).
This is a restricted, but faster, version of `rtweedie` from the `tweedie` package.

Value
A vector of random deviates from a Tweedie distribution, expected value vector `mu`, variance vector `phi*mu^p`.
Author(s)
Simon N. Wood <simon.wood@r-project.org>

References

See Also
ldTweedie, Tweedie

Examples
library(mgcv)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * (10 * x)^3 * (1 - x)^10
n <- 300
x <- runif(n)
mu <- exp(f2(x)/3+.1); x <- x*10 - 4
y <- rTweedie(mu,p=1.5,phi=1.3)
b <- gam(y~s(x,k=20),family=Tweedie(p=1.5))
b
plot(b)

---

Defining smooths in GAM formulae

Description
Function used in definition of smooth terms within gam model formulae. The function does not evaluate a (spline) smooth - it exists purely to help set up a model using spline based smooths.

Usage
s(..., k=-1,fx=FALSE,bs="tp",m=NA,by=NA,xt=NULL,id=NULL,sp=NULL,pc=NULL)

Arguments
... a list of variables that are the covariates that this smooth is a function of. Transformations whose form depends on the values of the data are best avoided here: e.g. s(log(x)) is fine, but s(I(x/sd(x))) is not (see predict.gam).
k the dimension of the basis used to represent the smooth term. The default depends on the number of variables that the smooth is a function of. k should not be less than the dimension of the null space of the penalty for the term (see null.space.dimension), but will be reset if it is. See choose.k for further information.
fx indicates whether the term is a fixed d.f. regression spline (TRUE) or a penalized regression spline (FALSE).
bs

a two letter character string indicating the (penalized) smoothing basis to use. (eg "tp" for thin plate regression spline, "cr" for cubic regression spline). see smooth.terms for an over view of what is available.

m

The order of the penalty for this term (e.g. 2 for normal cubic spline penalty with 2nd derivatives when using default t.p.r.s basis). NA signals autoinitialization. Only some smooth classes use this. The "ps" class can use a 2 item array giving the basis and penalty order separately.

by

a numeric or factor variable of the same dimension as each covariate. In the numeric vector case the elements multiply the smooth, evaluated at the corresponding covariate values (a ‘varying coefficient model’ results). For the numeric by variable case the resulting smooth is not usually subject to a centering constraint (so the by variable should not be added as an additional main effect). In the factor by variable case a replicate of the smooth is produced for each factor level (these smooths will be centered, so the factor usually needs to be added as a main effect as well). See gam.models for further details. A by variable may also be a matrix if covariates are matrices: in this case implements linear functional of a smooth (see gam.models and linear.functional.terms for details).

xt

Any extra information required to set up a particular basis. Used e.g. to set large data set handling behaviour for "tp" basis. If xt$sumConv exists and is FALSE then the summation convention for matrix arguments is turned off.

id

A label or integer identifying this term in order to link its smoothing parameters to others of the same type. If two or more terms have the same id then they will have the same smoothing parameters, and, by default, the same bases (first occurrence defines basis type, but data from all terms used in basis construction). An id with a factor by variable causes the smooths at each factor level to have the same smoothing parameter.

sp

any supplied smoothing parameters for this term. Must be an array of the same length as the number of penalties for this smooth. Positive or zero elements are taken as fixed smoothing parameters. Negative elements signal auto-initialization. Over-rides values supplied in sp argument to gam. Ignored by gamm.

pc

If not NULL, signals a point constraint: the smooth should pass through zero at the point given here (as a vector or list with names corresponding to the smooth names). Never ignored if supplied. See identifiability.

Details

The function does not evaluate the variable arguments. To use this function to specify use of your own smooths, note the relationships between the inputs and the output object and see the example in smooth.construct.

Value

A class xx.smooth.spec object, where xx is a basis identifying code given by the bs argument of s. These smooth.spec objects define smooths and are turned into bases and penalties by smooth.construct method functions.

The returned object contains the following items:

term

An array of text strings giving the names of the covariates that the term is a function of.
bs.dim  The dimension of the basis used to represent the smooth.

fixed  TRUE if the term is to be treated as a pure regression spline (with fixed degrees of freedom); FALSE if it is to be treated as a penalized regression spline.

dim  The dimension of the smoother - i.e. the number of covariates that it is a function of.

p.order  The order of the t.p.r.s. penalty, or 0 for auto-selection of the penalty order.

by  is the name of any by variable as text ("NA" for none).

label  A suitable text label for this smooth term.

xt  The object passed in as argument xt.

id  An identifying label or number for the smooth, linking it to other smooths. Defaults to NULL for no linkage.

sp  array of smoothing parameters for the term (negative for auto-estimation). Defaults to NULL.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


https://www.maths.ed.ac.uk/~swood34/

See Also

t, gam, gamm

Examples

# example utilising 'by' variables
library(mgcv)
set.seed(0)
n<-200; sig2<-4
x1 <- runif(n, 0, 1); x2 <- runif(n, 0, 1); x3 <- runif(n, 0, 1)
fac<-c(rep(1,n/2),rep(2,n/2)) # create factor
fac.1<-rep(0,n)+(fac==1); fac.2<-1-fac.1 # and dummy variables
fac<-as.factor(fac)
f1 <- exp(2 * x1) - 3.75887
f2 <- 0.2 * x1^11 * (10 * (1 - x1))^6 + 10 * (10 * x1)^3 * (1 - x1)^10
f<-f1*fac.1+f2*fac.2+x2
e <- rnorm(n, 0, sqrt(abs(sig2)))
y <- f + e
# NOTE: smooths will be centered, so need to include fac in model....
b<-gam(y~fac+s(x1,by=fac)+x2)
plot(b,pages=1)
Description

Family for use with gam or bam, implementing regression for the heavy tailed response variables, y, using a scaled t model. The idea is that $(y - \mu)/\sigma \sim t_\nu$ where $\mu$ is determined by a linear predictor, while $\sigma$ and $\nu$ are parameters to be estimated alongside the smoothing parameters.

Usage

```r
scat(theta = NULL, link = "identity", min.df = 3)
```

Arguments

- **theta** the parameters to be estimated $\nu = b + \exp(\theta_1)$ (where ‘b’ is min.df) and $\sigma = \exp(\theta_2)$. If supplied and both positive, then taken to be fixed values of $\nu$ and $\sigma$. If any negative, then absolute values taken as starting values.
- **link** The link function: one of "identity", "log" or "inverse".
- **min.df** minimum degrees of freedom. Should not be set to 2 or less as this implies infinite response variance.

Details

Useful in place of Gaussian, when data are heavy tailed. min.df can be modified, but lower values can occasionally lead to convergence problems in smoothing parameter estimation. In any case min.df should be >2, since only then does a t random variable have finite variance.

Value

An object of class extended.family.

Author(s)

Natalya Pya (nat.pya@gmail.com)

References


Examples

```r
library(mgcv)
## Simulate some t data...
set.seed(3);n<-400
dat <- gamSim(1,n=n)
dat$y <- dat$f + rt(n,df=4)*2
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=scat(link="identity"),data=dat)
```
sdiag

Extract or modify diagonals of a matrix

Description

Extracts or modifies sub- or super- diagonals of a matrix.

Usage

sdiag(A,k=0)
sdiag(A,k=0) <- value

Arguments

A  
a matrix

k  
sub- (negative) or super- (positive) diagonal of a matrix. 0 is the leading diagonal.

value  
single value, or vector of the same length as the diagonal.

Value

A vector containing the requested diagonal, or a matrix with the requested diagonal replaced by value.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

Examples

require(mgcv)
A <- matrix(1:35,7,5)
A
sdiag(A,1) ## first super diagonal
sdiag(A,-1) ## first sub diagonal

sdiag(A) <- 1 ## leading diagonal set to 1
sdiag(A,3) <- c(-1,-2) ## set 3rd super diagonal
shash

Sinh-arcsinh location scale and shape model family

Description

The shash family implements the four-parameter sinh-arcsinh (shash) distribution of Jones and Pewsey (2009). The location, scale, skewness and kurtosis of the density can depend on additive smooth predictors. Useable only with gam, the linear predictors are specified via a list of formulae. It is worth carefully considering whether the data are sufficient to support estimation of such a flexible model before using it.

Usage

shash(link = list("identity", "logeb", "identity", "identity"),
       b = 1e-2, phiPen = 1e-3)

Arguments

- **link**: vector of four characters indicating the link function for location, scale, skewness and kurtosis parameters.
- **b**: positive parameter of the logeb link function, see Details.
- **phiPen**: positive multiplier of a ridge penalty on kurtosis parameter. Do not touch it unless you know what you are doing, see Details.

Details

The density function of the shash family is

\[ p(y|\mu, \sigma, \epsilon, \delta) = C(z) \exp\{-S(z)^2/2\}\{2\pi(1 + z^2)\}^{-1/2}/\sigma, \]

where \( C(z) = (1 + S(z)^2)^{1/2}, \ S(z) = \sinh(\delta \sinh^{-1}(z) - \epsilon) \) and \( z = (y - \mu)/(\sigma \delta) \). Here \( \mu \) and \( \sigma > 0 \) control, respectively, location and scale, \( \epsilon \) determines skewness, while \( \delta > 0 \) controls tailweight. shash can model skewness to either side, depending on the sign of \( \epsilon \). Also, shash can have tails that are lighter (\( \delta > 1 \)) or heavier (\( 0 < \delta < 1 \)) than a normal. For fitting purposes, here we are using \( \tau = \log(\sigma) \) and \( \phi = \log(\delta) \).

The density is based on the expression given on the second line of section 4.1 and equation (2) of Jones and Pewsey (2009), and uses the simple reparameterization given in section 4.3.

The link function used for \( \tau \) is logeb with is \( \eta = \log\{\exp(\tau) - b\} \) so that the inverse link is \( \tau = \log(\sigma) = \log\{\exp(\eta) + b\} \). The point is that we are don’t allow \( \sigma \) to become smaller than a small constant \( b \). The likelihood includes a ridge penalty \( -\phi\text{Pen} * \phi^2 \), which shrinks \( \phi \) toward zero. When sufficient data is available the ridge penalty does not change the fit much, but it is useful to include it when fitting the model to small data sets, to avoid \( \phi \) diverging to +infinity (a problem already identified by Jones and Pewsey (2009)).

Value

An object inheriting from class general.family.

Author(s)

Matteo Fasiolo <matteo.fasiolo@gmail.com> and Simon N. Wood.
References


Examples

```
# Shash dataset
## Simulate some data from shash
set.seed(847)
N <- 1000
x <- seq(-4, 4, length.out = N)
X <- cbind(1, x, x^2)
mu <- X %*% beta
sigma = .5+0.4*(x+4)*.5 # Scale
eps = 2*sin(x) # Skewness
del = 1 + 0.2*cos(3*x) # Kurtosis
dat <- mu + (del*sigma)*sinh((1/del)*asinh(qnorm(runif(N)))) + (eps/del))
dataf <- data.frame(cbind(dat, x))
names(dataf) <- c("y", "x")

## Fit model
fit <- gam(list(y ~ s(x), ~ s(x), ~ s(x), ~ s(x, k = 20)),
data = dataf,
            family = shash, # <- new family
            optimizer = "efs")

## Plotting truth and estimates for each parameters of the density
muE <- fit$fitted[ , 1]
sigE <- exp(fit$fitted[ , 2])
epsE <- fit$fitted[ , 3]
delE <- exp(fit$fitted[ , 4])

par(mfrow = c(2, 2))
plot(x, muE, type = 'l', ylab = expression(mu(x)), lwd = 2)
lines(x, mu, col = 2, lty = 2, lwd = 2)
legend("top", c("estimated", "truth"), col = 1:2, lty = 1:2, lwd = 2)

plot(x, sigE, type = 'l', ylab = expression(sigma(x)), lwd = 2)
lines(x, sigma, col = 2, lty = 2, lwd = 2)

plot(x, epsE, type = 'l', ylab = expression(epsilon(x)), lwd = 2)
lines(x, eps, col = 2, lty = 2, lwd = 2)
```
Single index models contain smooth terms with arguments that are linear combinations of other covariates. e.g. $s(X_\alpha)$ where $\alpha$ has to be estimated. For identifiability, assume $\|\alpha\| = 1$ with positive first element. One simple way to fit such models is to use \texttt{gam} to profile out the smooth model coefficients and smoothing parameters, leaving only the $\alpha$ to be estimated by a general purpose optimizer.

Example code is provided below, which can be easily adapted to include multiple single index terms, parametric terms and further smooths. Note the initialization strategy. First estimate $\alpha$ without penalization to get starting values and then do the full fit. Otherwise it is easy to get trapped in a local optimum in which the smooth is linear. An alternative is to initialize using fixed penalization (via the \texttt{sp} argument to \texttt{gam}).
Author(s)
Simon N. Wood <simon.wood@r-project.org>

Examples

```r
require(mgcv)

si <- function(theta,y,x,z,opt=TRUE,k=10,fx=FALSE) {
## Fit single index model using gam call, given theta (defines alpha).
## Return ML if opt==TRUE and fitted gam with theta added otherwise.
## Suitable for calling from 'optim' to find optimal theta/alpha.
alpha <- c(1,theta) ## constrained alpha defined using free theta
kk <- sqrt(sum(alpha^2))
alpha <- alpha/kk ## so now ||alpha||=1
a <- x%*%alpha ## argument of smooth
b <- gam(y~s(a,fx=fx,k=k)+s(z),family=poisson,method="ML") ## fit model
if (opt) return(b$gcv.ubre) else {
b$balpha <- alpha ## add alpha
J <- outer(alpha,-theta/kk^2) ## compute Jacobian
for (j in 1:length(theta)) J[j+1,j] <- J[j+1,j] + 1/kk
b$J <- J ## dalpha_i/dtheta_j
return(b)
}
}
## simulate some data from a single index model...
set.seed(1)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * (10 * x)^3 * (1 - x)^10
n <- 200;m <- 3
x <- matrix(runif(n*m),n,m) ## the covariates for the single index part
z <- runif(n) ## another covariate
alpha <- c(1,-1,.5); alpha <- alpha/sqrt(sum(alpha^2))
eta <- as.numeric(f2((x%*%alpha+.41)/1.4)+1+z^2*2)/4
mu <- exp(eta)
y <- rpois(n,mu) ## Poi response
## now fit to the simulated data...
th0 <- c(-.8,.4) ## close to truth for speed
## get initial theta, using no penalization...
f0 <- nlm(si,th0,y=y,x=x,z=z,fx=FALSE,k=5)
## now get theta/alpha with smoothing parameter selection...
f1 <- nlm(si,f0$estimate,y=y,x=x,z=z,hessian=TRUE,k=10)
theta.est <-f1$estimate

## Alternative using 'optim'...
th0 <- rep(0,m-1)
## get initial theta, using no penalization...
f0 <- optim(th0,si,y=y,x=x,z=z,fx=FALSE,k=5)
## now get theta/alpha with smoothing parameter selection...
f1 <- optim(f0$par,si,y=y,x=x,z=z,hessian=TRUE,k=10)
theta.est <-f1$par
```
## extract and examine fitted model...

```r
b <- si(theta.est,y,x,z,opt=FALSE) ## extract best fit model
plot(b,pages=1)
```

```r
b
```

```r
b$alpha
```

## get sd for alpha...

```r
Vt <- b$J %*% solve(f1$hessian,t(b$J))
diag(Vt)^.5
```

---

### Sl.inirep

**Re-parametrizing model matrix X**

**Description**

INTERNAL routine to apply initial SI re-parameterization to model matrix X, or, if inverse==TRUE, to apply inverse re-parametrization to parameter vector or covariance matrix.

**Usage**

```r
Sl.inirep(Sl,X,l,r,nt=1)
```

```r
Sl.initial.repara(Sl, X, inverse = FALSE, both.sides = TRUE, cov = TRUE, nt = 1)
```

**Arguments**

- `Sl` the output of `Sl.setup`.
- `X` the model matrix.
- `l` if non-zero apply transform (positive) or inverse transform from left. 1 or -1 of transform, 2 or -2 for transpose.
- `r` if non-zero apply transform (positive) or inverse transform from right. 1 or -1 of transform, 2 or -2 for transpose.
- `inverse` if TRUE an inverse re-parametrization is performed.
- `both.sides` if inverse==TRUE and both.sides==FALSE then the re-parametrization only applied to rhs, as appropriate for a choleski factor. If both.sides==FALSE, X is a vector and inverse==FALSE then X is taken as a coefficient vector (so re-parametrization is inverse of that for the model matrix).
- `cov` boolean indicating whether X is a covariance matrix.
- `nt` number of parallel threads to be used.

**Value**

A re-parametrized version of X.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>.
Applying re-parameterization from log-determinant of penalty matrix to model matrix.

Description
INTERNAL routine to apply re-parameterization from log-determinant of penalty matrix, $\text{ldet} S$ to model matrix, $X$, blockwise.

Usage
Sl.repara(rp, X, inverse = FALSE, both.sides = TRUE)

Arguments
rp reparametrization.
X if $X$ is a matrix it is assumed to be a model matrix whereas if $X$ is a vector it is assumed to be a parameter vector.
inverse if TRUE an inverse re-parametrization is performed.
both.sides if inverse==TRUE and both.sides==FALSE then the re-parametrization only applied to rhs, as appropriate for a choleski factor. If both.sides==FALSE, $X$ is a vector and inverse==FALSE then $X$ is taken as a coefficient vector (so re-parametrization is inverse of that for the model matrix).

Value
A re-parametrized version of $X$.

Author(s)
Simon N. Wood <simon.wood@r-project.org>.

Setting up a list representing a block diagonal penalty matrix

Description
INTERNAL function for setting up a list representing a block diagonal penalty matrix from the object produced by gam.setup.

Usage
Sl.setup(G, cholesky=FALSE, no.repara=FALSE, sparse=FALSE)

Arguments
G the output of gam.setup.
cholesky re-parameterize using Cholesky only.
no.repara set to TRUE to turn off all initial reparameterization.
sparse sparse setup?
slanczos

Value

A list with an element for each block. For block, b, Sl[[b]] is a list with the following elements

- **repara**: should re-parameterization be applied to model matrix, etc? Usually FALSE if non-linear in coefficients.
- **start, stop**: such that start:stop are the indexes of the parameters of this block.
- **S**: a list of penalty matrices for the block (dim = stop-start+1) If length(S)==1 then this will be an identity penalty. Otherwise it is a multiple penalty, and an rS list of square root penalty matrices will be added. S (if repara==TRUE) and rS (always) will be projected into range space of total penalty matrix.
- **rS**: square root of penalty matrices if multiple penalties are used.
- **D**: a reparameterization matrix for the block. Applies to cols/params in start:stop. If numeric then X[,start:stop]%*%diag(D) is re-parametrization of X[,start:stop], and b.orig = D*b.repara (where b.orig is the original parameter vector). If matrix then X[,start:stop]%*%D is re-parametrization of X[,start:stop], and b.orig = D%*%b.repara (where b.orig is the original parameter vector).

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

slanczos                  Compute truncated eigen decomposition of a symmetric matrix

Description

Uses Lanczos iteration to find the truncated eigen-decomposition of a symmetric matrix.

Usage

slanczos(A,k=10,kl=-1,tol=.Machine$double.eps^.5,nt=1)

Arguments

A A symmetric matrix.

k Must be non-negative. If kl is negative, then the k largest magnitude eigenvalues are found, together with the corresponding eigenvectors. If k1 is non-negative then the k highest eigenvalues are found together with their eigenvectors and the k1 lowest eigenvalues with eigenvectors are also returned.

kl If k1 is non-negative then the k1 lowest eigenvalues are returned together with their corresponding eigenvectors (in addition to the k highest eigenvalues + vectors). negative k1 signals that the k largest magnitude eigenvalues should be returned, with eigenvectors.

tol tolerance to use for convergence testing of eigenvalues. Error in eigenvalues will be less than the magnitude of the dominant eigenvalue multiplied by tol (or the machine precision!).

nt number of threads to use for leading order iterative multiplication of A by vector. May show no speed improvement on two processor machine.
Details

If \( kl \) is non-negative, returns the highest \( k \) and lowest \( kl \) eigenvalues, with their corresponding eigenvectors. If \( kl \) is negative, returns the largest magnitude \( k \) eigenvalues, with corresponding eigenvectors.

The routine implements Lanczos iteration with full re-orthogonalization as described in Demmel (1997). Lanczos iteration iteratively constructs a tridiagonal matrix, the eigenvalues of which converge to the eigenvalues of \( A \), as the iteration proceeds (most extreme first). Eigenvectors can also be computed. For small \( k \) and \( kl \) the approach is faster than computing the full symmetric eigendecomposition. The tridiagonal eigenproblems are handled using LAPACK.

The implementation is not optimal: in particular the inner triadiagonal problems could be handled more efficiently, and there would be some savings to be made by not always returning eigenvectors.

Value

A list with elements values (array of eigenvalues); vectors (matrix with eigenvectors in its columns); iter (number of iterations required).

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

cyclic.p.spline

Examples

```
require(mgcv)
## create some x's and knots...
set.seed(1);
n <- 700;A <- matrix(runif(n*n),n,n);A <- A+t(A)

## compare timings of slanczos and eigen
system.time(er <- slanczos(A,10))
system.time(um <- eigen(A,symmetric=TRUE))

## confirm values are the same...
ind <- c(1:6,(n-3):n)
range(er$values-um$values[ind]);range(abs(er$vectors)-abs(um$vectors[,ind]))
```
Description

Smooth terms in a GAM formula are turned into smooth specification objects of class xx.smooth.spec during processing of the formula. Each of these objects is converted to a smooth object using an appropriate smooth.construct function. New smooth classes can be added by writing a new smooth.construct method function and a corresponding Predict.matrix method function (see example code below).

In practice, smooth.construct is usually called via smooth.construct2 and the wrapper function smoothCon, in order to handle by variables and centering constraints (see the smoothCon documentation if you need to handle these things directly, for a user defined smooth class).

Usage

smooth.construct(object, data, knots)
smooth.construct2(object, data, knots)

Arguments

object

is a smooth specification object, generated by an s or te term in a GAM formula. Objects generated by s terms have class xx.smooth.spec where xx is given by the bs argument of s (this convention allows the user to add their own smoothers). If object is not class tensor.smooth.spec it will have the following elements:

term The names of the covariates for this smooth, in an array.
bs.dim Argument k of the s term generating the object. This is the dimension of the basis used to represent the term (or, arguably, 1 greater than the basis dimension for cc terms). bs.dim<0 indicates that the constructor should set this to the default value.
fixed TRUE if the term is to be unpenalized, otherwise FALSE.
dim the number covariates of which this smooth is a function.
p.order the order of the smoothness penalty or NA for autoselection of this. This is argument m of the s term that generated object.
by the name of any by variable to multiply this term as supplied as an argument to s. "NA" if there is no such term.
label A suitable label for use with this term.
xt An object containing information that may be needed for basis setup (used, e.g. by "tp" smooths to pass optional information on big dataset handling).
id Any identity associated with this term — used for linking bases and smoothing parameters. NULL by default, indicating no linkage.
sp Smoothing parameters for the term. Any negative are estimated, otherwise they are fixed at the supplied value. Unless NULL (default), over-rides sp argument to gam.

If object is of class tensor.smooth.spec then it was generated by a te term in the GAM formula, and specifies a smooth of several variables with a basis generated as a tensor product of lower dimensional bases. In this case the object will be different and will have the following elements:

margin is a list of smooth specification objects of the type listed above, defining the bases which have their tensor product formed in order to construct this term.
term is the array of names of the covariates that are arguments of the smooth.
by is the name of any by variable, or "NA".
fx is an array, the elements of which indicate whether (TRUE) any of the margins in the tensor product should be unpenalized.

label A suitable label for use with this term.
dim is the number of covariates of which this smooth is a function.
mf TRUE if multiple penalties are to be used.
np TRUE if 1-D marginal smooths are to be re-parameterized in terms of function values.
id Any identity associated with this term — used for linking bases and smoothing parameters. NULL by default, indicating no linkage.
sp Smoothing parameters for the term. Any negative are estimated, otherwise they are fixed at the supplied value. Unless NULL (default), over-rides sp argument to gam.
data For smooth.construct a data frame or list containing the evaluation of the elements of object$term, with names given by object$term. The last entry will be the by variable, if object$by is not "NA". For smooth.construct2 data need only be an object within which object$term can be evaluated, the variables can be in any order, and there can be irrelevant variables present as well.
knots an optional data frame or list containing the knots relating to object$term. If it is NULL then the knot locations are generated automatically. The structure of knots should be as for data, depending on whether smooth.construct or smooth.construct2 is used.

Details

There are built in methods for objects with the following classes: tp.smooth.spec (thin plate regression splines: see tprs); ts.smooth.spec (thin plate regression splines with shrinkage-to-zero); cr.smooth.spec (cubic regression splines: see cubic.regression.spline; cs.smooth.spec (cubic regression splines with shrinkage-to-zero); cc.smooth.spec (cyclic cubic regression splines); ps.smooth.spec (Eilers and Marx (1986) style P-splines: see p.spline); cp.smooth.spec (cyclic P-splines); ad.smooth.spec (adaptive smooths of 1 or 2 variables: see adaptive.smooth); re.smooth.spec (simple random effect terms); mrf.smooth.spec (Markov random field smoothers for smoothing over discrete districts); tensor.smooth.spec (tensor product smooths).

There is an implicit assumption that the basis only depends on the knots and/or the set of unique covariate combinations; i.e. that the basis is the same whether generated from the full set of covariates, or just the unique combinations of covariates.

Plotting of smooths is handled by plot methods for smooth objects. A default mgcv.smooth method is used if there is no more specific method available. Plot methods can be added for specific smooth classes, see source code for mgcv:::plot.sos.smooth, mgcv:::plot.random.effect, mgcv:::plot.mgcv.smooth for example code.

Value

The input argument object, assigned a new class to indicate what type of smooth it is and with at least the following items added:

X The model matrix from this term. This may have an "offset" attribute: a vector of length nrow(X) containing any contribution of the smooth to the model offset term. by variables do not need to be dealt with here, but if they are then an item by.done must be added to the object.
A list of positive semi-definite penalty matrices that apply to this term. The list will be empty if the term is to be left un-penalized.

rank

An array giving the ranks of the penalties.

null.space.dim

The dimension of the penalty null space (before centering).

The following items may be added:

C

The matrix defining any identifiability constraints on the term, for use when fitting. If this is NULL then smoothCon will add an identifiability constraint that each term should sum to zero over the covariate values. Set to a zero row matrix if no constraints are required. If a supplied C has an attribute "always.apply" then it is never ignored, even if any by variables of a smooth imply that no constraint is actually needed. Code for creating C should check whether the specification object already contains a zero row matrix, and leave this unchanged if it is (since this signifies no constraint should be produced).

Cp

An optional matrix supplying alternative identifiability constraints for use when predicting. By default the fitting constrants are used. This option is useful when some sort of simple sparse constraint is required for fitting, but the usual sum-to-zero constraint is required for prediction so that, e.g. the CIs for model components are as narrow as possible.

no.rescale

if this is non-NULL then the penalty coefficient matrix of the smooth will not be rescaled for enhanced numerical stability (rescaling is the default, because gamm requires it). Turning off rescaling is useful if the values of the smoothing parameters should be interpretable in a model, for example because they are inverse variance components.

df

the degrees of freedom associated with this term (when unpenalized and unconstrained). If this is null then smoothCon will set it to the basis dimension. smoothCon will reduce this by the number of constraints.

te.ok

0 if this term should not be used as a tensor product marginal, 1 if it can be used and plotted, and 2 is it can be used but not plotted. Set to 1 if NULL.

plot.me

Set to FALSE if this smooth should not be plotted by plot.gam. Set to TRUE if NULL.

side.constrain

Set to FALSE to ensure that the smooth is never subject to side constraints as a result of nesting.

L

smooths may depend on fewer 'underlying' smoothing parameters than there are elements of S. In this case L is the matrix mapping the vector of underlying log smoothing parameters to the vector of logs of the smoothing parameters actually multiplying the S[[i]]. L=NULL signifies that there is one smoothing parameter per S[[i]].

Usually the returned object will also include extra information required to define the basis, and used by Predict.matrix methods to make predictions using the basis. See the Details section for links to the information included for the built in smooth classes.

tensor.smooth returned objects will additionally have each element of the margin list updated in the same way. tensor.smooths also have a list, XP, containing re-parameterization matrices for any 1-D marginal terms re-parameterized in terms of function values. This list will have NULL entries for marginal smooths that are not re-parameterized, and is only long enough to reach the last re-parameterized marginal in the list.
**WARNING**

User defined smooth objects should avoid having attributes names "qrc" or "nCons" as these are used internally to provide constraint free parameterizations.

**Author(s)**

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**References**


The code given in the example is based on the smooths advocated in:


However if you want p-splines, rather than splines with derivative based penalties, then the built in "ps" class is probably a marginally better bet. It’s based on


https://www.maths.ed.ac.uk/~swood34/

**See Also**

s, get.var, gamm, gam, Predict.matrix, smoothCon, PredictMat

**Examples**

```r
## Adding a penalized truncated power basis class and methods
## as favoured by Ruppert, Wand and Carroll (2003)
## Semiparametric regression CUP. (No advantage to actually
## using this, since mgcv can happily handle non-identity
## penalties.)

smooth.construct.tr.smooth.spec <- function(object, data, knots) {
  ## a truncated power spline constructor function
  ## object$p.order = null space dimension
  m <- object$p.order[1]
  if (is.na(m)) m <- 2 ## default
  if (m<1) stop("silly m supplied")
  if (object$bs.dim<0) object$bs.dim <- 10 ## default
  nk <- object$bs.dim-m-1 ## number of knots
  if (nk<0) stop("k too small for m")
  x <- data[[object$term]] ## the data
  x.shift <- mean(x) # shift used to enhance stability
  k <- knots[[object$term]] ## will be NULL if none supplied
  if (is.null(k)) k <- knots[[object$term]] ## will be NULL if none supplied
  if (is.null(k)) k <- knots[[object$term]] ## will be NULL if none supplied
  if (length(k)!=nk) # right number of knots?
    stop(paste("there should be ",nk," supplied knots"))
  x <- x - x.shift # basis stabilizing shift
```
k <- k - x.shift # knots treated the same!
X<-matrix(0,length(x),object$bs.dim)
for (i in 1:(m+1)) X[,i] <- x^(i-1)
for (i in 1:nk) X[,i+m+1]<-(x-k[i])^m*as.numeric(x>k[i])
object$X<-X # the finished model matrix
if (!object$fixed) # create the penalty matrix
  { object$S[[1]]<-diag(c(rep(0,m+1),rep(1,nk)))
}
object$rank<-nk # penalty rank
object$null.space.dim <- m+1 # dim. of unpenalized space
## store "tr" specific stuff ...
object$knots<-k;object$m<-m;object$x.shift <- x.shift
object$df<-ncol(object$X) # maximum DoF (if unconstrained)
class(object)<-"tr.smooth" # Give object a class
object
}

Predict.matrix.tr.smooth<-function(object,data) {
  ## prediction method function for the `tr' smooth class
  x <- data[[object$term]]
  x <- x - object$x.shift # stabilizing shift
  m <- object$m; # spline order (3=cubic)
  k<-object$knots # knot locations
  nk<-length(k) # number of knots
  X<-matrix(0,length(x),object$bs.dim)
  for (i in 1:(m+1)) X[,i] <- x^(i-1)
  for (i in 1:nk) X[,i+m+1]<-(x-k[i])^m*as.numeric(x>k[i])
  X # return the prediction matrix
}

# an example, using the new class....
require(mgcv)
set.seed(100)
dat <- gamSim(1,n=400,scale=2)
b<-gam(y~s(x0,bs="tr",m=2)+s(x1,bs="ps",m=c(1,3))+
  s(x2,bs="tr",m=3)+s(x3,bs="tr",m=2),data=dat)
plot(b,pages=1)
b<-gamm(y~s(x0,bs="tr",m=2)+s(x1,bs="ps",m=c(1,3))+
  s(x2,bs="tr",m=3)+s(x3,bs="tr",m=2),data=dat)
plot(b$gam,pages=1)
# another example using tensor products of the new class
dat <- gamSim(2,n=400, scale=.1)$data
b <- gam(y~te(x,z,bs=c("tr","tr"),m=c(2,2)),data=dat)
vis.gam(b)

smooth.construct.ad.smooth.spec

Adaptive smooths in GAMs

Description

`gam' can use adaptive smooths of one or two variables, specified via terms like
`s(...,bs="ad",...). (`gamm' can not use such terms — check out package AdaptFit if this is a
The basis for such a term is a (tensor product of) P-spline(s) or cubic regression spline(s). Discrete P-spline type penalties are applied directly to the coefficients of the basis, but the penalties themselves have a basis representation, allowing the strength of the penalty to vary with the covariates. The coefficients of the penalty basis are the smoothing parameters.

When invoking an adaptive smoother the \( k \) argument specifies the dimension of the smoothing basis (default 40 in 1D, 15 in 2D), while the \( m \) argument specifies the dimension of the penalty basis (default 5 in 1D, 3 in 2D). For an adaptive smooth of two variables \( k \) is taken as the dimension of both marginal bases: different marginal basis dimensions can be specified by making \( k \) a two element vector. Similarly, in the two dimensional case \( m \) is the dimension of both marginal bases for the penalties, unless it is a two element vector, which specifies different basis dimensions for each marginal (If the penalty basis is based on a thin plate spline then \( m \) specifies its dimension directly).

By default, P-splines are used for the smoothing and penalty bases, but this can be modified by supplying a list as argument \( xt \) with a character vector \( xt.bs \) specifying the smoothing basis type. Only "ps", "cp", "cc" and "cr" may be used for the smoothing basis. The penalty basis is always a B-spline, or a cyclic B-spline for cyclic bases.

The total number of smoothing parameters to be estimated for the term will be the dimension of the penalty basis. Bear in mind that adaptive smoothing places quite severe demands on the data. For example, setting \( m=10 \) for a univariate smooth of 200 data is rather like estimating 10 smoothing parameters, each from a data series of length 20. The problem is particularly serious for smooths of 2 variables, where the number of smoothing parameters required to get reasonable flexibility in the penalty can grow rather fast, but it often requires a very large smoothing basis dimension to make good use of this flexibility. In short, adaptive smooths should be used sparingly and with care.

In practice it is often as effective to simply transform the smoothing covariate as it is to use an adaptive smooth.

Usage

```r
## S3 method for class 'ad.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

- **object**: a smooth specification object, usually generated by a term `s(...,bs="ad",...)`
- **data**: a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
- **knots**: a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be NULL

Details

The constructor is not normally called directly, but is rather used internally by `gam`. To use for basis setup it is recommended to use `smooth.construct2`.

This class can not be used as a marginal basis in a tensor product smooth, nor by `gamm`.

Value

An object of class "pspline.smooth" in the 1D case or "tensor.smooth" in the 2D case.
Examples

## Comparison using an example taken from AdaptFit
## library(AdaptFit)
require(mgcv)
set.seed(0)
x <- 1:1000/1000
mu <- exp(-400*(x-.6)^2)+5*exp(-500*(x-.75)^2)/3+2*exp(-500*(x-.9)^2)
y <- mu+0.5*rnorm(1000)

##fit with default knots
## y.fit <- asp(y~f(x))
par(mfrow=c(2,2))
## plot(y.fit,main=round(cor(fitted(y.fit),mu),digits=4))
## lines(x,mu,col=2)

b <- gam(y~s(x,bs="ad",k=40,m=5)) ## adaptive
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

b <- gam(y~s(x,k=40)) ## non-adaptive
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

b <- gam(y~s(x,bs="ad",k=40,m=5,xt=list(bs="cr")))
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

## A 2D example (marked, 'Not run' purely to reduce
## checking load on CRAN).
##
par(mfrow=c(2,2),mar=c(1,1,1,1))
x <- seq(-.5, 1.5, length= 60)
z <- x
f3 <- function(x,z,k=15) { r<-sqrt(x^2+z^2);f<-exp(-r^2*k);f}
f <- outer(x, z, f3)
op <- par(bg = "white")

## Plot truth....
persp(x,z,f,theta=30,phi=30,col="lightblue",ticktype="detailed")

n <- 2000
x <- runif(n)*2-.5
z <- runif(n)*2-.5
f <- f3(x,z)
y <- f + rnorm(n)*.1

## Try tprs for comparison...
b0 <- gam(y-s(x,z,k=150))
vis.gam(b0,theta=30,phi=30,ticktype="detailed")

## Tensor product with non-adaptive version of adaptive penalty
### smooth.construct.bs.smooth.spec

#### Penalized B-splines in GAMs

**Description**

`gam` can use smoothing splines based on univariate B-spline bases with derivative based penalties, specified via terms like `s(x, bs="bs", m=c(3,2))`. `m[1]` controls the spline order, with `m[1]=3` being a cubic spline, `m[1]=2` being quadratic, and so on. The integrated square of the `m[2]`th derivative is used as the penalty. So `m=c(3,2)` is a conventional cubic spline. Any further elements of `m`, after the first 2, define the order of derivative in further penalties. If `m` is supplied as a single number, then it is taken to be `m[1]` and `m[2]=m[1]-1`, which is only a conventional smoothing spline in the `m=3`, cubic spline case. Notice that the definition of the spline order in terms of `m[1]` is intuitive, but differs to that used with the `tprs` and `p.spline` bases. See details for options for controlling the interval over which the penalty is evaluated (which can matter if it is necessary to extrapolate).

**Usage**

```r
## S3 method for class 'bs.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'Bspline.smooth'
Predict.matrix(object, data)
```

**Arguments**

- `object` a smooth specification object, usually generated by a term `s(x, bs="bs",...)`
- `data` a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
- `knots` a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be NULL. See details for further information.

**Details**

The basis and penalty are sparse (although sparse matrices are not used to represent them). `m[2]>m[1]` will generate an error, since in that case the penalty would be based on an undefined derivative of the basis, which makes no sense. The terms can have multiple penalties of different orders, for example `s(x, bs="bs", m=c(3,2,1,0))` specifies a cubic basis with 3 penalties: a conventional cubic spline penalty, an integrated square of first derivative penalty, and an integrated square of function value penalty.
The default basis dimension, \( k \), is the larger of 10 and \( m[1] \). \( m[1] \) is the lower limit on basis dimension. If knots are supplied, then the number of supplied knots should be \( k + m[1] + 1 \), and the range of the middle \( k-m[1]+1 \) knots should include all the covariate values. Alternatively, 2 knots can be supplied, denoting the lower and upper limits between which the spline can be evaluated (making this range too wide mean that there is no information about some basis coefficients, because the corresponding basis functions have a span that includes no data). Unlike P-splines, splines with derivative based penalties can have uneven knot spacing, without a problem.

Another option is to supply 4 knots. Then the outer 2 define the interval over which the penalty is to be evaluated, while the inner 2 define an interval within which all but the outermost 2 knots should lie. Normally the outer 2 knots would be the interval over which predictions might be required, while the inner 2 knots define the interval within which the data lie. This option allows the penalty to apply over a wider interval than the data, while still placing most of the basis functions where the data are. This is useful in situations in which it is necessary to extrapolate slightly with a smooth. Only applying the penalty over the interval containing the data amounts to a model in which the function could be less smooth outside the interval than within it, and leads to very wide extrapolation confidence intervals. However the alternative of evaluating the penalty over the whole real line amounts to asserting certainty that the function has some derivative zeroed away from the data, which is equally unreasonable. It is preferable to build a model in which the same smoothness assumptions apply over both data and extrapolation intervals, but not over the whole real line. See example code for practical illustration.

Linear extrapolation is used for prediction that requires extrapolation (i.e. prediction outside the range of the interior \( k-m[1]+1 \) knots — the interval over which the penalty is evaluated). Such extrapolation is not allowed in basis construction, but is when predicting.

It is possible to set a deriv flag in a smooth specification or smooth object, so that a model or prediction matrix produces the requested derivative of the spline, rather than evaluating it.

### Value

An object of class "Bspline.smooth". See `smooth.construct`, for the elements that this object will contain.

### WARNING

\( m[1] \) directly controls the spline order here, which is intuitively sensible, but different to other bases.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>. Extrapolation ideas joint with David Miller.

### References


### See Also

`p.spline`
Examples

```
require(mgcv)
set.seed(5)
dat <- gamSim(1,n=400,dist="normal",scale=2)
bs <- "bs"
## note the double penalty on the s(x2) term...
b <- gam(y~s(x0,bs=bs,m=c(4,2))+s(x1,bs=bs)+s(x2,k=15,bs=bs,m=c(4,3,0)) +
s(x3,bs=bs,m=c(1,0)),data=dat,method="REML")
plot(b,pages=1)

## Extrapolation example, illustrating the importance of considering
## the penalty carefully if extrapolating...

f3 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 * (10 * x)^3 *
    (1 - x)^4
## test function
n <- 100;x <- runif(n)
y <- f3(x) + rnorm(n)*2
## first a model with first order penalty over whole real line (red)
b0 <- gam(y~s(x,m=1,k=20),method="ML")
## now a model with first order penalty evaluated over (-.5,1.5) (black)
op <- options(warn=-1)
b <- gam(y~s(x,bs="bs",m=c(3,1),k=20),knots=list(x=c(-.5,0,1,1.5)),
          method="ML")
options(op)
## and the equivalent with same penalty over data range only (blue)

pd <- data.frame(x=seq(-.7,1.7,length=200))
fv <- predict(b,pd,se=TRUE)
ul <- fv$fit + fv$se.fit*2; ll <- fv$fit - fv$se.fit*2
plot(x,y,xlim=c(-.7,1.7),ylim=range(c(y,ll,ul)),main="Order 1 penalties: red tps; blue bs on (0,1); black bs on (-.5,1.5)"

## penalty defined on (-.5,1.5) gives plausible predictions and intervals
## over this range...
lines(pd$x,fv$fit);lines(pd$x,ul,lty=2);lines(pd$x,ll,lty=2)
fv <- predict(b0,pd,se=TRUE)
ul <- fv$fit + fv$se.fit*2; ll <- fv$fit - fv$se.fit*2
plot(x,y,xlim=c(-.7,1.7),ylim=range(c(y,ll,ul)),main="Order 1 penalties: red tps; blue bs on (0,1); black bs on (-.5,1.5)"

## penalty defined over whole real line gives constant width intervals away
## from data, as slope there must be zero, to avoid infinite penalty:
lines(pd$x,fv$fit,col=2)
lines(pd$x,ul,lty=2,col=2);lines(pd$x,ll,lty=2,col=2)
fv <- predict(b1,pd,se=TRUE)
ul <- fv$fit + fv$se.fit*2; ll <- fv$fit - fv$se.fit*2
## penalty defined on whole real line gives constant width intervals away
## from data, as slope there must be zero, to avoid infinite penalty:
lines(pd$x,fv$fit,col=2)
lines(pd$x,ul,lty=2,col=2);lines(pd$x,ll,lty=2,col=2)
fv <- predict(b1,pd,se=TRUE)
ul <- fv$fit + fv$se.fit*2; ll <- fv$fit - fv$se.fit*2
## penalty defined only over the data interval (0,1) gives wild and wide
## extrapolation since penalty has been `turned off' outside data range:
lines(pd$x,fv$fit,col=4)
lines(pd$x,ul,lty=2,col=4);lines(pd$x,ll,lty=2,col=4)

## construct smooth of x. Model matrix sm$X and penalty
## matrix sm$S[[1]] will have many zero entries...
x <- seq(0,1,length=100)
sm <- smoothCon(s(x,bs=bs"),data.frame(x))[[1]]

## another example checking penalty numerically...
m <- c(4,2); k <- 15; b <- runif(k)
sm <- smoothCon(s(x,bs=bs"),m=m,k=k),data.frame(x),
    scale.penalty=FALSE)[[1]]
sm$deriv <- m[2]
```
Penalized Cubic regression splines in GAMs

**Description**

`gam` can use univariate penalized cubic regression spline smooths, specified via terms like
`s(x, bs="cr")`. `s(x, bs="cs")` specifies a penalized cubic regression spline which has had its penalty modified to shrink towards zero at high enough smoothing parameters (as the smoothing parameter goes to infinity a normal cubic spline tends to a straight line.) `s(x, bs="cc")` specifies a cyclic penalized cubic regression spline smooth.

‘Cardinal’ spline bases are used: Wood (2017) sections 5.3.1 and 5.3.2 gives full details. These bases have very low setup costs. For a given basis dimension, k, they typically perform a little less well than thin plate regression splines, but a little better than p-splines. See `te` to use these bases in tensor product smooths of several variables.

Default `k` is 10.

**Usage**

```r
## S3 method for class 'cr.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'cs.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'cc.smooth.spec'
smooth.construct(object, data, knots)
```

**Arguments**

- `object`: a smooth specification object, usually generated by a term `s(..., bs="cr", ...), s(..., bs="cs", ...) or s(..., bs="cc", ...)`
- `data`: a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
knots       a list containing any knots supplied for basis setup — in same order and with same names as data. Can be NULL. See details.

Details
The constructor is not normally called directly, but is rather used internally by gam. To use for basis setup it is recommended to use smooth.construct2.

If they are not supplied then the knots of the spline are placed evenly throughout the covariate values to which the term refers: For example, if fitting 101 data with an 11 knot spline of x then there would be a knot at every 10th (ordered) x value. The parameterization used represents the spline in terms of its values at the knots. The values at neighbouring knots are connected by sections of cubic polynomial constrained to be continuous up to and including second derivative at the knots. The resulting curve is a natural cubic spline through the values at the knots (given two extra conditions specifying that the second derivative of the curve should be zero at the two end knots).

The shrinkage version of the smooth, eigen-decomposes the wiggliness penalty matrix, and sets its 2 zero eigenvalues to small multiples of the smallest strictly positive eigenvalue. The penalty is then set to the matrix with eigenvectors corresponding to those of the original penalty, but eigenvalues set to the perturbed versions. This penalty matrix has full rank and shrinks the curve to zero at high enough smoothing parameters.

Note that the cyclic smoother will wrap at the smallest and largest covariate values, unless knots are supplied. If only two knots are supplied then they are taken as the end points of the smoother (provided all the data lie between them), and the remaining knots are generated automatically.

The cyclic smooth is not subject to the condition that second derivatives go to zero at the first and last knots.

Value
An object of class "cr.smooth" "cs.smooth" or "cyclic.smooth". In addition to the usual elements of a smooth class documented under smooth.construct, this object will contain:

xp       giving the knot locations used to generate the basis.
F        For class "cr.smooth" and "cs.smooth" objects t(F) transforms function values at the knots to second derivatives at the knots.
BD       class "cyclic.smooth" objects include matrix BD which transforms function values at the knots to second derivatives at the knots.

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References

Examples
```r
## cyclic spline example...
require(mgcv)
set.seed(6)
x <- sort(runif(200)*10)
z <- runif(200)
```
f <- sin(x*2*pi/10)+.5
y <- rpois(exp(f),exp(f))

## finished simulating data, now fit model...
b <- gam(y ~ s(x,bs="cc",k=12) + s(z),family=poisson,
       knots=list(x=seq(0,10,length=12)))

## or more simply
b <- gam(y ~ s(x,bs="cc",k=12) + s(z),family=poisson,
       knots=list(x=c(0,10)))

## plot results...
par(mfrow=c(2,2))
plot(x,y);plot(b,select=1,shade=TRUE);lines(x,f-mean(f),col=2)
plot(b,select=2,shade=TRUE);plot(fitted(b),residuals(b))

smooth.construct.ds.smooth.spec

Low rank Duchon 1977 splines

Description

Thin plate spline smoothers are a special case of the isotropic splines discussed in Duchon (1977). A subset of this more general class can be invoked by terms like s(x,z,bs="ds",m=c(1,.5)) in a gam model formula. In the notation of Duchon (1977) m is given by m[1] (default value 2), while s is given by m[2] (default value 0).

Duchon’s (1977) construction generalizes the usual thin plate spline penalty as follows. The usual TPS penalty is given by the integral of the squared Euclidian norm of a vector of mixed partial mth order derivatives of the function w.r.t. its arguments. Duchon re-expresses this penalty in the Fourier domain, and then weights the squared norm in the integral by the Euclidean norm of the fourier frequencies, raised to the power 2s. s is a user selected constant taking integer values divided by 2. If d is the number of arguments of the smooth, then it is required that -d/2 < s < d/2. To obtain continuous functions we further require that m + s > d/2. If s=0 then the usual thin plate spline is recovered.

The construction is amenable to exactly the low rank approximation method given in Wood (2003) to thin plate splines, with similar optimality properties, so this approach to low rank smoothing is used here. For large datasets the same subsampling approach as is used in the tprs case is employed here to reduce computational costs.

These smoothers allow the use of lower orders of derivative in the penalty than conventional thin plate splines, while still yielding continuous functions. For example, we can set m = 1 and s = d/2 -.5 in order to use first derivative penalization for any d (which has the advantage that the dimension of the null space of unpenalized functions is only d+1).

Usage

## S3 method for class 'ds.smooth.spec'
smooth.construct(object, data, knots)

## S3 method for class 'duchon.spline'
Predict.matrix(object, data)
smooth.construct.ds.smooth.spec

Arguments

object 
a smooth specification object, usually generated by a term s(...,bs="ds", ...).

data 
a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.

knots 
a list containing any knots supplied for basis setup — in same order and with same names as data. Can be NULL.

Details

The default basis dimension for this class is \( k = M + k.\text{def} \) where \( M \) is the null space dimension (dimension of unpenalized function space) and \( k.\text{def} \) is 10 for dimension 1, 30 for dimension 2 and 100 for higher dimensions. This is essentially arbitrary, and should be checked, but as with all penalized regression smoothers, results are statistically insensitive to the exact choice, provided it is not so small that it forces oversmoothing (the smoother’s degrees of freedom are controlled primarily by its smoothing parameter).

The constructor is not normally called directly, but is rather used internally by \texttt{gam}. To use for basis setup it is recommended to use \texttt{smooth.construct2}.

For these classes the specification object will contain information on how to handle large datasets in their xt field. The default is to randomly subsample 2000 ‘knots’ from which to produce a reduced rank eigen approximation to the full basis, if the number of unique predictor variable combinations in excess of 2000. The default can be modified via the xt argument to \texttt{s}. This is supplied as a list with elements \texttt{max.knots} and \texttt{seed} containing a number to use in place of 2000, and the random number seed to use (either can be missing). Note that the random sampling will not effect the state of R’s RNG.

For these bases knots has two uses. Firstly, as mentioned already, for large datasets the calculation of the tp basis can be time-consuming. The user can retain most of the advantages of the approach by supplying a reduced set of covariate values from which to obtain the basis - typically the number of covariate values used will be substantially smaller than the number of data, and substantially larger than the basis dimension, \( k \). This approach is the one taken automatically if the number of unique covariate values (combinations) exceeds \texttt{max.knots}. The second possibility is to avoid the eigen-decomposition used to find the spline basis altogether and simply use the basis implied by the chosen knots: this will happen if the number of knots supplied matches the basis dimension, \( k \). For a given basis dimension the second option is faster, but gives poorer results (and the user must be quite careful in choosing knot locations).

Value

An object of class "duchon.spline". In addition to the usual elements of a smooth class documented under \texttt{smooth.construct}, this object will contain:

\begin{itemize}
  \item \texttt{shift} 
    A record of the shift applied to each covariate in order to center it around zero and avoid any co-linearity problems that might otherwise occur in the penalty null space basis of the term.
  \item \texttt{Xu} 
    A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).
  \item \texttt{UZ} 
    The matrix mapping the smoother parameters back to the parameters of a full Duchon spline.
\end{itemize}
null.space.dimension

The dimension of the space of functions that have zero wiggliness according to
the wiggliness penalty for this term.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

Duchon, J. (1977) Splines minimizing rotation-invariant semi-norms in Solobev spaces. in W.
Shemp and K. Zeller (eds) Construction theory of functions of several variables, 85-100, Springer,
Berlin.


See Also

Spherical.Spline

Examples

require(mgcv)
eg <- gamSim(2,n=200,scale=.05)
attach(eg)

op <- par(mfrow=c(2,2),mar=c(4,4,1,1))
b0 <- gam(y~s(x,z,bs="ds",m=c(2,0),k=50),data=data) ## tps
b <- gam(y~s(x,z,bs="ds",m=c(1,.5),k=50),data=data) ## first deriv penalty
b1 <- gam(y~s(x,z,bs="ds",m=c(2,.5),k=50),data=data) ## modified 2nd deriv

persp(truth$x,truth$z,truth$f,theta=30) ## truth
vis.gam(b0,theta=30)
vis.gam(b,theta=30)
vis.gam(b1,theta=30)

detach(eg)
smooth.construct.fs.smooth.spec

Usage

## S3 method for class 'fs.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'fs.interaction'
Predict.matrix(object, data)

Arguments

object
For the smooth.construct method a smooth specification object, usually generated by a term s(x,...,bs="fs",). May have a gamm attribute: see details. For the predict.Matrix method an object of class "fs.interaction" produced by the smooth.construct method.

data
a list containing just the data (including any by variable) required by this term, with names corresponding to object$term.

knots
a list containing any knots supplied for smooth basis setup.

Details

This class produces a smooth for each level of a single factor variable. Within a gam formula this is done with something like s(x,fac,bs="fs"), which is almost equivalent to s(x,by=fac, id=1) (with the gam argument select=TRUE). The terms are fully penalized, with separate penalties on each null space component: for this reason they are not centred (no sum-to-zero constraint).

The class is particularly useful for use with gamm, where estimation efficiently exploits the nesting of the smooth within the factor. Note however that: i) gamm only allows one conditioning factor for smooths, so s(x)+s(z,fac,bs="fs")+s(v,fac,bs="fs") is OK, but s(x)+s(z,fac1,bs="fs")+s(v,fac2,bs="fs") is not; ii) all additional random effects and correlation structures will be treated as nested within the factor of the smooth factor interaction. To facilitate this the constructor is called from gamm with an attribute "gamm" attached to the smooth specification object. The result differs from that resulting from the case where this is not done.

Note that gamm4 from the gamm4 package suffers from none of the restrictions that apply to gamm, and "fs" terms can be used without side-effects. Constructor is still called with a smooth specification object having a "gamm" attribute.

Any singly penalized basis can be used to smooth at each factor level. The default is "tp", but alternatives can be supplied in the xt argument of s (e.g. s(x,fac,bs="fs",xt="cr") or s(x,fac,bs="fs",xt=list(bs="cr")). The k argument to s(...,bs="fs") refers to the basis dimension to use for each level of the factor variable.

Note one computational bottleneck: currently gamm (or gamm4) will produce the full posterior covariance matrix for the smooths, including the smooths at each level of the factor. This matrix can get large and computationally costly if there are more than a few hundred levels of the factor. Even at one or two hundred levels, care should be taken to keep down k.

The plot method for this class has two schemes. scheme==0 is in colour, while scheme==1 is black and white.

Value

An object of class "fs.interaction" or a matrix mapping the coefficients of the factor smooth interaction to the smooths themselves. The contents of an "fs.interaction" object will depend on whether or not smooth.construct was called with an object with attribute gamm: see below.
Author(s)
Simon N. Wood <simon.wood@r-project.org> with input from Matteo Fasiolo.

See Also
factor.smooth, gamm, smooth.construct.sz.smooth.spec

Examples

library(mgcv)
set.seed(0)
## simulate data...
f0 <- function(x) 2 * sin(pi * x)
f1 <- function(x,a=2,b=-1) exp(a * x)+b
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
    (10 * x)^3 * (1 - x)^10
n <- 500; nf <- 25
fac <- sample(1:nf,n,replace=TRUE)
x0 <- runif(n); x1 <- runif(n); x2 <- runif(n)
a <- rnorm(nf)*.2 + 2; b <- rnorm(nf)*.5
f <- f0(x0) + f1(x1,a[fac],b[fac]) + f2(x2)
fac <- factor(fac)
y <- f + rnorm(n)*2
## so response depends on global smooths of x0 and
## x2, and a smooth of x1 for each level of fac.
## fit model...
bm <- gamm(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20))
plot(bm$gam,pages=1)
summary(bm$gam)
## Also efficient using bam(..., discrete=TRUE)
bd <- bam(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20),discrete=TRUE)
plot(bd,pages=1)
summary(bd)
## Could also use...
## b <- gam(y~s(x0)+ s(x1,fac,bs="fs",k=5)+s(x2,k=20),method="ML")
## ... but its slower (increasingly so with increasing nf)
## b <- gam(y~s(x0)+ t2(x1,fac,bs=c("tp","re"),k=5,full=TRUE)+
##    s(x2,k=20),method="ML")
## ... is exactly equivalent.

---

smooth.construct.gp.smooth.spec

Low rank Gaussian process smooths

Description

Gaussian process/kriging models based on simple covariance functions can be written in a very similar form to thin plate and Duchon spline models (e.g. Handcock, Meier, Nychka, 1994), and low rank versions produced by the eigen approximation method of Wood (2003). Kammann and Wand (2003) suggest a particularly simple form of the Matern covariance function with only a single smoothing parameter to estimate, and this class implements this and other similar models.
smooth.construct.gp.smooth.spec

Usually invoked by an `s(...,bs="gp")` term in a `gam` formula. Argument `m` selects the covariance function, sets the range parameter and any power parameter. If `m` is not supplied then it defaults to `NA` and the covariance function suggested by Kammann and Wand (2003) along with their suggested range parameter is used. Otherwise `abs(m[1])` between 1 and 5 selects the correlation function from respectively, spherical, power exponential, and Matern with kappa = 1.5, 2.5 or 3.5. The sign of `m[1]` determines whether a linear trend in the covariates is added to the Gaussian process (positive), or not (negative). The latter ensures stationarity. `m[2]`, if present, specifies the range parameter, with non-positive or absent indicating that the Kammann and Wand estimate should be used. `m[3]` can be used to specify the power for the power exponential which otherwise defaults to 1.

Usage

```r
## S3 method for class 'gp.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'gp.smooth'
Predict.matrix(object, data)
```

Arguments

- `object`: a smooth specification object, usually generated by a term `s(...,bs="ms",...)`.
- `data`: a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
- `knots`: a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`

Details

Let \( \rho > 0 \) be the range parameter, \( 0 < \kappa \leq 2 \) and \( d \) denote the distance between two points. Then the correlation functions indexed by `m[1]` are:

1. \( 1 - 1.5d/\rho + 0.5(d/\rho)^3 \) if \( d \leq \rho \) and 0 otherwise.
2. \( \exp(-(d/\rho)^\kappa) \).
3. \( \exp(-(d/\rho)(1 + d/\rho)) \).
4. \( \exp(-(d/\rho)(1 + d/\rho + (d/\rho)^2/3)) \).
5. \( \exp(-(d/\rho)(1 + d/\rho + 2(d/\rho)^2/5 + (d/\rho)^3/15)) \).

See Fahrmeir et al. (2013) section 8.1.6, for example. Note that setting \( r \) to too small a value will lead to unpleasant results, as most points become all but independent (especially for the spherical model. Note: Wood 2017, Figure 5.20 right is based on a buggy implementation).

The default basis dimension for this class is \( k=M+k.def \) where \( M \) is the null space dimension (dimension of unpenalized function space) and \( k.def \) is 10 for dimension 1, 30 for dimension 2 and 100 for higher dimensions. This is essentially arbitrary, and should be checked, but as with all penalized regression smoothers, results are statistically insensitive to the exact choice, provided it is not so small that it forces oversmoothing (the smoother’s degrees of freedom are controlled primarily by its smoothing parameter).

The constructor is not normally called directly, but is rather used internally by `gam`. To use for basis setup it is recommended to use `smooth.construct2`. 
For these classes the specification object will contain information on how to handle large datasets in their xt field. The default is to randomly subsample 2000 'knots' from which to produce a reduced rank eigen approximation to the full basis, if the number of unique predictor variable combinations in excess of 2000. The default can be modified via the xt argument to s. This is supplied as a list with elements max.knots and seed containing a number to use in place of 2000, and the random number seed to use (either can be missing). Note that the random sampling will not effect the state of R's RNG.

For these bases knots has two uses. Firstly, as mentioned already, for large datasets the calculation of the tp basis can be time-consuming. The user can retain most of the advantages of the approach by supplying a reduced set of covariate values from which to obtain the basis - typically the number of covariate values used will be substantially smaller than the number of data, and substantially larger than the basis dimension, k. This approach is the one taken automatically if the number of unique covariate values (combinations) exceeds max.knots. The second possibility is to avoid the eigen-decomposition used to find the spline basis altogether and simply use the basis implied by the chosen knots: this will happen if the number of knots supplied matches the basis dimension, k. For a given basis dimension the second option is faster, but gives poorer results (and the user must be quite careful in choosing knot locations).

Value

An object of class "gp.smooth". In addition to the usual elements of a smooth class documented under smooth.construct, this object will contain:

- shift: A record of the shift applied to each covariate in order to center it around zero and avoid any co-linearity problems that might otherwise occur in the penalty null space basis of the term.
- Xu: A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).
- UZ: The matrix mapping the smoother parameters back to the parameters of a full GF smooth.
- null.space.dimension: The dimension of the space of functions that have zero wiggliness according to the wiggliness penalty for this term.
- gp.defn: the type, range parameter and power parameter defining the correlation function.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

tprs
Examples

```r
require(mgcv)
eg <- gamSim(2,n=200, scale=.05)
attach(eg)
op <- par(mfrow=c(2,2), mar=c(4,4,1,1))
b0 <- gam(y~s(x,z,k=50),data=data)  ## tps
b <- gam(y~s(x,z,bs="gp",k=50),data=data)  ## Matern spline default range
b1 <- gam(y~s(x,z,bs="gp",k=50,m=c(1,.5)),data=data)  ## spherical
persp(truth$x,truth$z,truth$f,theta=30)  ## truth
vis.gam(b0,theta=30)
vis.gam(b,theta=30)
vis.gam(b1,theta=30)

## compare non-stationary (b1) and stationary (b2)
b2 <- gam(y~s(x,z,bs="gp",k=50,m=c(-1,.5)),data=data)  ## sph stationary
vis.gam(b1,theta=30);vis.gam(b2,theta=30)
x <- seq(-1,2,length=200); z <- rep(.5,200)
pd <- data.frame(x=x,z=z)
plot(x,predict(b1,pd),type="l");lines(x,predict(b2,pd),col=2)
abline(v=c(0,1))
plot(predict(b1),predict(b2))
detach(eg)
```

smooth.construct.mrf.smooth.spec

Markov Random Field Smooths

Description

For data observed over discrete spatial units, a simple Markov random field smoother is sometimes appropriate. These functions provide such a smoother class for mgcv. See details for how to deal with regions with missing data.

Usage

```r
## S3 method for class 'mrf.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'mrf.smooth'
Predict.matrix(object, data)
```

Arguments

- **object**: For the smooth.construct method a smooth specification object, usually generated by a term `s(x,...,bs="mrf",xt=list(polys=foo))`. `x` is a factor variable giving labels for geographic districts, and the `xt` argument is obligatory: see details. For the Predict.Matrix method an object of class "mrf.smooth" produced by the smooth.construct method.

- **data**: a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
If there are more geographic areas than data were observed for, then this argument is used to provide the labels for all the areas (observed and unobserved).

Details

A Markov random field smooth over a set of discrete areas is defined using a set of area labels, and a neighbourhood structure for the areas. The covariate of the smooth is the vector of area labels corresponding to each observation. This covariate should be a factor, or capable of being coerced to a factor.

The neighbourhood structure is supplied in the xt argument to s. This must contain at least one of the elements polys, nb or penalty.

polys contains the polygons defining the geographic areas. It is a list with as many elements as there are geographic areas. names(polys) must correspond to the levels of the argument of the smooth, in any order (i.e. it gives the area labels). polys[[i]] is a 2 column matrix the rows of which specify the vertices of the polygon(s) defining the boundary of the ith area.

A boundary may be made up of several closed loops: these must be separated by NA rows. A polygon within another is treated as a hole. The first polygon in any polys[[i]] should not be a hole. An example of the structure is provided by columb.polys (which contains an artificial hole in its second element, for illustration). Any list elements with duplicate names are combined into a single NA separated matrix.

Plotting of the smooth is not possible without a polys object.

If polys is the only element of xt provided, then the neighbourhood structure is computed from it automatically. To count as neighbours, polygons must exactly share one or more vertices.

nb is a named list defining the neighbourhood structure. names(nb) must correspond to the levels of the covariate of the smooth (i.e. the area labels), but can be in any order. nb[[i]] is a numeric vector indexing the neighbours of the ith area (and should not include i). All indices are relative to nb itself, but can be translated using names(nb). See example code. As an alternative each nb[[i]] can be an array of the names of the neighbours, but these will be converted to the arrays of numeric indices internally.

If no penalty is provided then it is computed automatically from this list. The ith row of the penalty matrix will be zero everwhere, except in the ith column, which will contain the number of neighbours of the ith geographic area, and the columns corresponding to those geographic neighbours, which will each contain -1.

penalty if this is supplied, then it is used as the penalty matrix. It should be positive semi-definite. Its row and column names should correspond to the levels of the covariate.

If no basis dimension is supplied then the constructor produces a full rank MRF, with a coefficient for each geographic area. Otherwise a low rank approximation is obtained based on truncation of the parameterization given in Wood (2017) Section 5.4.2. See Wood (2017, section 5.8.1).

Note that smooths of this class have a built in plot method, and that the utility function in.out can be useful for working with discrete area data. The plot method has two schemes, scheme==0 is colour, scheme==1 is grey scale.

The situation in which there are areas with no data requires special handling. You should set drop.unused.levels=FALSE in the model fitting function, gam, bam or gamm, having first ensured that any fixed effect factors do not contain unobserved levels. Also make sure that the basis dimension is set to ensure that the total number of coefficients is less than the number of observations.

Value

An object of class "mrf.smooth" or a matrix mapping the coefficients of the MRF smooth to the predictions for the areas listed in data.
Author(s)

Simon N. Wood <simon.wood@r-project.org> and Thomas Kneib (Fabian Scheipl prototyped the low rank MRF idea)

References


See Also

in.out, polys.plot

Examples

library(mgcv)
## Load Columbus Ohio crime data (see ?columbus for details and credits)
data(columb) ## data frame
data(columb.polys) ## district shapes list
xt <- list(polys=columb.polys) ## neighbourhood structure info for MRF
par(mfrow=c(2,2))
## First a full rank MRF...
b <- gam(crime ~ s(district,bs="mrf",xt=xt),data=columb,method="REML")
plot(b,scheme=1)
## Compare to reduced rank version...
b <- gam(crime ~ s(district,bs="mrf",k=20,xt=xt),data=columb,method="REML")
plot(b,scheme=1)
## An important covariate added...
b <- gam(crime ~ s(district,bs="mrf",k=20,xt=xt)+s(income),
data=columb,method="REML")
plot(b,scheme=c(0,1))
## plot fitted values by district
par(mfrow=c(1,1))
fv <- fitted(b)
names(fv) <- as.character(columb$district)
polys.plot(columb.polys,fv)

## Examine an example neighbourhood list - this one auto-generated from
## 'polys' above.

nb <- b$smooth[[1]]$xt$nb
head(nb)
names(nb) ## these have to match the factor levels of the smooth
## look at the indices of the neighbours of the first entry,
## named '0'...
nb[[0]] ## by name
nb[[1]] ## same by index
## ... and get the names of these neighbours from their indices...
names(nb)[nb[[0]]]
b1 <- gam(crime ~ s(district,bs="mrf",k=20,xt=list(nb=nb))+s(income),
data=columb,method="REML")
b1 ## fit unchanged
plot(b1) ## but now there is no information with which to plot the mrf
P-splines in GAMs

Description

`gam` can use univariate P-splines as proposed by Eilers and Marx (1996), specified via terms like `s(x,bs="ps")`. These terms use B-spline bases penalized by discrete penalties applied directly to the basis coefficients. Cyclic P-splines are specified by model terms like `s(x,bs="cp",...)`. These bases can be used in tensor product smooths (see `te`).

The advantage of P-splines is the flexible way that penalty and basis order can be mixed (but see also `d.spline`). This often provides a useful way of 'taming' an otherwise poorly behave smooth. However, in regular use, splines with derivative based penalties (e.g. "tp" or "cr" bases) tend to result in slightly better MSE performance, presumably because the good approximation theoretic properties of splines are rather closely connected to the use of derivative penalties.

Usage

```r
## S3 method for class 'ps.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'cp.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

- `object`: a smooth specification object, usually generated by a term `s(x,bs="ps",...)` or `s(x,bs="cp",...)`
- `data`: a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
- `knots`: a list containing any knots supplied for basis setup — in same order and with same names as data. Can be `NULL`. See details for further information.

Details

A smooth term of the form `s(x,bs="ps",m=c(2,3))` specifies a 2nd order P-spline basis (cubic spline), with a third order difference penalty (0th order is a ridge penalty) on the coefficients. If `m` is a single number then it is taken as the basis order and penalty order. The default is the 'cubic spline like' `m=c(2,2)`.

The default basis dimension, `k`, is the larger of 10 and `m[1]+1` for a "ps" terms and the larger of 10 and `m[1]` for a "cp" term. `m[1]+1` and `m[1]` are the lower limits on basis dimension for the two types.

If knots are supplied, then the number of knots should be one more than the basis dimension (i.e. `k+1`) for a "cp" smooth. For the "ps" basis the number of supplied knots should be `k + m[1] + 2`, and the range of the middle `k-m[1]` knots should include all the covariate values. See example.

Alternatively, for both types of smooth, 2 knots can be supplied, denoting the lower and upper limits between which the spline can be evaluated (Don’t make this range too wide, however, or you can end up with no information about some basis coefficients, because the corresponding basis functions
have a span that includes no data!). Note that P-splines don’t make much sense with uneven knot spacing.

Linear extrapolation is used for prediction that requires extrapolation (i.e. prediction outside the range of the interior \(k - m[1]\) knots). Such extrapolation is not allowed in basis construction, but is when predicting.

For the "ps" basis it is possible to set flags in the smooth specification object, requesting setup according to the SCOP-spline monotonic smoother construction of Pya and Wood (2015). As yet this is not supported by any modelling functions in \texttt{mgcv} (see package \texttt{scam}). Similarly it is possible to set a deriv flag in a smooth specification or smooth object, so that a model or prediction matrix produces the requested derivative of the spline, rather than evaluating it. See examples below.

**Value**

An object of class "pspline.smooth" or "cp.smooth". See \texttt{smooth.construct}, for the elements that this object will contain.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**


**See Also**

\texttt{cSplineDes}, \texttt{adaptive.smooth}, \texttt{d.spline}

**Examples**

```r
## see ?gam
## cyclic example ...
require(mgcv)
set.seed(6)
x <- sort(runif(200)*10)
z <- runif(200)
f <- sin(x*2*pi/10)+.5
y <- rpois(exp(f),exp(f))

## finished simulating data, now fit model...
b <- gam(y ~ s(x,bs="cp") + s(z,bs="ps"),family=poisson)

## example with supplied knot ranges for x and z (can do just one)
b <- gam(y ~ s(x,bs="cp") + s(z,bs="ps"),family=poisson,
      knots=list(x=c(0,10),z=c(0,1)))

## example with supplied knots...
bk <- gam(y ~ s(x,bs="cp",k=12) + s(z,bs="ps",k=13),family=poisson,
      knots=list(x=seq(0,10,length=13),z=(-3):13/10))

## plot results...
```
par(mfrow=c(2,2))
plot(b, select=1, shade=TRUE); lines(x, f-mean(f), col=2)
plot(b, select=2, shade=TRUE); lines(z, 0*z, col=2)
plot(bk, select=1, shade=TRUE); lines(x, f-mean(f), col=2)
plot(bk, select=2, shade=TRUE); lines(z, 0*z, col=2)

## Example using monotonic constraints via the SCOP-spline
## construction, and of computing derivatives...
x <- seq(0,1,length=100); dat <- data.frame(x)
sspec <- s(x, bs="ps")
sspec$mono <- 1
sm <- smoothCon(sspec, dat)[[1]]
sm$deriv <- 1
Xd <- PredictMat(sm, dat)

## generate random coefficients in the unconstrained
## parameterization...
b <- runif(10)*3-2.5
## exponentiate those parameters indicated by sm$g.index
## to obtain coefficients meeting the constraints...
b[sm$g.index] <- exp(b[sm$g.index])

## plot monotonic spline and its derivative
par(mfrow=c(2,2))
plot(x, sm$X%*%b, type="l", ylab="f(x)"
plot(x, Xd%*%b, type="l", ylab="f'(x)"

## repeat for decrease...
sspec$mono <- -1
sm1 <- smoothCon(sspec, dat)[[1]]
sm1$deriv <- 1
Xd1 <- PredictMat(sm1, dat)
plot(x, sm1$X%*%b, type="l", ylab="f(x)"
plot(x, Xd1%*%b, type="l", ylab="f'(x)"

## Now with sum to zero constraints as well...
sspec$mono <- -1
sm <- smoothCon(sspec, dat, absorb.cons=TRUE)[[1]]
sm$deriv <- 1
Xd <- PredictMat(sm, dat)
b <- b[-1] ## dropping first param
plot(x, sm$X%*%b, type="l", ylab="f(x)"
plot(x, Xd%*%b, type="l", ylab="f'(x)"

sspec$mono <- -1
sm1 <- smoothCon(sspec, dat, absorb.cons=TRUE)[[1]]
sm1$deriv <- 1
Xd1 <- PredictMat(sm1, dat)
plot(x, sm1$X%*%b, type="l", ylab="f(x)"
plot(x, Xd1%*%b, type="l", ylab="f'(x)"

---

smooth.construct.re.smooth.spec

*Simple random effects in GAMs*
smooth.construct.re.smooth.spec

Description

gam can deal with simple independent random effects, by exploiting the link between smooths and random effects to treat random effects as smooths. \( s(x, \text{bs}=\text{"re"}) \) implements this. Such terms can have any number of predictors, which can be any mixture of numeric or factor variables. The terms produce a parametric interaction of the predictors, and penalize the corresponding coefficients with a multiple of the identity matrix, corresponding to an assumption of i.i.d. normality. See details.

Usage

## S3 method for class 're.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'random.effect'
Predict.matrix(object, data)

Arguments

object
For the smooth.construct method a smooth specification object, usually generated by a term \( s(x, \ldots, \text{bs}=\text{"re"},) \). For the predict.Matrix method an object of class "random.effect" produced by the smooth.construct method.

data
a list containing just the data (including any by variable) required by this term, with names corresponding to object$term (and object$by). The by variable is the last element.

knots
generically a list containing any knots supplied for basis setup — unused at present.

Details

Exactly how the random effects are implemented is best seen by example. Consider the model term \( s(x,z, \text{bs}=\text{"re"}) \). This will result in the model matrix component corresponding to \( ~x:z-1 \) being added to the model matrix for the whole model. The coefficients associated with the model matrix component are assumed i.i.d. normal, with unknown variance (to be estimated). This assumption is equivalent to an identity penalty matrix (i.e. a ridge penalty) on the coefficients. Because such a penalty is full rank, random effects terms do not require centering constraints.

If the nature of the random effect specification is not clear, consider a couple more examples: \( s(x, \text{bs}=\text{"re"}) \) results in \( \text{model.matrix}(~x-1) \) being appended to the overall model matrix, while \( s(x,v,w, \text{bs}=\text{"re"}) \) would result in \( \text{model.matrix}(~x:v:w-1) \) being appended to the model matrix. In both cases the corresponding model coefficients are assumed i.i.d. normal, and are hence subject to ridge penalties.

Some models require differences between the coefficients corresponding to different levels of the same random effect. See \texttt{linear.functional.terms} for how to implement this.

If the random effect precision matrix is of the form \( \sum_j \lambda_j S_j \) for known matrices \( S_j \) and unknown parameters \( \lambda_j \), then a list containing the \( S_j \) can be supplied in the \texttt{xt} argument of \texttt{s}. In this case an array rank should also be supplied in \texttt{xt} giving the ranks of the \( S_j \) matrices. See simple example below.

Note that smooth ids are not supported for random effect terms. Unlike most smooth terms, side conditions are never applied to random effect terms in the event of nesting (since they are identifiable without side conditions).

Random effects implemented in this way do not exploit the sparse structure of many random effects, and may therefore be relatively inefficient for models with large numbers of random effects, when
gamm4 or gamm may be better alternatives. Note also that gam will not support models with more coefficients than data.

The situation in which factor variable random effects intentionally have unobserved levels requires special handling. You should set drop.unused.levels=FALSE in the model fitting function, gamm, bam or gamm, having first ensured that any fixed effect factors do not contain unobserved levels.

The implementation is designed so that supplying random effect factor levels to predict.gam that were not levels of the factor when fitting, will result in the corresponding random effect (or interactions involving it) being set to zero (with zero standard error) for prediction. See random.effects for an example. This is achieved by the Predict.matrix method zeroing any rows of the prediction matrix involving factors that are NA. predict.gam will set any factor observation to NA if it is a level not present in the fit data.

Value

An object of class "random.effect" or a matrix mapping the coefficients of the random effect to the random effects themselves.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

gam.vcomp, gamm

Examples

## see ?gam.vcomp

require(mgcv)
## simulate simple random effect example
set.seed(4)
nb <- 50; n <- 400
b <- rnorm(nb)*2 ## random effect
r <- sample(1:nb,n,replace=TRUE) ## r.e. levels
y <- 2 + b[r] + rnorm(n)
r <- factor(r)
## fit model....
b <- gam(y ~ s(r,bs="re"),method="REML")
gam.vcomp(b)

## example with supplied precision matrices...
b <- c(rnorm(nb/2)*2,rnorm(nb/2)*.5) ## random effect now with 2 variances
r <- sample(1:nb,n,replace=TRUE) ## r.e. levels
y <- 2 + b[r] + rnorm(n)
r <- factor(r)
## known precision matrix components...
S <- list(diag(rep(c(1,0),each=nb/2)), diag(rep(c(0,1),each=nb/2)))
b <- gam(y ~ s(r,bs="re"),xt=list(S=S,rank=c(nb/2,nb/2)),method="REML")
gam.vcomp(b)
Description

Sets up basis functions and wiggliness penalties for soap film smoothers (Wood, Bravington and Hedley, 2008). Soap film smoothers are based on the idea of constructing a 2-D smooth as a film of soap connecting a smoothly varying closed boundary. Unless smoothing very heavily, the film is distorted towards the data. The smooths are designed not to smooth across boundary features (peninsulas, for example).

The so version sets up the full smooth. The sf version sets up just the boundary interpolating soap film, while the sw version sets up the wiggly component of a soap film (zero on the boundary). The latter two are useful for forming tensor products with soap films, and can be used with gamm and gamm4. To use these to simply set up a basis, then call via the wrapper smooth.construct2 or smoothCon.

Usage

## S3 method for class 'so.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'sf.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'sw.smooth.spec'
smooth.construct(object, data, knots)

Arguments

object A smooth specification object as produced by a s(....,bs="so",xt=list(bnd=bnd,...)) term in a gam formula. Note that the xt argument to s *must* be supplied, and should be a list, containing at least a boundary specification list (see details). xt may also contain various options controlling the boundary smooth (see details), and PDE solution grid. The dimension of the bases for boundary loops is specified via the k argument of s, either as a single number to be used for each boundary loop, or as a vector of different basis dimensions for the various boundary loops.

data A list or data frame containing the arguments of the smooth.

knots list or data frame with two named columns specifying the knot locations within the boundary. The column names should match the names of the arguments of the smooth. The number of knots defines the *interior* basis dimension (i.e. it is *not* supplied via argument k of s).

Details

For soap film smooths the following *must* be supplied:

- k the basis dimension for each boundary loop smooth.
- xt$bnd the boundary specification for the smooth.
smooth.construct.so.smooth.spec

• knots the locations of the interior knots for the smooth.

When used in a GAM then k and xt are supplied via s while knots are supplied in the knots argument of gam.

The bnd element of the xt list is a list of lists (or data frames), specifying the loops that define the boundary. Each boundary loop list must contain 2 columns giving the co-ordinates of points defining a boundary loop (when joined sequentially by line segments). Loops should not intersect (not checked). A point is deemed to be in the region of interest if it is interior to an odd number of boundary loops. Each boundary loop list may also contain a column f giving known boundary conditions on a loop.

The bndSpec element of xt, if non-NULL, should contain

• bs the type of cyclic smoothing basis to use: one of "cc" and "cp". If not "cc" then a cyclic p-spline is used, and argument m must be supplied.
• knot.space set to "even" to get even knot spacing with the "cc" basis.
• m 1 or 2 element array specifying order of "cp" basis and penalty.

Currently the code will not deal with more than one level of nesting of loops, or with separate loops without an outer enclosing loop: if there are known boundary conditions (identifiability constraints get awkward).

Note that the function locator provides a simple means for defining boundaries graphically, using something like bnd <- as.data.frame(locator(type="l")), after producing a plot of the domain of interest (right click to stop). If the real boundary is very complicated, it is probably better to use a simpler smooth boundary enclosing the true boundary, which represents the major boundary features that you don’t want to smooth across, but doesn’t follow every tiny detail.

Model set up, and prediction, involves evaluating basis functions which are defined as the solution to PDEs. The PDEs are solved numerically on a grid using sparse matrix methods, with bilinear interpolation used to obtain values at any location within the smoothing domain. The dimension of the PDE solution grid can be controlled via element nmax (default 200) of the list supplied as argument xt of s in a gam formula: it gives the number of cells to use on the longest grid side.

A little theory: the soap film smooth \( f(x, y) \) is defined as the solution of

\[
\frac{\partial^2 f}{\partial x^2} + \frac{\partial^2 f}{\partial y^2} = g
\]

subject to the condition that \( f = s \), on the boundary curve, where \( s \) is a smooth function (usually a cyclic penalized regression spline). The function \( g \) is defined as the solution of

\[
\frac{\partial^2 g}{\partial x^2} + \frac{\partial^2 g}{\partial y^2} = 0
\]

where \( g = 0 \) on the boundary curve and \( g(x_k, y_k) = c_k \) at the ‘knots’ of the surface; the \( c_k \) are model coefficients.

In the simplest case, estimation of the coefficients of \( f \) (boundary coefficients plus \( c_k \’s \)) is by minimization of

\[
\|z - f\|^2 + \lambda_s J_s(s) + \lambda_f J_f(f)
\]

where \( J_s \) is usually some cubic spline type wiggliness penalty on the boundary smooth and \( J_f \) is the integral of \((f_x x + f_y y)^2\) over the interior of the boundary. Both penalties can be expressed as quadratic forms in the model coefficients. The \( \lambda \)’s are smoothing parameters, selectable by GCV, REML, AIC, etc. \( z \) represents noisy observations of \( f \).
Value

A list with all the elements of object plus

- **sd** A list defining the PDE solution grid and domain boundary, and including the sparse LU factorization of the PDE coefficient matrix.
- **X** The model matrix: this will have an "offset" attribute, if there are any known boundary conditions.
- **S** List of smoothing penalty matrices (in smallest non-zero submatrix form).
- **irng** A vector of scaling factors that have been applied to the model matrix, to ensure nice conditioning.

In addition there are all the elements usually added by smooth.construct methods.

WARNINGS

Soap film smooths are quite specialized, and require more setup than most smoothers (e.g. you have to supply the boundary and the interior knots, plus the boundary smooth basis dimension(s)). It is worth looking at the reference.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


https://www.maths.ed.ac.uk/~swood34/

See Also

Predict.matrix.soap.film

Examples

```r
require(mgcv)

# simple test function...

fsb <- list(fs.boundary())
nmax <- 100

knots <- data.frame(v=rep(seq(-.5,3,by=.5),4),
                    w=rep(c(-.6,-.3,.3,.6),rep(8,4)))

set.seed(0)
n <- 600
v <- runif(n)*5-1; w <- runif(n)*2-1
y <- fs.test(v, w, b=1)
names(fsb[[1]]) <- c("v", "w")
ind <- inside(fsb, x=v, y=w) ## remove outsiders
y <- y + rnorm(n)*.3 ## add noise
```
y <- y[ind]; v <- v[ind]; w <- w[ind]
n <- length(y)

par(mfrow=c(3,2))
## plot boundary with knot and data locations
plot(fsb[[1]]$v,fsb[[1]]$w,type="l");points(knots,pch=20,col=2)
points(v,w,pch=".");

## Now fit the soap film smoother. 'k' is dimension of boundary smooth.
## boundary supplied in 'xt', and knots in 'knots'

nmax <- 100 ## reduced from default for speed.
b <- gam(y~s(v,w,k=30,bs="so",xt=list(bnd=fsb,nmax=nmax)),knots=knots)

plot(b) ## default plot
plot(b,scheme=1)
plot(b,scheme=2)
plot(b,scheme=3)

vis.gam(b,plot.type="contour")

# Fit same model in two parts...
par(mfrow=c(2,2))
vis.gam(b,plot.type="contour")
b1 <- gam(y~s(v,w,k=30,bs="sf",xt=list(bnd=fsb,nmax=nmax))+s(v,w,k=30,bs="sw",xt=list(bnd=fsb,nmax=nmax)),knots=knots)
vis.gam(b1,plot.type="contour")
plot(b1)

# Now an example with known boundary condition...

# Evaluate known boundary condition at boundary nodes...
fsb[[1]]$f <- fs.test(fsb[[1]]$v,fsb[[1]]$w,b=1,exclude=FALSE)

# Now fit the smooth...
bk <- gam(y~s(v,w,bs="so",xt=list(bnd=fsb,nmax=nmax)),knots=knots)
plot(bk) ## default plot

# tensor product example...
set.seed(9)
n <- 10000
v <- runif(n)*5-1;w<-runif(n)*2-1
t <- runif(n)
y <- fs.test(v,w,b=1)
y <- y + 4.2
y <- y^.5+t
fsb <- list(fs.boundary())
names(fsb[[1]]) <- c("v","w")
```
ind <- inSide(fsb,x=v,y=w) ## remove outsiders
y <- y[ind]; v <- v[ind]; w <- w[ind]; t <- t[ind]
n <- length(y)
y <- y + rnorm(n)*.05 ## add noise
knots <- data.frame(v=rep(seq(-.5,3,by=.5),4),
w=rep(c(-.6,-.3,.3,.6),rep(8,4)))
## notice NULL element in 'xt' list - to indicate no xt object for "cr" basis...
bk <- gam(y~ te(v,w,t,bs=c("sf","cr"),k=c(25,4),d=c(2,1),
xt=list(list(bnd=fsb,nmax=nmax),NULL))+
te(v,w,t,bs=c("sw","cr"),k=c(25,4),d=c(2,1),
xt=list(list(bnd=fsb,nmax=nmax),NULL)),knots=knots)
par(mfrow=c(3,2))
m<-100;n<-50
xm <- seq(-1,3.5,length=m);yn<-seq(-1,1,length=n)
xx <- rep(xm,n);yy<-rep(yn,rep(m,n))
tru <- matrix(fs.test(xx,yy),m,n)+4.2 ## truth
image(xm,yn,tru^.5,col=heat.colors(100),xlab="v",ylab="w",
main="truth")
lines(fsb[[1]]$v,fsb[[1]]$w,lwd=3)
contour(xm,yn,tru^.5,add=TRUE)
vis.gam(bk,view=c("v","w"),cond=list(t=0),plot.type="contour")
image(xm,yn,tru,col=heat.colors(100),xlab="v",ylab="w",
main="truth")
lines(fsb[[1]]$v,fsb[[1]]$w,1w=3)
contour(xm,yn,tru,add=TRUE)
vis.gam(bk,view=c("v","w"),cond=list(t=.5),plot.type="contour")
image(xm,yn,tru^1.5,col=heat.colors(100),xlab="v",ylab="w",
main="truth")
lines(fsb[[1]]$v,fsb[[1]]$w,1w=3)
contour(xm,yn,tru^1.5,add=TRUE)
vis.gam(bk,view=c("v","w"),cond=list(t=1),plot.type="contour")

########################################################################
# nested boundary example...
########################################################################

bnd <- list(list(x=0,y=0),list(x=0,y=0))
seq(0,2*pi,length=100) -> theta
bnd[[1]]$x <- sin(theta);bnd[[1]]$y <- cos(theta)
bnd[[2]]$x <- -.3 + .3*sin(theta);
bnd[[2]]$y <- -.3 + .3*cos(theta)
plot(bnd[[1]]$x,bnd[[1]]$y,type="l")
lines(bnd[[2]]$x,bnd[[2]]$y)
## setup knots
k <- 8
xm <- seq(-1,1,length=k);ym <- seq(-1,1,length=k)
x=rep(xm,k);y=rep(ym,rep(k,k))
```
ind <- inSide(bnd,x,y)
knots <- data.frame(x=x[ind],y=y[ind])
points(knots$x,knots$y)

## a test function
f1 <- function(x,y) {
  exp(-(x-.3)^2-(y-.3)^2)
}

## plot the test function within the domain
par(mfrow=c(2,3))
m<-100;n<-100
xm <- seq(-1,1,length=m);yn<-seq(-1,1,length=n)
x <- rep(xm,n);y<-rep(yn,rep(m,n))
ff <- f1(x,y)
ind <- inSide(bnd,x,y)
ff[!ind] <- NA
image(xm,yn,matrix(ff,m,n),xlab="x",ylab="y")
contour(xm,yn,matrix(ff,m,n),add=TRUE)
lines(bnd[[1]]$x,bnd[[1]]$y,lwd=2);lines(bnd[[2]]$x,bnd[[2]]$y,lwd=2)

## Simulate data by noisy sampling from test function...
set.seed(1)
x <- runif(300)*2-1;y <- runif(300)*2-1
ind <- inSide(bnd,x,y)
x <- x[ind];y <- y[ind]
n <- length(x)
z <- f1(x,y) + rnorm(n)*.1

## Fit a soap film smooth to the noisy data
nmax <- 60
b <- gam(z~s(x,y,k=c(30,15),bs="so",xt=list(bnd=bnd,nmax=nmax)),
  knots=knots,method="REML")
plot(b) ## default plot
vis.gam(b,plot.type="contour") ## prettier version

## trying out separated fits....
ba <- gam(z=s(x,y,k=c(30,15),bs="sf",xt=list(bnd=bnd,nmax=nmax)) +
  s(x,y,k=c(30,15),bs="sw",xt=list(bnd=bnd,nmax=nmax)),
  knots=knots,method="REML")
plot(ba)
vis.gam(ba,plot.type="contour")

smooth.construct.sos.smooth.spec

Splines on the sphere

Description

gam can use isotropic smooths on the sphere, via terms like s(1a,1o,bs="sos",m=2,k=100). There must be exactly 2 arguments to such a smooth. The first is taken to be latitude (in degrees) and the second longitude (in degrees). m (default 0) is an integer in the range -1 to 4 determining
the order of the penalty used. For \( m \geq 0 \), \((m+2)/2\) is the penalty order, with \( m = 2 \) equivalent to the usual second derivative penalty. \( m = 0 \) signals to use the 2nd order spline on the sphere, computed by Wendelberger's (1981) method. \( m = -1 \) results in a Duchon spline being used (with \( m = 2 \) and \( s = 1/2 \)), following an unpublished suggestion of Jean Duchon.

\( k \) (default 50) is the basis dimension.

Usage

```r
## S3 method for class 'sos.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'sos.smooth'
Predict.matrix(object, data)
```

Arguments

- **object**: a smooth specification object, usually generated by a term `s(...,bs="sos",...)`.
- **data**: a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
- **knots**: a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be NULL

Details

For \( m \geq 0 \), the smooths implemented here are based on the pseudosplines on the sphere of Wahba (1981) (there is a correction of table 1 in 1982, but the correction has a misprint in the definition of \( A \) — the \( A \) given in the 1981 paper is correct). For \( m = 0 \) (default) then a second order spline on the sphere is used which is the analogue of a second order thin plate spline in 2D: the computation is based on Chapter 4 of Wendelberger, 1981. Optimal low rank approximations are obtained using exactly the approach given in Wood (2003). For \( m = -1 \) a smooth of the general type discussed in Duchon (1977) is used: the sphere is embedded in a 3D Euclidean space, but smoothing employs a penalty based on second derivatives (so that locally as the smoothing parameter tends to zero we recover a "normal" thin plate spline on the tangent space). This is an unpublished suggestion of Jean Duchon. \( m = -2 \) is the same but with first derivative penalization.

Note that the null space of the penalty is always the space of constant functions on the sphere, whatever the order of penalty.

This class has a plot method, with 3 schemes. `scheme==0` plots one hemisphere of the sphere, projected onto a circle. The plotting sphere has the north pole at the top, and the 0 meridian running down the middle of the plot, and towards the viewer. The smoothing sphere is rotated within the plotting sphere, by specifying the location of its pole in the co-ordinates of the viewing sphere. \( \theta \), \( \phi \) give the longitude and latitude of the smoothing sphere pole within the plotting sphere (in plotting sphere co-ordinates). (You can visualize the smoothing sphere as a globe, free to rotate within the fixed transparent plotting sphere.) The value of the smooth is shown by a heat map overlaid with a contour plot. \( \text{lat, lon gridlines are also plotted.} \)

`scheme==1` is as `scheme==0`, but in black and white, without the image plot. `scheme>1` calls the default plotting method with `scheme` decremented by 2.

Value

An object of class "sos.smooth". In addition to the usual elements of a smooth class documented under `smooth.construct`, this object will contain:
### smooth.construct.sos.smooth.spec

**Xu**
A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).

**UZ**
The matrix mapping the parameters of the reduced rank spline back to the parameters of a full spline.

**Author(s)**
Simon Wood <simon.wood@r-project.org>, with help from Grace Wahba (m=0 case) and Jean Duchon (m = -1 case).

**References**


**See Also**
Duchon.spline

**Examples**

```r
require(mgcv)
set.seed(0)
n <- 400

f <- function(la,lo) { ## a test function...
  sin(lo)*cos(la-.3)
}

## generate with uniform density on sphere...
lo <- runif(n)*2*pi-pi ## longitude
la <- runif(3*n)*pi-pi/2
ind <- runif(3*n)<=cos(la)
la <- la[ind];
la <- la[1:n]
ff <- f(la,lo)
y <- ff + rnorm(n)*.2 ## test data

## generate data for plotting truth...
lam <- seq(-pi/2,pi/2,length=30)
lom <- seq(-pi,pi,length=60)
gr <- expand.grid(la=lam,lo=lom)
fz <- f(gr$la,gr$lo)
zm <- matrix(fz,30,60)

require(mgcv)
dat <- data.frame(la = la *180/pi,lo = lo *180/pi,y=y)

## fit spline on sphere model...
bp <- gam(y~s(la,lo,bs="sos",k=60),data=dat)
```
smooth.construct.sz.smooth.spec

Description

Factor smooth interactions constructed to exclude main effects (and lower order factor smooth interactions). A smooth is constructed for each combination of the supplied factor levels. By appropriate application of sum to zero contrasts to equivalent smooth coefficients across factor levels, the required exclusion of lower order effects is achieved.

See factor.smooth for alternative factor smooth interactions.

Usage

## S3 method for class 'sz.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'sz.interaction'
Predict.matrix(object, data)

Arguments

object For the smooth.construct method a smooth specification object, usually generated by a term s(x, ..., bs = "sz",). For the predict.Matrix method an object of class "sz.interaction" produced by the smooth.construct method.

data a list containing just the data (including any by variable) required by this term, with names corresponding to object$term.

knots a list containing any knots supplied for smooth basis setup.
Details

This class produces a smooth for each combination of the levels of the supplied factor variables. \( s(fac, x, bs="sz") \) produces a smooth of \( x \) for each level of \( fac \), for example. The smooths are constrained to represent deviations from the main effect smooth, so that models such as

\[
g(\mu_i) = f(x_i) + f_k(i)(x_i)
\]

can be estimated in an identifiable manner, where \( k(i) \) indicates the level of some factor that applies for the \( i \)th observation. Identifiability in this case is ensured by constraining the coefficients of the splines representing the \( f_k \). In particular if \( \beta_{ki} \) is the \( i \)th coefficient of \( f_k \) then the constraints are \( \sum_k \beta_{ki} = 0 \).

Such sum to zero constraints are implemented using sum to zero contrasts: identity matrices with an extra row of -1s appended. Consider the case of a single factor first. The model matrix corresponding to a smooth per factor level is the row tensor product (see \texttt{tensor.prod.model.matrix} of the model matrix for the factor, and the model matrix for the smooth. The contrast matrix is then the Kronecker product of the sum to zero contrast for the factor, and an identity matrix of dimension determined by the number of coefficients of the smooth.

If there are multiple factors then the overall model matrix is the row Kronecker product of all the factor model matrices and the smooth, while the contrast is the Kronecker product of all the sum-to-zero contrasts for the factors and a final identity matrix. Notice that this construction means that the main effects (and any interactions) of the factors are included in the factor level dependent smooths. In other words the individual smooths are not each centered. This means that adding main effects or interactions of the factors will lead to a rank deficient model.

The terms can have a smoothing parameter per smooth, or a single smoothing parameter for all the smooths. The latter is specified by giving the smooth term an \( id \). e.g. \( s(fac, x, bs="sz", id=1) \).

The basis for the smooths can be selected by supplying a list as the \( xt \) argument to \texttt{s}, with a \texttt{bs} item. e.g. \( s(fac, x, xt=list(bs="cr")) \) selects the "cr" basis. The default is "tp"

The plot method for this class has two schemes. \texttt{scheme==0} is in colour, while \texttt{scheme==1} is black and white. Currently it only works for 1D smooths.

Value

An object of class "sz.interaction" or a matrix mapping the coefficients of the factor smooth interaction to the smooths themselves.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with input from Matteo Fasiolo.

See Also

gam.models, gamm, factor.smooth

Examples

library(mgcv)
set.seed(0)
dat <- gamSim(4)

b <- gam(y ~ s(x2)+s(fac,x2,bs="sz") + s(x0),data=dat,method="REML")
plot(b,pages=1)
summary(b)
## Example involving 2 factors

\[ f_1(x_2) = 2 \times \sin(\pi \times x_2) \]

\[ f_2(x_2) = \exp(2 \times x_2) - 3.7587 \]

\[ f_3(x_2) = 0.2 \times x_2^{11} \times (10 \times (1 - x_2))^{6} + 10 \times (10 \times x_2)^{3} \times (1 - x_2)^{10} \]

\[ n = 600 \]

\[ x \sim \text{runif}(n) \]

\[ f_1 \leftarrow \text{factor}(\text{sample}(c("a","b","c"),n,\text{replace=TRUE})) \]

\[ f_2 \leftarrow \text{factor}(\text{sample}(c("foo","bar"),n,\text{replace=TRUE})) \]

\[ \mu = f_3(x) \]

\[ \text{for (i in 1:3) } \mu \leftarrow \mu + \exp(2*(2-i)*x)*(f_1==\text{levels}(f_1)[i]) \]

\[ \text{for (i in 1:2) } \mu \leftarrow \mu + 10*i*x*(1-x)*(f_2==\text{levels}(f_2)[i]) \]

\[ y \sim \mu + \text{rnorm}(n) \]

\[ \text{dat} \leftarrow \text{data.frame}(y=y,x=x,f_1=f_1,f_2=f_2) \]

\[ b \leftarrow \text{gam}(y \sim s(x)+s(f_1,x,bs="sz") + s(f_2,x,bs="sz") + s(f_1,f_2,x,bs="sz",id=1), \text{data=} \text{dat, method="REML")} \]

\[ \text{plot}(b, \text{pages}=1, \text{scale}=0) \]

---

**smooth.construct.t2.smooth.spec**

*Tensor product smoothing constructor*

**Description**


**Usage**

```r
## S3 method for class 't2.smooth.spec'
smooth.construct(object, data, knots)
```

**Arguments**

- **object**: a smooth specification object of class `t2.smooth.spec`, usually generated by a term like `t2(x,z)` in a `gam` model formula
- **data**: a list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.
- **knots**: a list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`. See details for further information.
Tensor product smooths are smooths of several variables which allow the degree of smoothing to be different with respect to different variables. They are useful as smooth interaction terms, as they are invariant to linear rescaling of the covariates, which means, for example, that they are insensitive to the measurement units of the different covariates. They are also useful whenever isotropic smoothing is inappropriate. See t2, te, smooth.construct and smooth.terms. The construction employed here produces tensor smooths for which the smoothing penalties are non-overlapping portions of the identity matrix. This makes their estimation by mixed modelling software rather easy.

Value
An object of class "t2.smooth".

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References

See Also
t2

Examples
## see ?t2
Arguments

**object**

A smooth specification object of class `tensor.smooth.spec`, usually generated by a term like `te(x,z)` in a `gam` model formula.

**data**

A list containing just the data (including any by variable) required by this term, with names corresponding to `object$term` (and `object$by`). The by variable is the last element.

**knots**

A list containing any knots supplied for basis setup — in same order and with same names as `data`. Can be `NULL`. See details for further information.

Details

Tensor product smooths are smooths of several variables which allow the degree of smoothing to be different with respect to different variables. They are useful as smooth interaction terms, as they are invariant to linear rescaling of the covariates, which means, for example, that they are insensitive to the measurement units of the different covariates. They are also useful whenever isotropic smoothing is inappropriate. See `te`, `smooth.construct` and `smooth.terms`.

Value

An object of class "tensor.smooth". See `smooth.construct`, for the elements that this object will contain.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

cSplineDes

Examples

```
## see ?gam
```
Description

gam can use isotropic smooths of any number of variables, specified via terms like
\( s(x,z,bs=\text{"tp"},m=3) \) (or just \( s(x,z) \) as this is the default basis). These terms are based on thin
plate regression splines. \( m \) specifies the order of the derivatives in the thin plate spline penalty.

If \( m \) is a vector of length 2 and the second element is zero, then the penalty null space of the smooth
is not included in the smooth: this is useful if you need to test whether a smooth could be replaced
by a linear term, or construct models with odd nesting structures.

Thin plate regression splines are constructed by starting with the basis and penalty for a full thin
plate spline and then truncating this basis in an optimal manner, to obtain a low rank smoother.
Details are given in Wood (2003). One key advantage of the approach is that it avoids the knot
placement problems of conventional regression spline modelling, but it also has the advantage that
smooths of lower rank are nested within smooths of higher rank, so that it is legitimate to use
conventional hypothesis testing methods to compare models based on pure regression splines. Note
that the basis truncation does not change the meaning of the thin plate spline penalty (it penalizes
exactly what it would have penalized for a full thin plate spline).

The t.p.r.s. basis and penalties can become expensive to calculate for large datasets. For this reason
the default behaviour is to randomly subsample \( \text{max.knots} \) unique data locations if there are more
than \( \text{max.knots} \) such, and to use the sub-sample for basis construction. The sampling is always
done with the same random seed to ensure repeatability (does not reset R RNG). \( \text{max.knots} \) is 2000,
by default. Both seed and \( \text{max.knots} \) can be modified using the \( \text{xt} \) argument to \( s \). Alternatively the
user can supply knots from which to construct a basis.

The "ts" smooths are t.p.r.s. with the penalty modified so that the term is shrunk to zero for high
enough smoothing parameter, rather than being shrunk towards a function in the penalty null space
(see details).

Usage

```r
## S3 method for class 'tp.smooth.spec'
smooth.construct(object, data, knots)
## S3 method for class 'ts.smooth.spec'
smooth.construct(object, data, knots)
```

Arguments

- **object**: a smooth specification object, usually generated by a term
  \( s(\ldots,bs=\text{"tp"},\ldots) \) or \( s(\ldots,bs=\text{"ts"},\ldots) \)
- **data**: a list containing just the data (including any by variable) required by this term,
  with names corresponding to \( \text{object$term} \) (and \( \text{object$by} \)). The by variable
  is the last element.
- **knots**: a list containing any knots supplied for basis setup — in same order and with
  same names as \( \text{data} \). Can be NULL

Details

The default basis dimension for this class is \( k=M+k.\text{def} \) where \( M \) is the null space dimension (dimen-
sion of unpenalized function space) and \( k.\text{def} \) is 8 for dimension 1, 27 for dimension 2 and 100 for
higher dimensions. This is essentially arbitrary, and should be checked, but as with all penalized
regression smoothers, results are statistically insensitive to the exact chosie, provided it is not so
small that it forces oversmoothing (the smoother’s degrees of freedom are controlled primarily by
its smoothing parameter).
The default is to set \( m \) (the order of derivative in the thin plate spline penalty) to the smallest value satisfying \( 2m > d+1 \) where \( d \) if the number of covariates of the term: this yields ‘visually smooth’ functions. In any case \( 2m > d \) must be satisfied.

The constructor is not normally called directly, but is rather used internally by \texttt{gam}. To use for basis setup it is recommended to use \texttt{smooth.construct2}.

For these classes the specification object will contain information on how to handle large datasets in their \texttt{xt} field. The default is to randomly subsample 2000 ‘knots’ from which to produce a tprs basis, if the number of unique predictor variable combinations in excess of 2000. The default can be modified via the \texttt{xt} argument to \texttt{s}. This is supplied as a list with elements \texttt{max.knots} and \texttt{seed} containing a number to use in place of 2000, and the random number seed to use (either can be missing).

For these bases \texttt{knots} has two uses. Firstly, as mentioned already, for large datasets the calculation of the tps basis can be time-consuming. The user can retain most of the advantages of the t.p.r.s. approach by supplying a reduced set of covariate values from which to obtain the basis - typically the number of covariate values used will be substantially smaller than the number of data, and substantially larger than the basis dimension, \( k \). This approach is the one taken automatically if the number of unique covariate values (combinations) exceeds \texttt{max.knots}. The second possibility is to avoid the eigen-decomposition used to find the t.p.r.s. basis altogether and simply use the basis implied by the chosen knots: this will happen if the number of knots supplied matches the basis dimension, \( k \). For a given basis dimension the second option is faster, but gives poorer results (and the user must be quite careful in choosing knot locations).

The shrinkage version of the smooth, eigen-decomposes the wiggliness penalty matrix, and sets its zero eigenvalues to small multiples of the smallest strictly positive eigenvalue. The penalty is then set to the matrix with eigenvectors corresponding to those of the original penalty, but eigenvalues set to the perturbed versions. This penalty matrix has full rank and shrinks the curve to zero at high enough smoothing parameters.

**Value**

An object of class "tprs.smooth" or "ts.smooth". In addition to the usual elements of a smooth class documented under \texttt{smooth.construct}, this object will contain:

- \texttt{shift} A record of the shift applied to each covariate in order to center it around zero and avoid any co-linearity problems that might otherwise occur in the penalty null space basis of the term.
- \texttt{Xu} A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).
- \texttt{UZ} The matrix mapping the t.p.r.s. parameters back to the parameters of a full thin plate spline.
- \texttt{null.space.dimension} The dimension of the space of functions that have zero wiggliness according to the wiggliness penalty for this term.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Examples

```r
require(mgcv); n <- 100; set.seed(2)
x <- runif(n); y <- x + x^2*.2 + rnorm(n) *.1

## is smooth significantly different from straight line?
summary(gam(y~s(x,m=c(2,0))+x,method="REML")) ## not quite

## is smooth significatly different from zero?
summary(gam(y~s(x),method="REML")) ## yes!

## Fool bam(...,discrete=TRUE) into (strange) nested
## model fit...
set.seed(2) ## simulate some data...
dat <- gamSim(1,n=400,dist="normal",scale=2)
dat$x1a <- dat$x1 ## copy x1 so bam allows 2 copies of x1
## Following removes identifiability problem, by removing
## linear terms from second smooth, and then re-inserting
## the one that was not a duplicate (x2)...
b <- bam(y~s(x0,x1)+s(x1a,x2,m=c(2,0))+x2,data=dat,discrete=TRUE)

## example of knot based tprs...
k <- 10; m <- 2
y <- y[order(x)]; x <- x[order(x)]
b <- gam(y~s(x,k=k,m=m),method="REML",
       knots=list(x=seq(0,1,length=k)))
X <- model.matrix(b)
par(mfrow=c(1,2))
plot(x,X[,1],ylim=range(X),type="l")
for (i in 2:ncol(X)) lines(x,X[,i],col=i)

## compare with eigen based (default)
b1 <- gam(y~s(x,k=k,m=m),method="REML")
X1 <- model.matrix(b1)
plot(x,X1[,1],ylim=range(X1),type="l")
for (i in 1:ncol(X1)) lines(x,X1[,i],col=i)
## see ?gam
```

smooth.info

Generic function to provide extra information about smooth specification

Description

Takes a smooth specification object and adds extra basis specific information to it before smooth constructor called. Default method returns supplied object unmodified.

Usage

```
smooth.info(object)
```

Arguments

- `object` is a smooth specification object
smooth.terms

Details

Sometimes it is necessary to know something about a smoother before it is constructed, beyond what is in the initial smooth specification object. For example, some smooth terms could be set up as tensor product smooths and it is useful for bam to take advantage of this when discrete covariate methods are used. However, bam needs to know whether a smoother falls into this category before it is constructed in order to discretize its covariates marginally instead of jointly. Rather than bam having a hard coded list of such smooth classes it is preferable for the smooth specification object to report this themselves. smooth.info method functions are the means for achieving this. When interpreting a gam formula the smooth.info function is applied to each smooth specification object as soon as it is produced (in interpret.gam).

Value

A smooth specification object, which may be modified in some way.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

bam, smooth.construct, PredictMat

Examples

# See smooth.construct examples
spec <- s(a,bs="re")
class(spec)
spec$tensor.possible
spec <- smooth.info(spec)
spec$tensor.possible

---

smooth.terms Smooth terms in GAM

Description

Smooth terms are specified in a gam formula using s, te, ti and t2 terms. Various smooth classes are available, for different modelling tasks, and users can add smooth classes (see user.defined.smooth). What defines a smooth class is the basis used to represent the smooth function and quadratic penalty (or multiple penalties) used to penalize the basis coefficients in order to control the degree of smoothness. Smooth classes are invoked directly by s terms, or as building blocks for tensor product smoothing via te, ti or t2 terms (only smooth classes with single penalties can be used in tensor products). The smooths built into the mgcv package are all based one way or another on low rank versions of splines. For the full rank versions see Wahba (1990).
Note that smooths can be used rather flexibly in gam models. In particular the linear predictor of the GAM can depend on (a discrete approximation to) any linear functional of a smooth term, using by variables and the ‘summation convention’ explained in linear.functional.terms.

The single penalty built in smooth classes are summarized as follows

**Thin plate regression splines** bs="tp". These are low rank isotropic smoothers of any number of covariates. By isotropic is meant that rotation of the covariate co-ordinate system will not change the result of smoothing. By low rank is meant that they have far fewer coefficients than there are data to smooth. They are reduced rank versions of the thin plate splines and use the thin plate spline penalty. They are the default smooth for s terms because there is a defined sense in which they are the optimal smoother of any given basis dimension/rank (Wood, 2003). Thin plate regression splines do not have ‘knots’ (at least not in any conventional sense): a truncated eigen-decomposition is used to achieve the rank reduction. See tprs for further details.

bs="ts" is as "tp" but with a modification to the smoothing penalty, so that the null space is also penalized slightly and the whole term can therefore be shrunk to zero.

**Duchon splines** bs="ds". These generalize thin plate splines. In particular, for any given number of covariates they allow lower orders of derivative in the penalty than thin plate splines (and hence a smaller null space). See Duchon.spline for further details.

**Cubic regression splines** bs="cr". These have a cubic spline basis defined by a modest sized set of knots spread evenly through the covariate values. They are penalized by the conventional intergrated square second derivative cubic spline penalty. For details see cubic.regression.spline and e.g. Wood (2017).

bs="cs" specifies a shrinkage version of "cr".

bs="cc" specifies a cyclic cubic regression splines (see cyclic.cubic.spline). i.e. a penalized cubic regression splines whose ends match, up to second derivative.

**Splines on the sphere** bs="sos". These are two dimensional splines on a sphere. Arguments are latitude and longitude, and they are the analogue of thin plate splines for the sphere. Useful for data sampled over a large portion of the globe, when isotropy is appropriate. See Spherical.Spline for details.

**B-splines** bs="bs" B-spline basis with integrated squared derivative penalties. The order of basis and penalty can be chosen separately, and several penalties of different orders can be applied. Somewhat like a derivative penalty version of P-splines. See b.spline for details.

**P-splines** bs="ps". These are P-splines as proposed by Eilers and Marx (1996). They combine a B-spline basis, with a discrete penalty on the basis coefficients, and any sane combination of penalty and basis order is allowed. Although this penalty has no exact interpretation in terms of function shape, in the way that the derivative penalties do, P-splines perform almost as well as conventional splines in many standard applications, and can perform better in particular cases where it is advantageous to mix different orders of basis and penalty.

bs="cp" gives a cyclic version of a P-spline (see cyclic.p.spline).

**Random effects** bs="re". These are parametric terms penalized by a ridge penalty (i.e. the identity matrix). When such a smooth has multiple arguments then it represents the parametric interaction of these arguments, with the coefficients penalized by a ridge penalty. The ridge penalty is equivalent to an assumption that the coefficients are i.i.d. normal random effects. See smooth.construct.re.smooth.spec.

**Markov Random Fields** bs="mrf". These are popular when space is split up into discrete contiguous geographic units (districts of a town, for example). In this case a simple smoothing penalty is constructed based on the neighbourhood structure of the geographic units. See mrf for details and an example.
Gaussian process smooths bs="gp". Gaussian process models with a variety of simple correlation functions can be represented as smooths. See gp.smooth for details.

Soap film smooths bs="so" (actually not single penalited, but bs="sw" and bs="sf" allows splitting into single penalty components for use in tensor product smoothing). These are finite area smoothers designed to smooth within complicated geographical boundaries, where the boundary matters (e.g. you do not want to smooth across boundary features). See soap for details.

Broadly speaking the default penalized thin plate regression splines tend to give the best MSE performance, but they are slower to set up than the other bases. The knot based penalized cubic regression splines (with derivative based penalties) usually come next in MSE performance, with the P-splines doing just a little worse. However the P-splines are useful in non-standard situations.

All the preceding classes (and any user defined smooths with single penalties) may be used as marginal bases for tensor product smooths specified via te, ti or t2 terms. Tensor product smooths are smooth functions of several variables where the basis is built up from tensor products of bases for smooths of fewer (usually one) variable(s) (marginal bases). The multiple penalties for these smooths are produced automatically from the penalties of the marginal smooths. Wood (2006) and Wood, Scheipl and Faraway (2012), give the general recipe for these constructions.

te te smooths have one penalty per marginal basis, each of which is interpretable in a similar way to the marginal penalty from which it is derived. See Wood (2006).

ti ti smooths exclude the basis functions associated with the ‘main effects’ of the marginal smooths, plus interactions other than the highest order specified. These provide a stable an interpretable way of specifying models with main effects and interactions. For example if we are interested in linear predicto $f_1(x) + f_2(z) + f_3(x, z)$, we might use model formula $y~s(x)+s(z)+ti(x,z)$ or $y~ti(x)+ti(z)+ti(x,z)$. A similar construction involving te terms instead will be much less statistically stable.

t2 t2 uses an alternative tensor product construction that results in more penalties each having a simple non-overlapping structure allowing use with the gamm4 package. It is a natural generalization of the SS-ANOVA construction, but the penalties are a little harder to interpret. See Wood, Scheipl and Faraway (2012/13).

Tensor product smooths often perform better than isotropic smooths when the covariates of a smooth are not naturally on the same scale, so that their relative scaling is arbitrary. For example, if smoothing with respect to time and distance, an isotropic smoother will give very different results if the units are cm and minutes compared to if the units are metres and seconds: a tensor product smooth will give the same answer in both cases (see te for an example of this). Note that te terms are knot based, and the thin plate splines seem to offer no advantage over cubic or P-splines as marginal bases.

Some further specialist smoothers that are not suitable for use in tensor products are also available.

Adaptive smoothers bs="ad" Univariate and bivariate adaptive smooths are available (see adaptive.smooth). These are appropriate when the degree of smoothing should itself vary with the covariates to be smoothed, and the data contain sufficient information to be able to estimate the appropriate variation. Because this flexibility is achieved by splitting the penalty into several ‘basis penalties’ these terms are not suitable as components of tensor product smooths, and are not supported by gamm.

Factor smooth interactions bs="sz" Smooth factor interactions (see factor.smooth) are often produced using by variables (see gam.models), but it is often desirable to include smooths which represent the deviations from some main effect smooth that apply for each level of a factor (or combination of factors). See smooth.construct.sz.smooth.spec for details.
Random factor smooth interactions  bs="fs"  A special smoother class (see smooth.construct.fs.smooth.spec) is available for the case in which a smooth is required at each of a large number of factor levels (for example a smooth for each patient in a study), and each smooth should have the same smoothing parameter. The “fs” smoothers are set up to be efficient when used with gamm, and have penalties on each null space component (i.e. they are fully ‘random effects’).

Author(s)

Simon Wood <simon.wood@r-project.org>

References


Wahba (1990) Spline Models of Observational Data. SIAM


See Also

s, te, t2, tprs, Duchon.spline, cubic.regression.spline, p.spline, d.spline, mrf, soap, Spherical.Spline, adaptive.smooth, user.deined.smooth, smooth.construct.re.smooth.spec, smooth.construct.gp.smooth.spec, factor.smooth.interaction

Examples

## see examples for gam and gamm

smooth2random

Convert a smooth to a form suitable for estimating as random effect

Description

A generic function for converting mgcv smooth objects to forms suitable for estimation as random effects by e.g. lme. Exported mostly for use by other package developers.
**Usage**

```
smooth2random(object, vnames, type=1)
```

**Arguments**

- `object`: an mgcv smooth object.
- `vnames`: a vector of names to avoid as dummy variable names in the random effects form.
- `type`: 1 for lme, otherwise lmer.

**Details**

There is a duality between smooths and random effects which means that smooths can be estimated using mixed modelling software. This function converts standard mgcv smooth objects to forms suitable for estimation by lme, for example. A service routine for gamm exported for use by package developers. See examples for creating prediction matrices for new data, corresponding to the random and fixed effect matrices returned when type=2.

**Value**

A list.

- `rand`: a list of random effects, including grouping factors, and a fixed effects matrix. Grouping factors, model matrix and model matrix name attached as attributes, to each element. Alternatively, for type=2 a list of random effect model matrices, each corresponding to an i.i.d. Gaussian random effect with a single variance component.
- `trans.U`: A matrix, trans.U, that transforms coef, in order [rand1, rand2,... fix] back to original parameterization. If null, then not needed. If null then taken as identity.
- `Xf`: A matrix for the fixed effects, if any.
- `fixed`: TRUE/FALSE, indicating if term was unpenalized or not. If unpenalized then other stuff may not be returned (it’s not a random effect).
- `rind`: an index vector such that if br is the vector of random coefficients for the term, br[rind] is the coef in order for this term.
- `pen.ind`: index of which penalty penalizes each coefficient: 0 for unpenalized.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>.

**References**

See Also
gamm

Examples

```r
## Simple type 1 'lme' style...
library(mgcv)
x <- runif(30)
sm <- smoothCon(s(x),data.frame(x=x))[[1]]
smooth2random(sm,"")

## Now type 2 'lme4' style...
z <- runif(30)
dat <- data.frame(x=x,z=z)
sm <- smoothCon(t2(x,z),dat)[[1]]
re <- smooth2random(sm,"",2)
str(re)

## For prediction after fitting we might transform parameters back to
## original parameterization using 'rind', 'trans.D' and 'trans.U',
## and call PredictMat(sm,newdata) to get the prediction matrix to
## multiply these transformed parameters by.
## Alternatively we could obtain fixed and random effect Prediction
## matrices corresponding to the results from smooth2random, which
## can be used with the fit parameters without transforming them.
## The following shows how...

s2rPred <- function(sm,re,data) {
  ## Function to aid prediction from smooths represented as type==2
  ## random effects. re must be the result of smooth2random(sm,...,type=2).
  X <- PredictMat(sm,data)  ## get prediction matrix for new data
  ## transform to r.e. parameterization
  if (!is.null(re$trans.U)) X <- X%*%re$trans.U
  X <- t(t(X)*re$trans.D)
  ## re-order columns according to random effect re-ordering...
  X[,re$rind] <- X[,re$pen.ind!=0]
  ## re-order penalization index in same way
  pen.ind <- re$pen.ind; pen.ind[re$rind] <- pen.ind[pen.ind>0]
  ## start return object...
  r <- list(rand=list(),Xf=X[,which(re$pen.ind==0),drop=FALSE])
  for (i in 1:length(re$rand)) {  ## loop over random effect matrices
    r$rand[[i]] <- X[,which(pen.ind==i),drop=FALSE]
    attr(r$rand[[i]],"s.label") <- attr(re$rand[[i]],"s.label")
  }
  names(r$rand) <- names(re$rand)
  r
}
## s2rPred

## use function to obtain prediction random and fixed effect matrices
## for first 10 elements of 'dat'. Then confirm that these match the
## first 10 rows of the original model matrices, as they should...

r <- s2rPred(sm,re,dat[1:10,])
range(r$Xf-re$Xf[1:10,])
range(r$rand[[1]]-re$rand[[1]][1:10,])
```
smoothCon

Prediction/Construction wrapper functions for GAM smooth terms

Description

Wrapper functions for construction of and prediction from smooth terms in a GAM. The purpose of the wrappers is to allow user-transparent re-parameterization of smooth terms, in order to allow identifiability constraints to be absorbed into the parameterization of each term, if required. The routine also handles ‘by’ variables and construction of identifiability constraints automatically, although this behaviour can be over-ridden.

Usage

```r
smoothCon(object, data, knots = NULL, absorb.cons = FALSE, 
scale.penalty = TRUE, n = nrow(data), dataX = NULL, 
null.space.penalty = FALSE, sparse.cons = 0, 
diagonal.penalty = FALSE, apply.by = TRUE, modCon = 0)
```

```r
PredictMat(object, data, n = nrow(data))
```

Arguments

- **object**: is a smooth specification object or a smooth object.
- **data**: A data frame, model frame or list containing the values of the (named) covariates at which the smooth term is to be evaluated. If it’s a list then n must be supplied.
- **knots**: An optional data frame supplying any knot locations to be supplied for basis construction.
- **absorb.cons**: Set to `TRUE` in order to have identifiability constraints absorbed into the basis.
- **scale.penalty**: should the penalty coefficient matrix be scaled to have approximately the same ‘size’ as the inner product of the terms model matrix with itself? This can improve the performance of `gamm` fitting.
- **n**: number of values for each covariate, or if a covariate is a matrix, the number of rows in that matrix: must be supplied explicitly if `data` is a list.
- **dataX**: Sometimes the basis should be set up using data in `data`, but the model matrix should be constructed with another set of data provided in `dataX` — n is assumed to be the same for both. Facilitates smooth id’s.
- **null.space.penalty**: Should an extra penalty be added to the smooth which will penalize the components of the smooth in the penalty null space: provides a way of penalizing terms out of the model altogether.
- **apply.by**: set to `FALSE` to have basis setup exactly as in default case, but to return add an additional matrix X0 to the return object, containing the model matrix without the by variable, if a by variable is present. Useful for `bam` discrete method setup.
- **sparse.cons**: If 0 then default sum to zero constraints are used. If -1 then sweep and drop sum to zero constraints are used (default with `bam`). If 1 then one coefficient is set to zero as constraint for sparse smooths. If 2 then sparse coefficient sum to zero constraints are used for sparse smooths. None of these options has an effect if the smooth supplies its own constraint.
smoothCon

diagonal.penalty

If TRUE then the smooth is reparameterized to turn the penalty into an identity matrix, with the final diagonal elements zeroed (corresponding to the penalty nullspace). May result in a matrix diagRP in the returned object for use by PredictMat.

modCon

force modification of any smooth supplied constraints. 0 - do nothing. 1 - delete supplied constraints, replacing with automatically generated ones. 2 - set fit and predict constraint to predict constraint. 3 - set fit and predict constraint to fit constraint.

Details

These wrapper functions exist to allow smooths specified using smooth.construct and Predict.matrix method functions to be re-parameterized so that identifiability constraints are no longer required in fitting. This is done in a user transparent manner, but is typically of no importance in use of GAMs. The routine’s also handle by variables and will create default identifiability constraints.

If a user defined smooth constructor handles by variables itself, then its returned smooth object should contain an object by.done. If this does not exist then smoothCon will use the default code. Similarly if a user defined Predict.matrix method handles by variables internally then the returned matrix should have a "by.done" attribute.

Default centering constraints, that terms should sum to zero over the covariates, are produced unless the smooth constructor includes a matrix C of constraints. To have no constraints (in which case you had better have a full rank penalty!) the matrix C should have no rows. There is an option to use centering constraint that generate no, or limited infil, if the smoother has a sparse model matrix.

smoothCon returns a list of smooths because factor by variables result in multiple copies of a smooth, each multiplied by the dummy variable associated with one factor level. smoothCon modifies the smooth object labels in the presence of by variables, to ensure that they are unique, it also stores the level of a by variable factor associated with a smooth, for later use by PredictMat.

The parameterization used by gam can be controlled via gam.control.

Value

From smoothCon a list of smooth objects returned by the appropriate smooth.construct method function. If constraints are to be absorbed then the objects will have attributes "qrc" and "nCons". "nCons" is the number of constraints. "qrc" is usually the qr decomposition of the constraint matrix (returned by qr), but if it is a single positive integer it is the index of the coefficient to set to zero, and if it is a negative number then this indicates that the parameters are to sum to zero.

For predictMat a matrix which will map the parameters associated with the smooth to the vector of values of the smooth evaluated at the covariate values given in object.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

https://www.maths.ed.ac.uk/~swood34/

See Also

gam.control, smooth.construct, Predict.matrix
Examples

```r
## example of using smoothCon and PredictMat to set up a basis
## to use for regression and make predictions using the result
library(MASS)  ## load for mcycle data.
## set up a smoother...
sm <- smoothCon(s(times,k=10),data=mcycle,knots=NULL)[[1]]
## use it to fit a regression spline model...
beta <- coef(lm(mcycle$accel~sm$X-1))
with(mcycle,plot(times,accel))  ## plot data
times <- seq(0,60,length=200)  ## creat prediction times
## Get matrix mapping beta to spline prediction at 'times'
Xp <- PredictMat(sm,data.frame(times=times))
lines(times,Xp%*%beta)  ## add smooth to plot

## Same again but using a penalized regression spline of
## rank 30....
sm <- smoothCon(s(times,k=30),data=mcycle,knots=NULL)[[1]]
E <- t(mroot(sm$S[[1]]))  ## square root penalty
X <- rbind(sm$X,0.1*E)  ## augmented model matrix
y <- c(mcycle$accel,rep(0,nrow(E)))  ## augmented data
beta <- coef(lm(y~X-1))  ## fit penalized regression spline
Xp <- PredictMat(sm,data.frame(times=times))  ## prediction matrix
with(mcycle,plot(times,accel))  ## plot data
lines(times,Xp%*%beta)  ## overlay smooth
```

Description

Extracts the estimated covariance matrix for the log smoothing parameter estimates from a (RE)ML estimated gam object, provided the fit was with a method that evaluated the required Hessian.

Usage

```r
sp.vcov(x, edge.correct=TRUE, reg=1e-3)
```

Arguments

- `x` a fitted model object of class `gam` as produced by `gam()`.
- `edge.correct` if the model was fitted with `edge.correct=TRUE` (see `gam.control`), then the returned covariance matrix will be for the edge corrected log smoothing parameters.
- `reg` regularizer for Hessian - default is equivalent to prior variance of 1000 on log smoothing parameters.

Details

Just extracts the inverse of the hessian matrix of the negative (restricted) log likelihood w.r.t the log smoothing parameters, if this has been obtained as part of fitting.
spasm.construct

Value
A matrix corresponding to the estimated covariance matrix of the log smoothing parameter estimators, if this can be extracted, otherwise NULL. If the scale parameter has been (RE)ML estimated (i.e. if the method was "ML" or "REML" and the scale parameter was unknown) then the last row and column relate to the log scale parameter. If edge.correct=TRUE and this was used in fitting then the edge corrected smoothing parameters are in attribute 1sp of the returned matrix.

Author(s)
Simon N. Wood <simon.wood@r-project.org>

References

See Also
gam, gam.vcomp

Examples
require(mgcv)
n <- 100
x <- runif(n); z <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=10)+s(z),knots=list(x=seq(0,1,length=10)),
method="REML")
sp.vcov(mod)

spasm.construct Experimental sparse smoothers

Description
These are experimental sparse smoothing functions, and should be left well alone!

Usage
spasm.construct(object, data)
spasm.sp(object, sp, w=rep(1,object$nobs), get.trH=TRUE, block=0, centre=FALSE)
spasm.smooth(object, X, residual=FALSE, block=0)

Arguments
object sparse smooth object
data data frame
sp smoothing parameter value
w optional weights
get.trH Should (estimated) trace of sparse smoother matrix be returned
There is no `step.gam` in package `mgcv`. The `mgcv` default for model selection is to use either prediction error criteria such as GCV, GACV, Mallows’ Cp/AIC/UBRE or the likelihood based methods of REML or ML. Since the smoothness estimation part of model selection is done in this way it is logically most consistent to perform the rest of model selection in the same way, i.e. to decide which terms to include or omit by looking at changes in GCV, AIC, REML etc.

To facilitate fully automatic model selection the package implements two smooth modification techniques which can be used to allow smooths to be shrunk to zero as part of smoothness selection.

**Shrinkage smoothers** are smoothers in which a small multiple of the identity matrix is added to the smoothing penalty, so that strong enough penalization will shrink all the coefficients of the smooth to zero. Such smoothers can effectively be penalized out of the model altogether, as part of smoothing parameter estimation. 2 classes of these shrinkage smoothers are implemented: “cs” and “ts”, based on cubic regression spline and thin plate regression spline smoothers (see `s`)

**Null space penalization** An alternative is to construct an extra penalty for each smooth which penalizes the space of functions of zero wiggliness according to its existing penalties. If all the smoothing parameters for such a term tend to infinity then the term is penalized to zero, and is effectively dropped from the model. The advantage of this approach is that it can be implemented automatically for any smooth. The `select` argument to `gam` causes this latter approach to be used. Unpenalized terms (e.g. `s(x,fx=TRUE)`) remain unpenalized.

REML and ML smoothness selection are equivalent under this approach, and simulation evidence suggests that they tend to perform a little better than prediction error criteria, for model selection.

**References**

Marra, G. and S.N. Wood (2011) Practical variable selection for generalized additive models Computational Statistics and Data Analysis 55,2372-2387
See Also
gam.selection

Examples

## an example of GCV based model selection as
## an alternative to stepwise selection, using
## shrinkage smoothers...
library(mgcv)
set.seed(0);n <- 400
dat <- gamSim(1,n=n, scale=2)
dat$x4 <- runif(n, 0, 1)
dat$x5 <- runif(n, 0, 1)
attach(dat)
## Note the increased gamma parameter below to favour
## slightly smoother models...
b<-gam(y~s(x0,bs="ts") + s(x1,bs="ts") +
    s(x2,bs="ts") +
    s(x3,bs="ts") + s(x4,bs="ts") + s(x5,bs="ts"),
    gamma=1.4)
summary(b)
plot(b,pages=1)

## Same again using REML/ML
b<-gam(y~s(x0,bs="ts") + s(x1,bs="ts") + s(x2,bs="ts") +
    s(x3,bs="ts") + s(x4,bs="ts") + s(x5,bs="ts"),
    method="REML")
summary(b)
plot(b,pages=1)

## And once more, but using the null space penalization
b<-gam(y~s(x0,bs="cr") + s(x1,bs="cr") + s(x2,bs="cr") +
    s(x3,bs="cr") + s(x4,bs="cr") + s(x5,bs="cr"),
    method="REML",select=TRUE)
summary(b)
plot(b,pages=1)

detach(dat);rm(dat)

summary.gam

Summary for a GAM fit

Description

Takes a fitted gam object produced by gam() and produces various useful summaries from it. (See sink to divert output to a file.)

Usage

## S3 method for class 'gam'
summary(object, dispersion=NULL, freq=FALSE, re.test=TRUE, ...)

## S3 method for class 'summary.gam'
print(x,digits = max(3, getOption("digits") - 3),
    signif.stars = getOption("show.signif.stars"),...)
**Arguments**

- **object**: a fitted `gam` object as produced by `gam()`.
- **x**: a `summary.gam` object produced by `summary.gam()`.
- **dispersion**: A known dispersion parameter. NULL to use estimate or default (e.g. 1 for Poisson).
- **freq**: By default p-values for parametric terms are calculated using the Bayesian estimated covariance matrix of the parameter estimators. If this is set to TRUE then the frequentist covariance matrix of the parameters is used instead.
- **re.test**: Should tests be performed for random effect terms (including any term with a zero dimensional null space)? For large models these tests can be computationally expensive.
- **digits**: controls number of digits printed in output.
- **signif.stars**: Should significance stars be printed alongside output.
- **...**: other arguments.

**Details**

Model degrees of freedom are taken as the trace of the influence (or hat) matrix $A$ for the model fit. Residual degrees of freedom are taken as number of data minus model degrees of freedom. Let $P_i$ be the matrix giving the parameters of the $i$th smooth when applied to the data (or pseudodata in the generalized case) and let $X$ be the design matrix of the model. Then $\text{tr}(XP_i)$ is the edf for the $i$th term. Clearly this definition causes the edf’s to add up properly! An alternative version of EDF is more appropriate for p-value computation, and is based on the trace of $2A - AA$.

`print.summary.gam` tries to print various bits of summary information useful for term selection in a pretty way.

P-values for smooth terms are usually based on a test statistic motivated by an extension of Nychka’s (1988) analysis of the frequentist properties of Bayesian confidence intervals for smooths (Marra and Wood, 2012). These have better frequentist performance (in terms of power and distribution under the null) than the alternative strictly frequentist approximation. When the Bayesian intervals have good across the function properties then the p-values have close to the correct null distribution and reasonable power (but there are no optimality results for the power). Full details are in Wood (2013b), although what is computed is actually a slight variant in which the components of the test statistic are weighted by the iterative fitting weights.

Note that for terms with no unpenalized terms (such as Gaussian random effects) the Nychka (1988) requirement for smoothing bias to be substantially less than variance breaks down (see e.g. appendix of Marra and Wood, 2012), and this results in incorrect null distribution for p-values computed using the above approach. In this case it is necessary to use an alternative approach designed for random effects variance components, and this is done. See Wood (2013a) for details: the test is based on a likelihood ratio statistic (with the reference distribution appropriate for the null hypothesis on the boundary of the parameter space).

All p-values are computed without considering uncertainty in the smoothing parameter estimates. In simulations the p-values have best behaviour under ML smoothness selection, with REML coming second. In general the p-values behave well, but neglecting smoothing parameter uncertainty means that they may be somewhat too low when smoothing parameters are highly uncertain. High uncertainty happens in particular when smoothing parameters are poorly identified, which can occur with nested smooths or highly correlated covariates (high concurrence).

By default the p-values for parametric model terms are also based on Wald tests using the Bayesian covariance matrix for the coefficients. This is appropriate when there are ”re” terms present, and
is otherwise rather similar to the results using the frequentist covariance matrix (freq=TRUE), since
the parametric terms themselves are usually unpenalized. Default P-values for parametric terms
that are penalized using the paraPen argument will not be good. However if such terms represent
conventional random effects with full rank penalties, then setting freq=TRUE is appropriate.

**Value**

`summary.gam` produces a list of summary information for a fitted `gam` object.

- **p.coef**: an array of estimates of the strictly parametric model coefficients.
- **p.t**: an array of the `p.coef`s divided by their standard errors.
- **p.pv**: an array of p-values for the null hypothesis that the corresponding parameter
  is zero. Calculated with reference to the t distribution with the estimated residual
  degrees of freedom for the model fit if the dispersion parameter has been estimated, and the standard normal if not.
- **m**: The number of smooth terms in the model.
- **chi.sq**: An array of test statistics for assessing the significance of model smooth terms.
  See details.
- **s.pv**: An array of approximate p-values for the null hypotheses that each smooth term
  is zero. Be warned, these are only approximate.
- **se**: array of standard error estimates for all parameter estimates.
- **r.sq**: The adjusted r-squared for the model. Defined as the proportion of variance ex-
  plained, where original variance and residual variance are both estimated using
  unbiased estimators. This quantity can be negative if your model is worse than
  a one parameter constant model, and can be higher for the smaller of two nested
  models! The proportion null deviance explained is probably more appropriate
  for non-normal errors. Note that `r.sq` does not include any offset in the one
  parameter model.
- **dev.expl**: The proportion of the null deviance explained by the model. The null deviance is
  computed taking account of any offset, so `dev.expl` can be substantially lower
  than `r.sq` when an offset is present.
- **edf**: array of estimated degrees of freedom for the model terms.
- **residual.df**: estimated residual degrees of freedom.
- **n**: number of data.
- **np**: number of model coefficients (regression coefficients, not smoothing parameters
  or other parameters of likelihood).
- **rank**: apparent model rank.
- **method**: The smoothing selection criterion used.
- **sp.criterion**: The minimized value of the smoothness selection criterion. Note that for ML
  and REML methods, what is reported is the negative log marginal likelihood or
  negative log restricted likelihood.
- **scale**: estimated (or given) scale parameter.
- **family**: the family used.
- **formula**: the original GAM formula.
- **dispersion**: the scale parameter.
- **pTerms.df**: the degrees of freedom associated with each parametric term (excluding the con-
  stant).
summary.gam

pTerms.chi.sq  a Wald statistic for testing the null hypothesis that the each parametric term is zero.
pTerms.pv  p-values associated with the tests that each term is zero. For penalized fits these are approximate. The reference distribution is an appropriate chi-squared when the scale parameter is known, and is based on an F when it is not.
cov.unscaled  The estimated covariance matrix of the parameters (or estimators if freq=TRUE), divided by scale parameter.
cov.scaled  The estimated covariance matrix of the parameters (estimators if freq=TRUE).
p.table  significance table for parameters
s.table  significance table for smooths
p.Terms  significance table for parametric model terms

WARNING

The p-values are approximate and neglect smoothing parameter uncertainty. They are likely to be somewhat too low when smoothing parameter estimates are highly uncertain: do read the details section. If the exact values matter, read Wood (2013a or b).
P-values for terms penalized via ‘paraPen’ are unlikely to be correct.

Author(s)

Simon N. Wood <simon.wood@r-project.org> with substantial improvements by Henric Nilsson.

References


See Also

`gam`, `predict.gam`, `gam.check`, `anova.gam`, `gam.vcomp`, `sp.vcov`

Examples

```r
library(mgcv)
set.seed(0)

dat <- gamSim(1,n=200,scale=2) ## simulate data

b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)
summary(b)
```
## Define alternative tensor product smooths in GAM formulae

**Description**

Alternative to `te` for defining tensor product smooths in a `gam` formula. Results in a construction in which the penalties are non-overlapping multiples of identity matrices (with some rows and columns zeroed). The construction, which is due to Fabian Scheipl (mgcv implementation, 2010), is analogous to Smoothing Spline ANOVA (Gu, 2002), but using low rank penalized regression spline marginals. The main advantage of this construction is that it is useable with `gamm4` from package `gamm4`. 

```r
## now check the p-values by using a pure regression spline.....
b.d <- round(summary(b)$edf)+1  # get edf per smooth
b.d <- pmax(b.d,3)  # can't have basis dimension less than 3!
bc<gam(y~s(x0,k=b.d[1],fx=TRUE)+s(x1,k=b.d[2],fx=TRUE)+
s(x2,k=b.d[3],fx=TRUE)+s(x3,k=b.d[4],fx=TRUE),data=dat)
plot(bc,pages=1)
summary(bc)

## Example where some p-values are less reliable...
dat <- gamSim(6,n=200, scale=2)
b <- gam(y~s(x0,m=1)+s(x1)+s(x2)+s(x3)+s(fac,bs="re"),data=dat)
# Here s(x0,m=1) can be penalized to zero, so p-value approximation
## cruder than usual...
summary(b)

## p-value check - increase k to make this useful!
k<-20;n <- 200;p <- rep(NA,k)
for (i in 1:k)
  ( b<gam(y~te(x,z),data=data.frame(y=rnorm(n),x=runif(n),z=runif(n)),
method="ML")
  p[i]<-summary(b)$s.p[i]
}
plot(((1:k)-0.5)/k,sort(p))
abline(0,1,col=2)
ks.test(p,"punif")  # how close to uniform are the p-values?

## A Gamma example, by modify `gamSim` output...
dat <- gamSim(1,n=400,dist="normal",scale=1)
dat$f <- dat$f/4  # true linear predictor
Ey <- exp(dat$f);scale <- .5  # mean and GLM scale parameter
# Note that 'shape' and 'scale' in 'rgamma' are almost
## opposite terminology to that used with GLM/GAM...
dat$y <- rgamma(Ey*0,shape=1/scale,scale=Ey*scale)
bg <- gam(y~ s(x0)+ s(x1)+s(x2)+s(x3),family=Gamma(link=log),
data=dat,method="REML")
summary(bg)
```
Usage

\[ t2(..., k=NA, bs="cr", m=NA, d=NA, by=NA, xt=NULL, \\ id=NULL, sp=NULL, full=FALSE, ord=NULL, pc=NULL) \]

Arguments

- **...**  
  a list of variables that are the covariates that this smooth is a function of. Transformations whose form depends on the values of the data are best avoided here: e.g. \( t2(\log(x), z) \) is fine, but \( t2(I(x/sd(x)), z) \) is not (see `predict.gam`).

- **k**  
  the dimension(s) of the bases used to represent the smooth term. If not supplied then set to \( 5^d \). If supplied as a single number then this basis dimension is used for each basis. If supplied as an array then the elements are the dimensions of the component (marginal) bases of the tensor product. See `choose.k` for further information.

- **bs**  
  array (or single character string) specifying the type for each marginal basis. "cr" for cubic regression spline; "cs" for cubic regression spline with shrinkage; "cc" for periodic/cyclic cubic regression spline; "tp" for thin plate regression spline; "ts" for t.p.r.s. with extra shrinkage. See `smooth.terms` for details and full list. User defined bases can also be used here (see `smooth.construct` for an example). If only one basis code is given then this is used for all bases.

- **m**  
  The order of the spline and its penalty (for smooth classes that use this) for each term. If a single number is given then it is used for all terms. A vector can be used to supply a different \( m \) for each margin. For marginals that take vector \( m \) (e.g. `p.spline` and `Duchon.spline`), then a list can be supplied, with a vector element for each margin. NA autoinitializes. \( m \) is ignored by some bases (e.g. "cr").

- **d**  
  array of marginal basis dimensions. For example if you want a smooth for 3 covariates made up of a tensor product of a 2 dimensional t.p.r.s. basis and a 1-dimensional basis, then set \( d=c(2,1) \). Incompatibilities between built in basis types and dimension will be resolved by resetting the basis type.

- **by**  
  a numeric or factor variable of the same dimension as each covariate. In the numeric vector case the elements multiply the smooth evaluated at the corresponding covariate values (a 'varying coefficient model' results). In the factor case causes a replicate of the smooth to be produced for each factor level. See `gam.models` for further details. May also be a matrix if covariates are matrices: in this case implements linear functional of a smooth (see `gam.models` and `linear.functional.terms` for details).

- **xt**  
  Either a single object, providing any extra information to be passed to each marginal basis constructor, or a list of such objects, one for each marginal basis.

- **id**  
  A label or integer identifying this term in order to link its smoothing parameters to others of the same type. If two or more smooth terms have the same id then they will have the same smoothing parameters, and, by default, the same bases (first occurrence defines basis type, but data from all terms used in basis construction).

- **sp**  
  any supplied smoothing parameters for this term. Must be an array of the same length as the number of penalties for this smooth. Positive or zero elements are taken as fixed smoothing parameters. Negative elements signal auto-initialization. Over-rides values supplied in sp argument to `gam`. Ignored by `gamm`. 
**full**

If TRUE then there is a separate penalty for each combination of null space column and range space. This gives strict invariance. If FALSE each combination of null space and range space generates one penalty, but the columns of each null space basis are treated as one group. The latter is more parsimonious, but does mean that invariance is only achieved by an arbitrary rescaling of null space basis vectors.

**ord**

An array giving the orders of terms to retain. Here order means number of marginal range spaces used in the construction of the component. NULL to retain everything.

**pc**

If not NULL, signals a point constraint: the smooth should pass through zero at the point given here (as a vector or list with names corresponding to the smooth names). Never ignored if supplied. See `identifiability`.

**Details**

Smooths of several covariates can be constructed from tensor products of the bases used to represent smooths of one (or sometimes more) of the covariates. To do this ‘marginal’ bases are produced with associated model matrices and penalty matrices. These are reparameterized so that the penalty is zero everywhere, except for some elements on the leading diagonal, which all have the same non-zero value. This reparameterization results in an unpenalized and a penalized subset of parameters, for each marginal basis (see e.g. appendix of Wood, 2004, for details).

The re-parameterized marginal bases are then combined to produce a basis for a single function of all the covariates (dimension given by the product of the dimensions of the marginal bases). In this set up there are multiple penalty matrices — all zero, but for a mixture of a constant and zeros on the leading diagonal. No two penalties have a non-zero entry in the same place.

Essentially the basis for the tensor product can be thought of as being constructed from a set of products of the penalized (range) or unpenalized (null) space bases of the marginal smooths (see Gu, 2002, section 2.4). To construct one of the set, choose either the null space or the range space from each marginal, and from these bases construct a product basis. The result is subject to a ridge penalty (unless it happens to be a product entirely of marginal null spaces). The whole basis for the smooth is constructed from all the different product bases that can be constructed in this way. The separately penalized components of the smooth basis each have an interpretation in terms of the ANOVA - decomposition of the term. See `pen.edf` for some further information.

Note that there are two ways to construct the product. When `full=FALSE` then the null space bases are treated as a whole in each product, but when `full=TRUE` each null space column is treated as a separate null space. The latter results in more penalties, but is the strict analog of the SS-ANOVA approach.

Tensor product smooths are especially useful for representing functions of covariates measured in different units, although they are typically not quite as nicely behaved as t.p.r.s. smooths for well scaled covariates.

Note also that GAMs constructed from lower rank tensor product smooths are nested within GAMs constructed from higher rank tensor product smooths if the same marginal bases are used in both cases (the marginal smooths themselves are just special cases of tensor product smooths.)

Note that tensor product smooths should not be centred (have identifiability constraints imposed) if any marginals would not need centering. The constructor for tensor product smooths ensures that this happens.

The function does not evaluate the variable arguments.
Value

A class t2.smooth.spec object defining a tensor product smooth to be turned into a basis and penalties by the smooth.construct.tensor.smooth.spec function.

The returned object contains the following items:

- **margin**: A list of smooth.spec objects of the type returned by s, defining the basis from which the tensor product smooth is constructed.
- **term**: An array of text strings giving the names of the covariates that the term is a function of.
- **by**: is the name of any by variable as text ("NA" for none).
- **fx**: logical array with element for each penalty of the term (tensor product smooths have multiple penalties). TRUE if the penalty is to be ignored, FALSE, otherwise.
- **label**: A suitable text label for this smooth term.
- **dim**: The dimension of the smoother - i.e. the number of covariates that it is a function of.
- **mp**: TRUE is multiple penalties are to be used (default).
- **np**: TRUE to re-parameterize 1-D marginal smooths in terms of function values (default).
- **id**: the id argument supplied to te.
- **sp**: the sp argument supplied to te.

Author(s)

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References


Alternative approaches to functional ANOVA decompositions, *not* implemented by t2 terms, are discussed in:


See Also
tes,gam,gamm,
Examples

# following shows how tensor product deals nicely with
# badly scaled covariates (range of x 5% of range of z)
require(mgcv)
test1<-function(x,z,sx=0.3,sz=0.4)
  { x<-x*20
    (pi**sx*sz)*(1.2*exp(-(-x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
       0.8*exp(-(-x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
  }
n<-500
old.par<-par(mfrow=c(2,2))
x<-runif(n)/20;z<-runif(n);
x<-(1:30)/20;zs<-seq(0,1,length=30)
pr<-data.frame(x=rep(xs,30),z=rep(zs,rep(30,30)))
truth<-matrix(test1(pr$x,pr$z),30,30)
f <- test1(x,z)
y <- f + rnorm(n)*0.2
b1<-gam(y~s(x,z))
persp(xs,zs,truth);title("truth")
vis.gam(b1);title("t.p.r.s")
b2<-gam(y~t2(x,z))
vis.gam(b2);title("tensor product")
b3<-gam(y~t2(x,z,bs=c("tp","tp"))
vis.gam(b3);title("tensor product")
par(old.par)
test2<-function(u,v,w,sv=0.3,sw=0.4)
  { ((pi**sv*sw)*(1.2*exp(-(-v-0.2)^2/sv^2-(w-0.3)^2/sw^2)+
       0.8*exp(-(-v-0.7)^2/sv^2-(w-0.8)^2/sw^2))*(u-0.5)^2*20
  }
n <- 500
v <- runif(n);w<-runif(n);u<-runif(n)
f <- test2(u,v,w)
y <- f + rnorm(n)*0.2

## tensor product of 2D Duchon spline and 1D cr spline
m <- list(c(1,.5),0)
b <- gam(y~t2(v,w,u,k=c(30,5),d=c(2,1),bs=c("ds","cr"),m=m))

## look at the edf per penalty. "rr" denotes interaction term
## (range space range space). "rn" is interaction of null space
## for u with range space for v,w...
pen.edf(b)

## plot results...
op <- par(mfrow=c(2,2))
vis.gam(b,cond=list(u=0),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=.33),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=.67),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=1),color="heat",zlim=c(-0.2,3.5))
par(op)

b <- gam(y~t2(v,w,u,k=c(25,5),d=c(2,1),bs=c("tp","cr"),full=TRUE),
  method="ML")

## more penalties now. numbers in labels like "r1" indicate which
## basis function of a null space is involved in the term.
Define tensor product smooths or tensor product interactions in GAM formulae

Description

Functions used for the definition of tensor product smooths and interactions within gam model formulae. te produces a full tensor product smooth, while ti produces a tensor product interaction, appropriate when the main effects (and any lower interactions) are also present.

The functions do not evaluate the smooth - they exists purely to help set up a model using tensor product based smooths. Designed to construct tensor products from any marginal smooths with a basis-penalty representation (with the restriction that each marginal smooth must have only one penalty).

Usage

```r
te(..., k=NA, bs="cr", m=NA, d=NA, by=NA, fx=FALSE,
np=TRUE, xt=NULL, id=NULL, sp=NULL, pc=NULL)
ti(..., k=NA, bs="cr", m=NA, d=NA, by=NA, fx=FALSE,
np=TRUE, xt=NULL, id=NULL, sp=NULL, mc=FALSE, pc=NULL)
```

Arguments

... a list of variables that are the covariates that this smooth is a function of. Transformations whose form depends on the values of the data are best avoided here: e.g. te(log(x), z) is fine, but te(I(x/sd(x)), z) is not (see predict.gam).

k the dimension(s) of the bases used to represent the smooth term. If not supplied then set to 5^d. If supplied as a single number then this basis dimension is used for each basis. If supplied as an array then the elements are the dimensions of the component (marginal) bases of the tensor product. See choose.k for further information.

bs array (or single character string) specifying the type for each marginal basis. "cr" for cubic regression spline; "cs" for cubic regression spline with shrinkage; "cc" for periodic/cyclic cubic regression spline; "tp" for thin plate regression spline; "ts" for t.p.r.s. with extra shrinkage. See smooth.terms for details and full list. User defined bases can also be used here (see smooth.construct for an example). If only one basis code is given then this is used for all bases.

m The order of the spline and its penalty (for smooth classes that use this) for each term. If a single number is given then it is used for all terms. A vector can be used to supply a different m for each margin. For marginals that take vector m (e.g. p.spline and Duchon.spline), then a list can be supplied, with a vector element for each margin. NA autoinitializes. m is ignored by some bases (e.g. "cr").

d array of marginal basis dimensions. For example if you want a smooth for 3 covariates made up of a tensor product of a 2 dimensional t.p.r.s. basis and a 1-dimensional basis, then set d=c(2,1). Incompatibilities between built in basis types and dimension will be resolved by resetting the basis type.
by a numeric or factor variable of the same dimension as each covariate. In the
numeric vector case the elements multiply the smooth evaluated at the corre-
sponding covariate values (a ‘varying coefficient model’ results). In the factor
case causes a replicate of the smooth to be produced for each factor level. See
gam.models for further details. May also be a matrix if covariates are matric-
es: in this case implements linear functional of a smooth (see gam.models and
linear.functional.terms for details).

fx indicates whether the term is a fixed d.f. regression spline (TRUE) or a penalized
regression spline (FALSE).

np TRUE to use the ‘normal parameterization’ for a tensor product smooth. This
represents any 1-d marginal smooths via parameters that are function values at
‘knots’, spread evenly through the data. The parameterization makes the penal-
ties easily interpretable, however it can reduce numerical stability in some cases.

xt Either a single object, providing any extra information to be passed to each
marginal basis constructor, or a list of such objects, one for each marginal basis.

id A label or integer identifying this term in order to link its smoothing parameters
to others of the same type. If two or more smooth terms have the same id
then they will have the same smoothing parameters, and, by default, the same
bases (first occurrence defines basis type, but data from all terms used in basis
construction).

sp any supplied smoothing parameters for this term. Must be an array of the
same length as the number of penalties for this smooth. Positive or zero ele-
ments are taken as fixed smoothing parameters. Negative elements signal auto-
initialization. Over-rides values supplied in sp argument to gam. Ignored by
gamm.

mc For ti smooths you can specify which marginals should have centering con-
straints applied, by supplying 0/1 or FALSE/TRUE values for each marginal in
this vector. By default all marginals are constrained, which is what is appropri-
ate for, e.g., functional ANOVA models. Note that ’ti’ only applies constraints
to the marginals, so if you turn off all marginal constraints the term will have no
identifiability constraints. Only use this if you really understand how marginal
constraints work.

pc If not NULL, signals a point constraint: the smooth should pass through zero at
the point given here (as a vector or list with names corresponding to the smooth
names). Never ignored if supplied. See identifiability.

Details

Smooths of several covariates can be constructed from tensor products of the bases used to represent
smooths of one (or sometimes more) of the covariates. To do this ‘marginal’ bases are produced
with associated model matrices and penalty matrices, and these are then combined in the manner de-
scribed in tensor.prod.model.matrix and tensor.prod.penalties, to produce a single model
matrix for the smooth, but multiple penalties (one for each marginal basis). The basis dimension of
the whole smooth is the product of the basis dimensions of the marginal smooths.

Tensor product smooths are especially useful for representing functions of covariates measured in
different units, although they are typically not quite as nicely behaved as t.p.r.s. smooths for well
scaled covariates.

It is sometimes useful to investigate smooth models with a main-effects + interactions structure, for
example

\[ f_1(x) + f_2(z) + f_3(x, z) \]
This functional ANOVA decomposition is supported by ti terms, which produce tensor product interactions from which the main effects have been excluded, under the assumption that they will be included separately. For example the ~ ti(x) + ti(z) + ti(x,z) would produce the above main effects + interaction structure. This is much better than attempting the same thing with sor te terms representing the interactions (although mgcv does not forbid it). Technically ti terms are very simple: they simply construct tensor product bases from marginal smooths to which identifiability constraints (usually sum-to-zero) have already been applied: correct nesting is then automatic (as with all interactions in a GLM framework). See Wood (2017, section 5.6.3).

The 'normal parameterization' (np=TRUE) re-parameterizes the marginal smooths of a tensor product smooth so that the parameters are function values at a set of points spread evenly through the range of values of the covariate of the smooth. This means that the penalty of the tensor product associated with any particular covariate direction can be interpreted as the penalty of the appropriate marginal smooth applied in that direction and averaged over the smooth. Currently this is only done for marginals of a single variable. This parameterization can reduce numerical stability when used with marginal smooths other than "cc", "cr" and "cs": if this causes problems, set np=FALSE.

Note that tensor product smooths should not be centred (have identifiability constraints imposed) if any marginals would not need centering. The constructor for tensor product smooths ensures that this happens.

The function does not evaluate the variable arguments.

**Value**

A class tensor.smooth.spec object defining a tensor product smooth to be turned into a basis and penalties by the smooth.construct.tensor.smooth.spec function.

The returned object contains the following items:

- margin: A list of smooth.spec objects of the type returned by s, defining the basis from which the tensor product smooth is constructed.
- term: An array of text strings giving the names of the covariates that the term is a function of.
- by: is the name of any by variable as text ("NA" for none).
- fx: logical array with element for each penalty of the term (tensor product smooths have multiple penalties). TRUE if the penalty is to be ignored, FALSE, otherwise.
- label: A suitable text label for this smooth term.
- dim: The dimension of the smoother - i.e. the number of covariates that it is a function of.
- mp: TRUE is multiple penalties are to be used (default).
- np: TRUE to re-parameterize 1-D marginal smooths in terms of function values (default).
- id: the id argument supplied to te.
- sp: the sp argument supplied to te.
- inter: TRUE if the term was generated by ti, FALSE otherwise.
- mc: the argument mc supplied to ti.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>
References


https://www.maths.ed.ac.uk/~swood34/

See Also

s.gam.gamm, smooth.construct.tensor.smooth.spec

Examples

# following shows how tensor product deals nicely with
# badly scaled covariates (range of x 5% of range of z )
require(mgcv)
test1 <- function(x,z,sx=0.3,sz=0.4) {
  x <- x*20
  (pi**sx*sz)*(1.2*exp(-(x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
    0.8*exp(-(x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
}
n <- 500
old.par <- par(mfrow=c(2,2))
x <- runif(n)/20;z <- runif(n);
xs <- seq(0,1,length=30)/20;zs <- seq(0,1,length=30)
pr <- data.frame(x=rep(xs,30),z=rep(zs,rep(30,30)))
truth <- matrix(test1(pr$x,pr$z),30,30)
f <- test1(x,z)
y <- f + rnorm(n)*0.2
b1 <- gam(y~s(x,z))
persp(xs,zs,truth);title("truth")
vis.gam(b1);title("t.p.r.s")
b2 <- gam(y~te(x,z))
vis.gam(b2);title("tensor product")
b3 <- gam(y~ ti(x) + ti(z) + ti(x,z))
vis.gam(b3);title("tensor anova")

## now illustrate partial ANOVA decomp...
vis.gam(b3);title("full anova")
b4 <- gam(y~ ti(x) + ti(x,z,mc=c(0,1))) ## note z constrained!
vis.gam(b4);title("partial anova")
plot(b4)

par(old.par)

## now with a multivariate marginal....

test2<-function(u,v,w,sv=0.3,sw=0.4)
{ ((pi**sv*sw)*(1.2*exp(-(v-0.2)^2/sw^2-(w-0.3)^2/sw^2)+
    0.8*exp(-(v-0.7)^2/sw^2-(w-0.8)^2/sw^2)))*(u-0.5)^2*20
}
n <- 500
v <- runif(n);w<-runif(n);u<-runif(n)
f <- test2(u,v,w)
y <- f + rnorm(n)*0.2
# tensor product of 2D Duchon spline and 1D cr spline
m <- list(c(1,.5),rep(0,0)) ## example of list form of m
b <- gam(y~te(v,w,u,k=c(30,5),d=c(2,1),bs=c("ds","cr"),m=m))
plot(b)

tensor.prod.model.matrix

Row Kronecker product/ tensor product smooth construction

Description
Produce model matrices or penalty matrices for a tensor product smooth from the model matrices or penalty matrices for the marginal bases of the smooth (marginals and results can be sparse). The model matrix construction uses row Kronecker products.

Usage
  tensor.prod.model.matrix(X)
  tensor.prod.penalties(S)
  a%o%b

Arguments
X
  a list of model matrices for the marginal bases of a smooth. Items can be class
  "matrix" or "dgCMatrix", but not a mixture of the two.
S
  a list of penalties for the marginal bases of a smooth.
  a
da matrix with the same number of rows as X.
  b
ab a matrix with the same number of rows as B.

Details
If X[[1]], X[[2]] ... X[[m]] are the model matrices of the marginal bases of a tensor product smooth then the ith row of the model matrix for the whole tensor product smooth is given by
X[[1]][i,] %x% X[[2]][i,] %x% ... X[[m]][i,], where %x% is the Kronecker product. Of course
the routine operates column-wise, not row-wise!
A%o%B is the operator form of this 'row Kronecker product'.
If S[[1]], S[[2]] ... S[[m]] are the penalty matrices for the marginal bases, and I[[1]], I[[2]] ...
  I[[m]] are corresponding identity matrices, each of the same dimension as its corresponding
penalty, then the tensor product smooth has m associate penalties of the form:
S[[1]]%o%I[[2]]%x% ... I[[m]],
I[[1]]%o%S[[2]]%x% ... I[[m]]
...
I[[1]]%o%I[[2]]%x% ... S[[m]].
Of course it's important that the model matrices and penalty matrices are presented in the same
order when constructing tensor product smooths.
totalPenaltySpace

Value

Either a single model matrix for a tensor product smooth (of the same class as the marginals), or a list of penalty terms for a tensor product smooth.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

te, smooth.construct.tensor.smooth.spec

Examples

```r
require(mgcv)
## Dense row Kronecker product example...
X <- list(matrix(0:3,2,2),matrix(c(5:8,0,0),2,3))
tensor.prod.model.matrix(X)
X[[1]]%.%X[[2]]

## sparse equivalent...
Xs <- lapply(X,as,"dgCMatrix")
tensor.prod.model.matrix(Xs)
Xs[[1]]%.%Xs[[2]]

S <- list(matrix(c(2,1,1,2),2,2),matrix(c(2,1,0,1,2,1,0,1,2,3,3)))
tensor.prod.penalties(S)
## Sparse equivalent...
Ss <- lapply(S,as,"dgCMatrix")
tensor.prod.penalties(Ss)
```

`totalPenaltySpace`  
Obtaining (orthogonal) basis for null space and range of the penalty matrix

Description

INTERNAL function to obtain (orthogonal) basis for the null space and range space of the penalty, and obtain actual null space dimension components are roughly rescaled to avoid any dominating.

Usage

`totalPenaltySpace(S, H, off, p)`
Arguments

- **S**: a list of penalty matrices, in packed form.
- **H**: the coefficient matrix of an user supplied fixed quadratic penalty on the parameters of the GAM.
- **off**: a vector where the i-th element is the offset for the i-th matrix.
- **p**: total number of parameters.

Value

A list of matrix square roots such that $S[i] = B[i] \times B[i]$.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

**trichol**

*Choleski decomposition of a tri-diagonal matrix*

Description

Computes Choleski decomposition of a (symmetric positive definite) tri-diagonal matrix stored as a leading diagonal and sub/super diagonal.

Usage

```
trichol(ld, sd)
```

Arguments

- **ld**: leading diagonal of matrix
- **sd**: sub/super diagonal of matrix

Details

Calls `dpotrf` from LAPACK. The point of this is that it has $O(n)$ computational cost, rather than the $O(n^3)$ required by dense matrix methods.

Value

A list with elements ld and sd. ld is the leading diagonal and sd is the super diagonal of bidiagonal matrix $B$ where $B^T B = T$ and $T$ is the original tridiagonal matrix.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References

See Also

bandchol

Examples

require(mgcv)
## simulate some diagonals...
set.seed(19); k <- 7
ld <- runif(k)+1
sd <- runif(k-1) -.5

## get diagonals of chol factor...
trichol(ld,sd)

## compare to dense matrix result...
A <- diag(ld); for (i in 1:(k-1)) A[i,i+1] <- A[i+1,i] <- sd[i]
R <- chol(A)
diag(R);diag(R[,,-1])

trind.generator

Generates index arrays for upper triangular storage

Description

Generates index arrays for upper triangular storage up to order four. Useful when working with higher order derivatives, which generate symmetric arrays. Mainly intended for internal use.

Usage

trind.generator(K = 2, ifunc=FALSE, reverse= !ifunc)

Arguments

K positive integer determining the size of the array.
ifunc if TRUE index functions are returned in place of index arrays.
reverse should the reverse indices be computed? Probably not if ifunc==TRUE.

Details

Suppose that m=1 and you fill an array using code like for(i in 1:K) for(j in i:K) for(k in j:K) for(l in k:K) {a[i,m] <- something; m <- m+1} and do this because actually the same "something" would be stored for any permutation of the indices i,j,k,l. Clearly in storage we have the restriction l>=k>=j>=i, but for access we want no restriction on the indices. 14[i,j,k,l] produces the appropriate m for unrestricted indices. 13 and 2 do the same for 3d and 2d arrays. If ifunc==TRUE then 12, 13 and 14 are functions, so 14(i,j,k,l) returns appropriate m. For high K the function versions save storage, but are slower.

If computed, the reverse indices pick out the unique elements of a symmetric array stored redundantly. The indices refer to the location of the elements when the redundant array is accessed as its underlying vector. For example the reverse indices for a 3 by 3 symmetric matrix are 1,2,3,5,6,9.
Tweedie

Value

A list where the entries $i_1$ to $i_4$ are arrays in up to four dimensions, containing $K$ indexes along each dimension. If ifunc==TRUE index functions are returned in place of index arrays. If reverse==TRUE reverse indices $i_1r$ to $i_4r$ are returned (always as arrays).

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

Examples

library(mgcv)
A <- trind.generator(3, reverse=TRUE)

# All permutations of c(1, 2, 3) point to the same index (5)
A$i3[1, 2, 3]
A$i3[2, 1, 3]
A$i3[2, 3, 1]
A$i3[3, 1, 2]
A$i3[1, 3, 2]

## use reverse indices to pick out unique elements
## just for illustration...
A$i2[A$i2[A$i2r]]
A$i3[A$i3r]

## same again using function indices...
A <- trind.generator(3, ifunc=TRUE)
A$i3(1, 2, 3)
A$i3(2, 1, 3)
A$i3(2, 3, 1)
A$i3(3, 1, 2)
A$i3(1, 3, 2)

Tweedie

GAM Tweedie families

Description

Tweedie families, designed for use with gm from the mgcv library. Restricted to variance function powers between 1 and 2. A useful alternative to quasi when a full likelihood is desirable. Tweedie is for use with fixed $p$. tw is for use when $p$ is to be estimated during fitting. For fixed $p$ between 1 and 2 the Tweedie is an exponential family distribution with variance given by the mean to the power $p$.

tw is only useable with gm and bam but not gamm. Tweedie works with all three.

Usage

Tweedie(p=1, link = power(0))
tw(theta = NULL, link = "log", a=1.01, b=1.99)
Arguments

p

the variance of an observation is proportional to its mean to the power \( p \). \( p \) must be greater than 1 and less than or equal to 2. 1 would be Poisson, 2 is gamma.

link

The link function: one of "log", "identity", "inverse", "sqrt", or a power link (Tweedie only).

theta

Related to the Tweedie power parameter by \( p = (a + b \exp(\theta))/(1 + \exp(\theta)) \).

If this is supplied as a positive value then it is taken as the fixed value for \( p \). If it is a negative values then its absolute value is taken as the initial value for \( p \).

a

lower limit on \( p \) for optimization.

b

upper limit on \( p \) for optimization.

Details

A Tweedie random variable with 1<\( p <2 \) is a sum of \( N \) gamma random variables where \( N \) has a Poisson distribution. The \( p=1 \) case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For 1<\( p <2 \) the distribution is supported on the positive reals with a point mass at zero. \( p=2 \) is a gamma distribution. As \( p \) gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at \( p=1 \), and is therefore highly multimodal. See \texttt{ldTweedie} for more on this behaviour.

Tweedie is based partly on the \texttt{poisson} family, and partly on \texttt{tweedie} from the \texttt{statmod} package. It includes extra components to work with all \texttt{mgcv} GAM fitting methods as well as an \texttt{aic} function.

The Tweedie density involves a normalizing constant with no closed form, so this is evaluated using the series evaluation method of Dunn and Smyth (2005), with extensions to also compute the derivatives w.r.t. \( p \) and the scale parameter. Without restricting \( p \) to (1,2) the calculation of Tweedie densities is more difficult, and there does not currently seem to be an implementation which offers any benefit over \texttt{quasi}. If you need this case then the \texttt{tweedie} package is the place to start.

Value

For \texttt{Tweedie}, an object inheriting from class \texttt{family}, with additional elements

\texttt{dvar}

the function giving the first derivative of the variance function w.r.t. \texttt{mu}.

\texttt{d2var}

the function giving the second derivative of the variance function w.r.t. \texttt{mu}.

\texttt{ls}

A function returning a 3 element array: the saturated log likelihood followed by its first 2 derivatives w.r.t. the scale parameter.

For \texttt{tw}, an object of class \texttt{extended.family}.

Author(s)

Simon N. Wood \(<\text{simon.wood@r-project.org}>\).

References


See Also

1dTweedie, rTweedie

Examples

library(mgcv)
set.seed(3)
n<-400
## Simulate data...
dat <- gamSim(1,n=n,dist="poisson",scale=.2)
dat$y <- rTweedie(exp(dat$f),p=1.3,phi=.5) ## Tweedie response

## Fit a fixed p Tweedie, with wrong link ...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=Tweedie(1.25,power(.1)),
data=dat)
plot(b,pages=1)
print(b)

## Same by approximate REML...
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=Tweedie(1.25,power(.1)),
data=dat,method="REML")
plot(b1,pages=1)
print(b1)

## estimate p as part of fitting
b2 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=tw(),
data=dat,method="REML")
plot(b2,pages=1)
print(b2)
rm(dat)

twlss  

Tweedie location scale family

Description

Tweedie family in which the mean, power and scale parameters can all depend on smooth linear predictors. Restricted to estimation via the extended Fellner Schall method of Wood and Fasiolo (2017). Only usable with gam. Tweedie distributions are exponential family with variance given by $\phi \mu^p$ where $\phi$ is a scale parameter, $p$ a parameter (here between 1 and 2) and $\mu$ is the mean.

Usage

twlss(link=list("log","identity","identity"),a=1.01,b=1.99)
Arguments

- **link**: The link function list: currently no choice.
- **a**: lower limit on the power parameter relating variance to mean.
- **b**: upper limit on power parameter.

Details

A Tweedie random variable with $1 < p < 2$ is a sum of $N$ gamma random variables where $N$ has a Poisson distribution. The $p=1$ case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For $1 < p < 2$ the distribution is supported on the positive reals with a point mass at zero. $p=2$ is a gamma distribution. As $p$ gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at $p=1$, and is therefore highly multimodal. See `ldTweedie` for more on this behaviour.

The Tweedie density involves a normalizing constant with no closed form, so this is evaluated using the series evaluation method of Dunn and Smyth (2005), with extensions to also compute the derivatives w.r.t. $p$ and the scale parameter. Without restricting $p$ to (1,2) the calculation of Tweedie densities is more difficult, and there does not currently seem to be an implementation which offers any benefit over `quasi`. If you need this case then the `tweedie` package is the place to start.

Value

An object inheriting from class `general.family`.

Author(s)

Simon N. Wood <simon.wood@r-project.org>.

References


See Also

`Tweedie`, `ldTweedie`, `rTweedie`

Examples

```r
library(mgcv)
set.seed(3)
n <- 400
## Simulate data...
```
dat <- gamSim(1,n=n,dist="poisson",scale=.2)
dat$y <- rTweedie(exp(dat$f),p=1.3,phi=.5) ## Tweedie response

## Fit a fixed p Tweedie, with wrong link ...
b <- gam(list(y~s(x0)+s(x1)+s(x2)+s(x3),~1,~1),family=twlss(),
data=dat)
plot(b,pages=1)
print(b)
rm(dat)

---

**uniquecombs**

*find the unique rows in a matrix*

**Description**

This routine returns a matrix or data frame containing all the unique rows of the matrix or data frame supplied as its argument. That is, all the duplicate rows are stripped out. Note that the ordering of the rows on exit need not be the same as on entry. It also returns an index attribute for relating the result back to the original matrix.

**Usage**

`uniquecombs(x, ordered=FALSE)`

**Arguments**

- `x` is an `R` matrix (numeric), or data frame.
- `ordered` set to `TRUE` to have the rows of the returned object in the same order regardless of input ordering.

**Details**

Models with more parameters than unique combinations of covariates are not identifiable. This routine provides a means of evaluating the number of unique combinations of covariates in a model.

When `x` has only one column then the routine uses `unique` and `match` to get the index. When there are multiple columns then it uses `paste0` to produce labels for each row, which should be unique if the row is unique. Then `unique` and `match` can be used as in the single column case. Obviously the pasting is inefficient, but still quicker for large `n` than the C based code that used to be called by this routine, which had `O(nlog(n))` cost. In principle a hash table based solution in C would be only `O(n)` and much quicker in the multicolumn case.

`unique` and `duplicated`, can be used in place of this, if the full index is not needed. Relative performance is variable.

If `x` is not a matrix or data frame on entry then an attempt is made to coerce it to a data frame.

**Value**

A matrix or data frame consisting of the unique rows of `x` (in arbitrary order).

The matrix or data frame has an "index" attribute. `index[i]` gives the row of the returned matrix that contains row `i` of the original matrix.
WARNINGS

If a dataframe contains variables of a type other than numeric, logical, factor or character, which either have no as.character method, or whose as.character method is a many to one mapping, then the routine is likely to fail.

If the character representation of a dataframe variable (other than of class factor of character) contains * then in principle the method could fail (but with a warning).

Author(s)

Simon N. Wood <simon.wood@r-project.org> with thanks to Jonathan Rougier

See Also

unique, duplicated, match.

Examples

```r
require(mgcv)

## matrix example...
X <- matrix(c(1,2,3,1,2,3,4,5,6,1,3,2,4,5,6,1,1,1,6,3,byrow=TRUE)
print(X)
Xu <- uniquecombs(X);Xu
ind <- attr(Xu,"index")
## find the value for row 3 of the original from Xu
Xu[ind[3],];X[3,]

## same with fixed output ordering
Xu <- uniquecombs(X,TRUE);Xu
ind <- attr(Xu,"index")
## find the value for row 3 of the original from Xu
Xu[ind[3],];X[3,]

## data frame example...
df <- data.frame(f=factor(c("er",3,"b","er",3,3,1,2,"b")),
x=c(.5,1,1.4,.5,1,.6,4,3,1.7),
bb = c(rep(TRUE,5),rep(FALSE,4)),
fred = c("foo","a","b","foo","a","vf","er","r","g"),
stringsAsFactors=FALSE)
uniquecombs(df)
```

vcov.gam

### Extract parameter (estimator) covariance matrix from GAM fit

**Description**

Extracts the Bayesian posterior covariance matrix of the parameters or frequentist covariance matrix of the parameter estimators from a fitted `gam` object.

**Usage**

```r
## S3 method for class 'gam'
vcov(object, sandwich=FALSE, freq = FALSE, dispersion = NULL, unconditional=FALSE, ...)
```
vcov.gam

Arguments

- object: fitted model object of class `gam` as produced by `gam()`.
- sandwich: compute sandwich estimate of covariance matrix. Currently expensive for discrete bam fits.
- freq: TRUE to return the frequentist covariance matrix of the parameter estimators, FALSE to return the Bayesian posterior covariance matrix of the parameters. The latter option includes the expected squared bias according to the Bayesian smoothing prior.
- dispersion: a value for the dispersion parameter: not normally used.
- unconditional: if TRUE (and freq==FALSE) then the Bayesian smoothing parameter uncertainty corrected covariance matrix is returned, if available.
- ... other arguments, currently ignored.

Details

Basically, just extracts object$Ve, object$Vp or object$Vc (if available) from a `gamObject`, unless sandwich==TRUE in which case the sandwich estimate is computed (with or without the squared bias component).

Value

A matrix corresponding to the estimated frequentist covariance matrix of the model parameter estimators/coefficients, or the estimated posterior covariance matrix of the parameters, depending on the argument freq.

Author(s)

Henric Nilsson. Maintained by Simon N. Wood <simon.wood@r-project.org>

References


See Also

gam

Examples

```r
require(mgcv)
n <- 100
x <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=10),knots=list(x=seq(0,1,length=10)))
diag(vcov(mod))
```
vis.gam

Visualization of GAM objects

Description

Produces perspective or contour plot views of gam model predictions, fixing all but the values in view to the values supplied in cond.

Usage

vis.gam(x, view=NULL, cond=list(), n.grid=30, too.far=0, col=NA, color="heat", contour.col=NULL, se=-1, type="link", plot.type="persp", zlim=NULL, nCol=50, lp=1, ...)

Arguments

x
  a gam object, produced by gam()

view
  an array containing the names of the two main effect terms to be displayed on the x and y dimensions of the plot. If omitted the first two suitable terms will be used. Note that variables coerced to factors in the model formula won’t work as view variables, and vis.gam cannot detect that this has happened when setting defaults.

cond
  a named list of the values to use for the other predictor terms (not in view). Variables omitted from this list will have the closest observed value to the median for continuous variables, or the most commonly occuring level for factors. Parametric matrix variables have all the entries in each column set to the observed column entry closest to the column median.

n.grid
  The number of grid nodes in each direction used for calculating the plotted surface.

too.far
  plot grid nodes that are too far from the points defined by the variables given in view can be excluded from the plot. too.far determines what is too far. The grid is scaled into the unit square along with the view variables and then grid nodes more than too.far from the predictor variables are excluded.

col
  The colours for the facets of the plot. If this is NA then if se>0 the facets are transparent, otherwise the colour scheme specified in color is used. If col is not NA then it is used as the facet colour.

color
  the colour scheme to use for plots when se<=0. One of "topo", "heat", "cm", "terrain", "gray" or "bw". Schemes "gray" and "bw" also modify the colors used when se>0.

contour.col
  sets the colour of contours when using plot.type="contour". Default scheme used if NULL.

se
  if less than or equal to zero then only the predicted surface is plotted, but if greater than zero, then 3 surfaces are plotted, one at the predicted values minus se standard errors, one at the predicted values and one at the predicted values plus se standard errors.

type
  "link" to plot on linear predictor scale and "response" to plot on the response scale.

plot.type
  one of "contour" or "persp".
zlim  a two item array giving the lower and upper limits for the z-axis scale. NULL to choose automatically.

ncol  The number of colors to use in color schemes.

lp selects the linear predictor for models with more than one.

other options to pass on to persp, image or contour. In particular ticktype="detailed" will add proper axes labelling to the plots.

Details

The x and y limits are determined by the ranges of the terms named in view. If se<=0 then a single (height colour coded, by default) surface is produced, otherwise three (by default see-through) meshes are produced at mean and +/- se standard errors. Parts of the x-y plane too far from data can be excluded by setting too.far.

All options to the underlying graphics functions can be reset by passing them as extra arguments ...: such supplied values will always over-ride the default values used by vis.gam.

Value

Simply produces a plot.

WARNINGS

The routine can not detect that a variable has been coerced to factor within a model formula, and will therefore fail if such a variable is used as a view variable. When setting default view variables it can not detect this situation either, which can cause failures if the coerced variables are the first, otherwise suitable, variables encountered.

Author(s)

Simon Wood  <simon.wood@r-project.org>

Based on an original idea and design by Mike Lonergan.

See Also

persp and gam.

Examples

library(mgcv)
set.seed(0)
n<-200;sig2<-4
x0 <- runif(n, 0, 1);x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1)
y<-x0^2+x1*x2 +runif(n,-0.3,0.3)
g<-gam(y~s(x0,x1,x2))
old.par<par(mfrow=c(2,2))
# display the prediction surface in x0, x1 ....
vis.gam(g,ticktype="detailed",color="heat",theta=-35)
vis.gam(g,se=2,theta=-35) # with twice standard error surfaces
vis.gam(g, view=c("x1","x2"),cond=list(x0=0.75)) # different view
vis.gam(g, view=c("x1","x2"),cond=list(x0=.75),theta=210,phi=40,
too.far=.07)
# .... areas where there is no data are not plotted
# contour examples....
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="heat")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="terrain")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="topo")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="cm")

par(old.par)

# Examples with factor and "by" variables

fac<-rep(1:4,20)
x<-runif(80)
y<-fac+2*x^2+rnorm(80)*0.1
fac<-factor(fac)
b<-gam(y~fac+s(x))

vis.gam(b,theta=-35,color="heat") # factor example

z<-rnorm(80)*0.4
y<-as.numeric(fac)+3*x^2*z+rnorm(80)*0.1
b<-gam(y~fac+s(x,by=z))

vis.gam(b,theta=-35,color="heat",cond=list(z=1)) # by variable example

vis.gam(b,view=c("z","x"),theta= -135) # plot against by variable

---

**XWXd**

*Internal functions for discretized model matrix handling*

## Description

Routines for computing with discretized model matrices as described in Wood et al. (2017) and Li and Wood (2019).

## Usage

```r
XWXd(X,w,k,ks,ts,dt,v,qc,ntthreads=1,drop=NULL,ar.stop=-1,ar.row=-1,ar.w=-1,
     lt=NULL,rt=NULL)
XWyd(X,w,y,k,ks,ts,dt,v,qc,drop=NULL,ar.stop=-1,ar.row=-1,ar.w=-1,lt=NULL)
Xbd(X,beta,k,ks,ts,dt,v,qc,drop=NULL,lt=NULL)
diagXVXd(X,V,k,ks,ts,dt,v,qc,drop=NULL,ntthreads=1,lt=NULL,rt=NULL)
```

## Arguments

- **X**: A list of the matrices containing the unique rows of model matrices for terms of a full model matrix, or the model matrices of the terms margins. if term subsetting arguments `lt` and `rt` are non-NULL then this requires an "lpip" attribute: see details. The elements of `X` may be sparse matrices of class "dgCMatrix", in which case the list requires attributes "r" and "off" defining reverse indices (see details).
- **w**: An n-vector of weights
y  n-vector of data.
beta  coefficient vector.
k  A matrix whose columns are index n-vectors each selecting the rows of an X[[i]] required to create the full matrix.
ks  The ith term has index vectors ks[i,1]: (ks[i,2]-1). The corresponding full model matrices are summed over.
ts  The element of X at which each model term starts.
dt  How many elements of X contribute to each term.
v  v[i] is Householder vector for ith term, if qc[i]>0.
qc  if qc[i]>0 then term has a constraint.
nthreads  number of threads to use
.drop  list of columns of model matrix/parameters to drop
.ar.stop  Negative to ignore. Otherwise sum rows (ar.stop[i-1]+1): ar.stop[i] of the rows selected by ar.row and weighted by ar.w to get ith row of model matrix to use.
ar.row  extract these rows...
ar.w  weight by these weights, and sum up according to ar.stop. Used to implement AR models.
l t  use only columns of X corresponding to these model matrix terms (for left hand X in XWXd). If NULL set to rt.
rt  as lt for right hand X. If NULL set to lt. If lt and rt are NULL use all columns.
V  Coefficient covariance matrix.

Details

These functions are really intended to be internal, but are exported so that they can be used in the initialization code of families without problem. They are primarily used by bam to implement the methods given in the references. XWXd produces $X^T W X$, XWy produces $X^T W y$, Xbd produces $X \beta$ and diagXVXd produces the diagonal of $XVX^T$.

The "lpip" attribute of X is a list of the coefficient indices for each term. Required if subsetting via lt and rt.

X can be a list of sparse matrices of class "dgCMatrix", in which case reverse indices are needed, mapping stored matrix rows to rows in the full matrix (that is the reverse of k which maps full matrix rows to the stored unique matrix rows). r is the same dimension as k while off is a list with as many elements as k has columns. r and off are supplied as attributes to X. For simplicity let r and codeoff denote a single column and element corresponding to each other: then coder[off[j]: (off[j+1]-1)] contains the rows of the full matrix corresponding to row j of the stored matrix. The reverse indices are essential for efficient computation with sparse matrices. See the example code for how to create them efficiently from the forward index matrix, k.

Author(s)

Simon N. Wood <simon.wood@r-project.org>
References


Examples

library(mgcv);library(Matrix)
## simulate some data creating a marginal matrix sequence...
set.seed(0);n <- 4000
dat <- gamSim(1,n=n,dist="normal",scale=2)
dat$x4 <- runif(n)
dat$y <- dat$y + 3*exp(dat$x4*15-5)/(1+exp(dat$x4*15-5))
dat$fac <- factor(sample(1:20,n,replace=TRUE))
G <- gam(y ~ te(x0,x2,k=5,bs="bs",m=1)+s(x1)+s(x4)+s(x3,bs="fs"),
       fit=FALSE,data=dat,discrete=TRUE)
p <- ncol(G$X)
## create a sparse version...
Xs <- list(); r <- G$kd*0; off <- list()
for (i in 1:length(G$Xd)) Xs[[i]] <- as(G$Xd[[i]],"dgCMatrix")
for (j in 1:nrow(G$ks)) { ## create the reverse indices...
  nr <- nrow(Xs[[j]]) # make sure we always tab to final stored row
  for (i in G$ks[j,1]:(G$ks[j,2]-1)) {
    r[,i] <- (1:length(G$kd[,i]))[order(G$kd[,i])]
    off[[i]] <- cumsum(c(1,tabulate(G$kd[,i],nbins=nr)))-1
  }
}
attr(Xs,"off") <- off;attr(Xs,"r") <- r
par(mfrow=c(2,3))
beta <- runif(p)
Xb0 <- Xbd(G$Xd,beta,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
Xb1 <- Xbd(Xs,beta,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(Xb0-Xb1);plot(Xb0,Xb1,pch=".
bb <- cbind(beta,beta+runif(p)*.3)
Xb0 <- Xbd(G$Xd,bb,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
Xb1 <- Xbd(Xs,bb,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(Xb0-Xb1);plot(Xb0,Xb1,pch=".
w <- runif(n)
XWy0 <- XWyd(G$Xd,w,y=dat$y,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
XWy1 <- XWyd(Xs,w,y=dat$y,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(XWy1-XWy0);plot(XWy1,XWy0,pch=".
yy <- cbind(dat$y,dat$y+runif(n)-.5)
XWy0 <- XWyd(G$Xd,w,y=yy,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
XWy1 <- XWyd(Xs,w,y=yy,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(XWy1-XWy0);plot(XWy1,XWy0,pch=".
A <- XWXd(G$Xd,w,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
B <- XWXd(Xs,w,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(A-B);plot(A,B,pch=".

3168 XWXd
ziP = GAM zero-inflated (hurdle) Poisson regression family

Description

Family for use with \texttt{gam} or \texttt{bam}, implementing regression for zero inflated Poisson data when the complimentary log log of the zero probability is linearly dependent on the log of the Poisson parameter. Use with great care, noting that simply having many zero response observations is not an indication of zero inflation: the question is whether you have too many zeroes given the specified model.

This sort of model is really only appropriate when none of your covariates help to explain the zeroes in your data. If your covariates predict which observations are likely to have zero mean then adding a zero inflated model on top of this is likely to lead to identifiability problems. Identifiability problems may lead to fit failures, or absurd values for the linear predictor or predicted values.

Usage

\texttt{ziP(theta = NULL, link = "identity", b=0)}

Arguments

- \texttt{theta} the 2 parameters controlling the slope and intercept of the linear transform of the mean controlling the zero inflation rate. If supplied then treated as fixed parameters ($\theta_1$ and $\theta_2$), otherwise estimated.
- \texttt{link} The link function: only the "identity" is currently supported.
- \texttt{b} a non-negative constant, specifying the minimum dependence of the zero inflation rate on the linear predictor.

Details

The probability of a zero count is given by $1 - p$, whereas the probability of count $y > 0$ is given by the truncated Poisson probability function $p \mu^y / ((\exp(\mu) - 1) y!)$. The linear predictor gives $\log \mu$, while $\eta = \log(-\log(1 - p))$ and $\theta = \theta_1 + \{b + \exp(\theta_2)\} \log \mu$. The theta parameters are estimated alongside the smoothing parameters. Increasing the b parameter from zero can greatly reduce identifiability problems, particularly when there are very few non-zero data.

The fitted values for this model are the log of the Poisson parameter. Use the \texttt{predict} function with \texttt{type="response"} to get the predicted expected response. Note that the theta parameters reported in model summaries are $\theta_1$ and $b + \exp(\theta_2)$.

These models should be subject to very careful checking, especially if fitting has not converged. It is quite easy to set up models with identifiability problems, particularly if the data are not really zero inflated, but simply have many zeroes because the mean is very low in some parts of the covariate space. See example for some obvious checks. Take convergence warnings seriously.

\begin{verbatim}
V <- crossprod(matrix(runif(p*p),p,p))
ii <- c(20:30,100:200)
jj <- c(50:90,150:160)
V[ii,jj] <- 0;V[jj,ii] <- 0
d1 <- diagXVXd(G$Xd,V,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
Vs <- as(V,"dgCMatrix")
d2 <- diagXVXd(Xs,Vs,G$kd,G$ks,G$ts,G$dt,G$v,G$qc)
range(d1-d2);plot(d1,d2,pch=".")
\end{verbatim}
Value

An object of class `extended.family`.

WARNINGS

Zero inflated models are often over-used. Having lots of zeroes in the data does not in itself imply zero inflation. Having too many zeroes *given the model mean* may imply zero inflation.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


See Also

ziplss

Examples

```r
rzip <- function(gamma,theta= c(-2,.3)) {
  ## generate zero inflated Poisson random variables, where
  ## lambda = exp(gamma), eta = theta[1] + exp(theta[2])*gamma
  ## and 1-p = exp(-exp(eta)).
  y <- gamma; n <- length(y)
  lambda <- exp(gamma)
  eta <- theta[1] + exp(theta[2])*gamma
  p <- 1- exp(-exp(eta))
  ind <- p > runif(n)
  y[ind] <- 0
  np <- sum(ind)
  ## generate from zero truncated Poisson, given presence...
  y[ind] <- qpois(runif(np,dpois(0,lambda[ind]),1),lambda[ind])
  y
}
```

```R
library(mgcv)
## Simulate some ziP data...
set.seed(1);n<-400
dat <- gamSim(1,n=n)
dat$y <- rzip(dat$f/4-1)

b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ziP(),data=dat)

b$outer.info ## check convergence!!
```

```R
b plot(b,pages=1)
plot(b,pages=1,unconditional=TRUE) ## add s.p. uncertainty
gam.check(b)
## more checking...
## 1. If the zero inflation rate becomes decoupled from the linear predictor,
## it is possible for the linear predictor to be almost unbounded in regions
```
## containing many zeroes. So examine if the range of predicted values
## is sane for the zero cases?
range(predict(b,type="response"))[b$y==0])

## 2. Further plots...
par(mfrow=c(2,2))
plot(predict(b,type="response"),residuals(b))
plot(predict(b,type="response"),b$y);abline(0,1,col=2)
plot(b$linear.predictors,b$y)
qq.gam(b,rep=20,level=1)

## 3. Refit fixing the theta parameters at their estimated values, to check we
## get essentially the same fit...
thb <- b$family$getTheta()
b0 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ziP(theta=thb),data=dat)
b;b0

## Example fit forcing minimum linkage of prob present and
## linear predictor. Can fix some identifiability problems.
b2 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=ziP(b=.3),data=dat)

---

### Description

The `ziplss` family implements a zero inflated (hurdle) Poisson model in which one linear predictor controls the probability of presence and the other controls the mean given presence. Useable only with `gam`, the linear predictors are specified via a list of formulae. Should be used with care: simply having a large number of zeroes is not an indication of zero inflation.

Requires integer count data.

### Usage

```r
ziplss(link=list("identity","identity"))
zipll(y,g,eta,deriv=0)
```

### Arguments

- **link**: two item list specifying the link - currently only identity links are possible, as parameterization is directly in terms of log of Poisson response and logit of probability of presence.
- **y**: response
- **g**: gamma vector
- **eta**: eta vector
- **deriv**: number of derivatives to compute
Details

ziplss is used with gam to fit 2 stage zero inflated Poisson models. gam is called with a list containing 2 formulae, the first specifies the response on the left hand side and the structure of the linear predictor for the Poisson parameter on the right hand side. The second is one sided, specifying the linear predictor for the probability of presence on the right hand side.

The fitted values for this family will be a two column matrix. The first column is the log of the Poisson parameter, and the second column is the complimentary log log of probability of presence. Predictions using predict.gam will also produce 2 column matrices for type "link" and "response".

The null deviance computed for this model assumes that a single probability of presence and a single Poisson parameter are estimated.

For data with large areas of covariate space over which the response is zero it may be advisable to use low order penalties to avoid problems. For 1D smooths uses e.g. s(x,m=1) and for isotropic smooths use Duchon.splines in place of thin plate terms with order 1 penalties, e.g s(x,z,m=c(1,.5)) — such smooths penalize towards constants, thereby avoiding extreme estimates when the data are uninformative.

zipl1 is a function used by ziplss, exported only to allow external use of the ziplss family. It is not usually called directly.

Value

For ziplss An object inheriting from class general.family.

WARNINGS

Zero inflated models are often over-used. Having lots of zeroes in the data does not in itself imply zero inflation. Having too many zeroes *given the model mean* may imply zero inflation.

Author(s)

Simon N. Wood <simon.wood@r-project.org>

References


Examples

library(mgcv)
## simulate some data...
f0 <- function(x) 2 * sin(pi * x); f1 <- function(x) exp(2 * x)
f2 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 + 10 *
  (10 * x)^3 * (1 - x)^10
n <- 500;set.seed(5)
x0 <- runif(n); x1 <- runif(n)
x2 <- runif(n); x3 <- runif(n)

## Simulate probability of potential presence...
eta1 <- f0(x0) + f1(x1) - 3
p <- binomial()$linkinv(eta1)
y <- as.numeric(runif(n)<p) ## 1 for presence, 0 for absence
## Simulate y given potentially present (not exactly model fitted!)...

```r
ind <- y>0
eta2 <- f2(x2[ind])/3
y[ind] <- rpois(exp(eta2),exp(eta2))
```

## Fit ZIP model...

```r
b <- gam(list(y~s(x2)+s(x3),~s(x0)+s(x1)),family=ziplss())
b$outer.info ## check convergence
```

```r
summary(b)
plot(b,pages=1)
```
Chapter 25

The nlme package

---

ACF  
**Autocorrelation Function**

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: gls and lme.

Usage

ACF(object, maxLag, ...)

Arguments

- **object**: any object from which an autocorrelation function can be obtained. Generally an object resulting from a model fit, from which residuals can be extracted.
- **maxLag**: maximum lag for which the autocorrelation should be calculated.
- **...**: some methods for this generic require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <Bates@stat.wisc.edu>

References


See Also

ACF.gls, ACF.lme, plot.ACF
Examples

```r
## see the method function documentation
```

### Description

This method function calculates the empirical autocorrelation function for the residuals from a `gls` fit. If a grouping variable is specified in `form`, the autocorrelation values are calculated using pairs of residuals within the same group; otherwise all possible residual pairs are used. The autocorrelation function is useful for investigating serial correlation models for equally spaced data.

### Usage

```r
## S3 method for class 'gls'
ACF(object, maxLag, resType, form, na.action, ...)
```

### Arguments

- **object**: an object inheriting from class "gls", representing a generalized least squares fitted model.
- **maxLag**: an optional integer giving the maximum lag for which the autocorrelation should be calculated. Defaults to maximum lag in the residuals.
- **resType**: an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
- **form**: an optional one sided formula of the form `~ t`, or `~ t | g`, specifying a time covariate `t` and, optionally, a grouping factor `g`. The time covariate must be integer valued. When a grouping factor is present in `form`, the autocorrelations are calculated using residual pairs within the same group. Defaults to `~ 1`, which corresponds to using the order of the observations in the data as a covariate, and no groups.
- **na.action**: a function that indicates what should happen when the data contain `NA`s. The default action (na.fail) causes `ACF.gls` to print an error message and terminate if there are any incomplete observations.
- **...**: some methods for this generic require additional arguments.

### Value

A data frame with columns `lag` and `ACF` representing, respectively, the lag between residuals within a pair and the corresponding empirical autocorrelation. The returned value inherits from class ACF.

### Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
References


See Also

ACF.lme, plot.ACF

Examples

fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
ACF(fm1, form = ~ 1 | Mare)

# Pinheiro and Bates, p. 255-257
fm1Dial.gls <- gls(rate ~
(pressure+I(pressure^2)+I(pressure^3)+I(pressure^4))*QB,
Dialyzer)

fm2Dial.gls <- update(fm1Dial.gls,
weights = varPower(form = ~ pressure))

ACF(fm2Dial.gls, form = ~ 1 | Subject)

---

ACF.lme

**Autocorrelation Function for lme Residuals**

Description

This method function calculates the empirical autocorrelation function for the within-group residuals from an lme fit. The autocorrelation values are calculated using pairs of residuals within the innermost group level. The autocorrelation function is useful for investigating serial correlation models for equally spaced data.

Usage

```r
## S3 method for class 'lme'
ACF(object, maxLag, resType, ...)
```

Arguments

- **object**: an object inheriting from class "lme", representing a fitted linear mixed-effects model.
- **maxLag**: an optional integer giving the maximum lag for which the autocorrelation should be calculated. Defaults to maximum lag in the within-group residuals.
- **resType**: an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
- **...**: some methods for this generic require additional arguments – not used.
Value

a data frame with columns lag and ACF representing, respectively, the lag between residuals within a pair and the corresponding empirical autocorrelation. The returned value inherits from class ACF.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

ACF.gls, plot.ACF

Examples

fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
          Ovary, random = ~ sin(2*pi*Time) | Mare)
ACF(fm1, maxLag = 11)

# Pinheiro and Bates, p240-241
fm1Over.lme <- lme(follicles ~ sin(2*pi*Time) +
                    cos(2*pi*Time), data=Ovary,
                    random=pdDiag(~sin(2*pi*Time)))
(ACF.fm1Over <- ACF(fm1Over.lme, maxLag=10))
plot(ACF.fm1Over, alpha=0.01)

---

Alfalfa

Split-Plot Experiment on Varieties of Alfalfa

Description

The Alfalfa data frame has 72 rows and 4 columns.

Format

This data frame contains the following columns:

- **Variety** a factor with levels Cossack, Ladak, and Ranger
- **Date** a factor with levels None S1 S20 07
- **Block** a factor with levels 1 2 3 4 5 6
- **Yield** a numeric vector
Details

These data are described in Snedecor and Cochran (1980) as an example of a split-plot design. The treatment structure used in the experiment was a $3 \times 4$ full factorial, with three varieties of alfalfa and four dates of third cutting in 1943. The experimental units were arranged into six blocks, each subdivided into four plots. The varieties of alfalfa (Cossac, Ladak, and Ranger) were assigned randomly to the blocks and the dates of third cutting (None, S1—September 1, S20—September 20, and O7—October 7) were randomly assigned to the plots. All four dates were used on each block.

Source


allCoef

Extract Coefficients from a Set of Objects

Description

The extractor function is applied to each object in ..., with the result being converted to a vector. A map attribute is included to indicate which pieces of the returned vector correspond to the original objects in dots.

Usage

allCoef(..., extract)

Arguments

... objects to which extract will be applied. Generally these will be model components, such as corStruct and varFunc objects.

extract an optional extractor function. Defaults to coef.

Value

a vector with all elements, generally coefficients, obtained by applying extract to the objects in ....

Author(s)

José' Pinheiro and Douglas Bates

See Also

lmeStruct, nlmeStruct

Examples

cs1 <- corAR1(0.1)
vf1 <- varPower(0.5)
allCoef(cs1, vf1)
Description

When only one fitted model object is present, a data frame with the numerator degrees of freedom, F-values, and P-values for Wald tests for the terms in the model (when Terms and L are NULL), a combination of model terms (when Terms is not NULL), or linear combinations of the model coefficients (when L is not NULL). Otherwise, when multiple fitted objects are being compared, a data frame with the degrees of freedom, the (restricted) log-likelihood, the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC) of each object is returned. If test=TRUE, whenever two consecutive objects have different number of degrees of freedom, a likelihood ratio statistic with the associated p-value is included in the returned data frame.

Usage

### S3 method for class 'gls'

```r
anova(object, ..., test, type, adjustSigma, Terms, L, verbose)
```

Arguments

- **object**: an object inheriting from class "gls", representing a generalized least squares fit.
- **...**: other optional fitted model objects inheriting from classes "gls", "gnls", "lm", "lme", "lmlist", "nlme", "nlslist", or "nls".
- **test**: an optional logical value controlling whether likelihood ratio tests should be used to compare the fitted models represented by `object` and the objects in .... Defaults to `TRUE`.
- **type**: an optional character string specifying the type of sum of squares to be used in F-tests for the terms in the model. If "sequential", the sequential sum of squares obtained by including the terms in the order they appear in the model is used; else, if "marginal", the marginal sum of squares obtained by deleting a term from the model at a time is used. This argument is only used when a single fitted object is passed to the function. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "sequential".
- **adjustSigma**: an optional logical value. If TRUE and the estimation method used to obtain `object` was maximum likelihood, the residual standard error is multiplied by \( \sqrt{\frac{n_{obs}}{n_{obs} - n_{par}}} \), converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is `TRUE`.
- **Terms**: an optional integer or character vector specifying which terms in the model should be jointly tested to be zero using a Wald F-test. If given as a character vector, its elements must correspond to term names; else, if given as an integer vector, its elements must correspond to the order in which terms are included in the model. This argument is only used when a single fitted object is passed to the function. Default is NULL.
- **L**: an optional numeric vector or array specifying linear combinations of the coefficients in the model that should be tested to be zero. If given as an array, its rows define the linear combinations to be tested. If names are assigned to the vector elements (array columns), they must correspond to coefficients names and will...
be used to map the linear combination(s) to the coefficients; else, if no names are
available, the vector elements (array columns) are assumed in the same order as
the coefficients appear in the model. This argument is only used when a single
fitted object is passed to the function. Default is NULL.

verbose

an optional logical value. If TRUE, the calling sequences for each fitted model
object are printed with the rest of the output, being omitted if verbose = FALSE.
Defaults to FALSE.

Value

a data frame inheriting from class "anova.lme".

Note

Likelihood comparisons are not meaningful for objects fit using restricted maximum likelihood and
with different fixed effects.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

York.

See Also

gls, gnls, nlme, lme, logLik.gls, AIC, BIC, print.anova.lme

Examples

# AR(1) errors within each Mare
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
correlation = corAR1(form = ~ 1 | Mare))
anova(fm1)
# variance changes with a power of the absolute fitted values?
fm2 <- update(fm1, weights = varPower())
anova(fm1, fm2)

# Pinheiro and Bates, p. 251-252
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
correlation = corSymm(form = ~ 1 | Subject),
weights = varIdent(form = ~ 1 | age))
fm2Orth.gls <- update(fm1Orth.gls,
corr = corCompSymm(form = ~ 1 | Subject))
anova(fm1Orth.gls, fm2Orth.gls)

# Pinheiro and Bates, pp. 215-215, 255-260
# p. 215
fm1Dial.lme <-
  lme(rate ~ (pressure + I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
      Dialyzer, ~ pressure + I(pressure^2))
# p. 216
fm2Dial.lme <- update(fm1Dial.lme,
anova.lme

Compare Likelihoods of Fitted Objects

Description

When only one fitted model object is present, a data frame with the numerator degrees of freedom, denominator degrees of freedom, F-values, and P-values for Wald tests for the terms in the model (when Terms and L are NULL), a combination of model terms (when Terms in not NULL), or linear combinations of the model coefficients (when L is not NULL). Otherwise, when multiple fitted objects are being compared, a data frame with the degrees of freedom, the (restricted) log-likelihood, the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC) of each object is returned. If test=TRUE, whenever two consecutive objects have different number of degrees of freedom, a likelihood ratio statistic with the associated p-value is included in the returned data frame.

Usage

## S3 method for class 'lme'
anova(object, ..., test, type, adjustSigma, Terms, L, verbose)

Arguments

- object: an object inheriting from class "lme", representing a fitted linear mixed-effects model.
- ...: other optional fitted model objects inheriting from classes "gls", "gnls", "lm", "lme", "lmList", "nlme", "nlsList", or "nls".
test an optional logical value controlling whether likelihood ratio tests should be used to compare the fitted models represented by object and the objects in ... Defaults to TRUE.

type an optional character string specifying the type of sum of squares to be used in F-tests for the terms in the model. If "sequential", the sequential sum of squares obtained by including the terms in the order they appear in the model is used; else, if "marginal", the marginal sum of squares obtained by deleting a term from the model at a time is used. This argument is only used when a single fitted object is passed to the function. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "sequential".

adjustSigma an optional logical value. If TRUE and the estimation method used to obtain object was maximum likelihood, the residual standard error is multiplied by \( \sqrt{n_{obs}}(n_{obs} - n_{par}) \), converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is TRUE.

Terms an optional integer or character vector specifying which terms in the model should be jointly tested to be zero using a Wald F-test. If given as a character vector, its elements must correspond to term names; else, if given as an integer vector, its elements must correspond to the order in which terms are included in the model. This argument is only used when a single fitted object is passed to the function. Default is NULL.

L an optional numeric vector or array specifying linear combinations of the coefficients in the model that should be tested to be zero. If given as an array, its rows define the linear combinations to be tested. If names are assigned to the vector elements (array columns), they must correspond to coefficients names and will be used to map the linear combination(s) to the coefficients; else, if no names are available, the vector elements (array columns) are assumed in the same order as the coefficients appear in the model. This argument is only used when a single fitted object is passed to the function. Default is NULL.

x an object inheriting from class "anova.lme"

verbose an optional logical value. If TRUE, the calling sequences for each fitted model object are printed with the rest of the output, being omitted if verbose = FALSE. Defaults to FALSE.

Value a data frame inheriting from class "anova.lme".

Note Likelihood comparisons are not meaningful for objects fit using restricted maximum likelihood and with different fixed effects.

Author(s) José Pinheiro and Douglas Bates <bates@stat.wisc.edu>


See Also gls, gls, nlme, lme, AIC, BIC, print.anova.lme, logLik.lme,
Examples

```r
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
anova(fm1)
fm2 <- update(fm1, random = pdDiag(~age))
anova(fm1, fm2)
```

## Pinheiro and Bates, pp. 251-254 ------------------------------------------

```r
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
correlation = corSymm(form = ~ 1 | Subject),
weights = varIdent(form = ~ 1 | age))
fm2Orth.gls <- update(fm1Orth.gls,
corr = corCompSymm(form = ~ 1 | Subject))
```

## anova.gls examples:
anova(fm1Orth.gls, fm2Orth.gls)

```r
fm3Orth.gls <- update(fm2Orth.gls, weights = NULL)
anova(fm2Orth.gls, fm3Orth.gls)
fm4Orth.gls <- update(fm3Orth.gls, weights = varIdent(form = ~ 1 | Sex))
anova(fm3Orth.gls, fm4Orth.gls)
```

# not in book but needed for the following command

```r
fm3Orth.lme <- lme(distance ~ Sex*I(age-11), data = Orthodont,
random = ~ I(age-11) | Subject,
weights = varIdent(form = ~ 1 | Sex))
```

# Compare an "lme" object with a "gls" object (test would be non-sensical!)

```r
anova(fm3Orth.lme, fm4Orth.gls, test = FALSE)
```

## Pinheiro and Bates, pp. 222-225 ------------------------------------------

```r
op <- options(contrasts = c("contr.treatment", "contr.poly"))
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight, random = ~ Time)
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# Test a specific contrast
anova(fm2BW.lme, L = c("Time:Diet2" = 1, "Time:Diet3" = -1))
```

## Pinheiro and Bates, pp. 352-365 ------------------------------------------

```r
fm1Theo.lis <- nlsList(
  conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data=Theoph)
fm1Theo.lis
fm1Theo.nlme <- nlme(fm1Theo.lis)
fm2Theo.nlme <- update(fm1Theo.nlme, random= pdDiag(lKe+lKa+lCl~1) )
fm3Theo.nlme <- update(fm2Theo.nlme, random= pdDiag( lKa+lCl~1) )
```

# Comparing the 3 nlme models

```r
anova(fm1Theo.nlme, fm3Theo.nlme, fm2Theo.nlme)
```

options(op) # (set back to previous state)

---

**as.matrix.corStruct**  
*Matrix of a corStruct Object*

**Description**

This method function extracts the correlation matrix, or list of correlation matrices, associated with object.
Usage

## S3 method for class 'corStruct'
as.matrix(x, ...)

Arguments

x | an object inheriting from class "corStruct", representing a correlation structure.
...
| further arguments passed from other methods.

Value

If the correlation structure includes a grouping factor, the returned value will be a list with components given by the correlation matrices for each group. Otherwise, the returned value will be a matrix representing the correlation structure associated with object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

corClasses, corMatrix

Examples

cst1 <- corAR1(form = ~1|Subject)
cst1 <- Initialize(cst1, data = Orthodont)
as.matrix(cst1)

Description

This method function extracts the positive-definite matrix represented by x.

Usage

## S3 method for class 'pdMat'
as.matrix(x, ...)

Arguments

x | an object inheriting from class "pdMat", representing a positive-definite matrix.
...
| further arguments passed from other methods.
as.matrix.reStruct

**Value**

a matrix corresponding to the positive-definite matrix represented by x.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**


**See Also**

pdMat, corMatrix

**Examples**

```r
as.matrix(pdSymm(diag(4)))
```

---

**as.matrix.reStruct**

*Matrices of an reStruct Object*

**Description**

This method function extracts the positive-definite matrices corresponding to the pdMat elements of object.

**Usage**

```r
## S3 method for class 'reStruct'
as.matrix(x, ...)
```

**Arguments**

- `x` an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
- `...` further arguments passed from other methods.

**Value**

a list with components given by the positive-definite matrices corresponding to the elements of object.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**

asOneFormula

See Also

as.matrix.pdMat, reStruct.pdMat

Examples

rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
as.matrix(rs1)

asOneFormula Combine Formulas of a Set of Objects

Description

The names of all variables used in the formulas extracted from the objects defined in ... are con-
verted into a single linear formula, with the variables names separated by +.

Usage

asOneFormula(..., omit)

Arguments

... objects, or lists of objects, from which a formula can be extracted.
omit an optional character vector with the names of variables to be omitted from the
returned formula. Defaults to c(".", "pi").

Value

a one-sided linear formula with all variables named in the formulas extracted from the objects in
..., except the ones listed in omit.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

formula, all.vars

Examples

asOneFormula(y ~ x + z | g, list(~ w, ~ t * sin(2 * pi)))
**Assay**  
*Bioassay on Cell Culture Plate*

### Description

The *Assay* data frame has 60 rows and 4 columns.

### Format

This data frame contains the following columns:

- **Block** an ordered factor with levels 2 < 1 identifying the block where the wells are measured.
- **sample** a factor with levels a to f identifying the sample corresponding to the well.
- **dilut** a factor with levels 1 to 5 indicating the dilution applied to the well
- **logDens** a numeric vector of the log-optical density

### Details

These data, courtesy of Rich Wolfe and David Lansky from Searle, Inc., come from a bioassay run on a 96-well cell culture plate. The assay is performed using a split-block design. The 8 rows on the plate are labeled A–H from top to bottom and the 12 columns on the plate are labeled 1–12 from left to right. Only the central 60 wells of the plate are used for the bioassay (the intersection of rows B–G and columns 2–11). There are two blocks in the design: Block 1 contains columns 2–6 and Block 2 contains columns 7–11. Within each block, six samples are assigned randomly to rows and five (serial) dilutions are assigned randomly to columns. The response variable is the logarithm of the optical density. The cells are treated with a compound that they metabolize to produce the stain. Only live cells can make the stain, so the optical density is a measure of the number of cells that are alive and healthy.

### Source


---

**asTable**  
*Convert groupedData to a matrix*

### Description

Create a tabular representation of the response in a balanced groupedData object.

### Usage

`asTable(object)`

### Arguments

- **object** A balanced groupedData object
Details

A balanced groupedData object can be represented as a matrix or table of response values corresponding to the values of a primary covariate for each level of a grouping factor. This function creates such a matrix representation of the data in object.

Value

A matrix. The data in the matrix are the values of the response. The columns correspond to the distinct values of the primary covariate and are labelled as such. The rows correspond to the distinct levels of the grouping factor and are labelled as such.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

groupedData, isBalanced, balancedGrouped

Examples

```
asTable(Orthodont)
```

# Pinheiro and Bates, p. 109
```
ergoStool.mat <- asTable(ergoStool)
```

---

### augPred

**Augmented Predictions**

Description

Predicted values are obtained at the specified values of `primary`. If `object` has a grouping structure (i.e. `getGroups(object)` is not `NULL`), predicted values are obtained for each group. If `level` has more than one element, predictions are obtained for each level of the `max(level)` grouping factor. If other covariates besides `primary` are used in the prediction model, their average (numeric covariates) or most frequent value (categorical covariates) are used to obtain the predicted values. The original observations are also included in the returned object.

Usage

```
augPred(object, primary, minimum, maximum, length.out, ...)
```

## S3 method for class 'lme'
augPred(object, primary = NULL,
minimum = min(primary), maximum = max(primary),
length.out = 51, level = Q, ...)
Arguments

- **object**: a fitted model object from which predictions can be extracted, using a `predict` method.
- **primary**: an optional one-sided formula specifying the primary covariate to be used to generate the augmented predictions. By default, if a covariate can be extracted from the data used to generate `object` (using `getCovariate`), it will be used as primary.
- **minimum**: an optional lower limit for the primary covariate. Defaults to `min(primary)`.
- **maximum**: an optional upper limit for the primary covariate. Defaults to `max(primary)`.
- **length.out**: an optional integer with the number of primary covariate values at which to evaluate the predictions. Defaults to 51.
- **level**: an optional integer vector specifying the desired prediction levels. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Defaults to the innermost level.
- **...**: some methods for the generic may require additional arguments.

Value

A data frame with four columns representing, respectively, the values of the primary covariate, the groups (if `object` does not have a grouping structure, all elements will be 1), the predicted or observed values, and the type of value in the third column: `original` for the observed values and `predicted` (single or no grouping factor) or `predict.groupVar` (multiple levels of grouping), with `groupVar` replaced by the actual grouping variable name (`fixed` is used for population predictions). The returned object inherits from class "augPred".

Note

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls`, `lme`, and `lmList`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

- `plot.augPred`, `getGroups`, `predict`

Examples

```r
fm1 <- lme(Orthodont, random = ~1)
augPred(fm1, length.out = 2, level = c(0,1))
```
balancedGrouped  

Create a groupedData object from a matrix

Description

Create a groupedData object from a data matrix. This function can be used only with balanced data. The opposite conversion, from a groupedData object to a matrix, is done with asTable.

Usage

balancedGrouped(form, data, labels=NULL, units=NULL)

Arguments

form  
A formula of the form y ~ x | g giving the name of the response, the primary covariate, and the grouping factor.

data  
A matrix or data frame containing the values of the response grouped according to the levels of the grouping factor (rows) and the distinct levels of the primary covariate (columns). The dimnames of the matrix are used to construct the levels of the grouping factor and the primary covariate.

labels  
an optional list of character strings giving labels for the response and the primary covariate. The label for the primary covariate is named x and that for the response is named y. Either label can be omitted.

units  
an optional list of character strings giving the units for the response and the primary covariate. The units string for the primary covariate is named x and that for the response is named y. Either units string can be omitted.

Value

A balanced groupedData object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

groupedData, isBalanced, asTable

Examples

OrthoMat <- asTable(Orthodont)
Orth2 <- balancedGrouped(distance ~ age | Subject, data = OrthoMat,
labels = list(x = "Age",
y = "Distance from pituitary to pterygomaxillary fissure"),
units = list(x = "(yr)", y = "(mm)"))
Orth2[1:10,]  ## check the first few entries
# Pinheiro and Bates, p. 109
```
ergoStool.mat <- aTable(ergoStool)
balancedGrouped(effort~Type|Subject,
              data=ergoStool.mat)
```

## bdf

### Language scores

**Description**

The bdf data frame has 2287 rows and 25 columns of language scores from grade 8 pupils in elementary schools in The Netherlands.

**Usage**

```
data(bdf)
```

**Format**

- `schoolNR` a factor denoting the school.
- `pupilNR` a factor denoting the pupil.
- `IQ.verb` a numeric vector of verbal IQ scores
- `IQ.perf` a numeric vector of IQ scores.
- `sex` Sex of the student.
- `Minority` a factor indicating if the student is a member of a minority group.
- `repeatgr` an ordered factor indicating if one or more grades have been repeated.
- `aritPRET` a numeric vector
- `classNR` a numeric vector
- `aritPOST` a numeric vector
- `langPRET` a numeric vector
- `langPOST` a numeric vector
- `ses` a numeric vector of socioeconomic status indicators.
- `denomina` a factor indicating of the school is a public school, a Protestant private school, a Catholic private school, or a non-denominational private school.
- `schoolSES` a numeric vector
- `satiprin` a numeric vector
- `natitest` a factor with levels 0 and 1
- `meetings` a numeric vector
- `currmeet` a numeric vector
- `mixedgra` a factor indicating if the class is a mixed-grade class.
- `permino` a numeric vector
- `aritdiff` a numeric vector
- `homework` a numeric vector
- `classsiz` a numeric vector
- `groupsiz` a numeric vector
Source


References


Examples

summary(bdf)

## More examples, including lme() fits reproducing parts in the above book, are available in the R script files
system.file("mlbook", "ch04.R", package ="nlme") # and
system.file("mlbook", "ch05.R", package ="nlme")

BodyWeight  Rat weight over time for different diets

Description

The BodyWeight data frame has 176 rows and 4 columns.

Format

This data frame contains the following columns:

weight  a numeric vector giving the body weight of the rat (grams).

Time  a numeric vector giving the time at which the measurement is made (days).

Rat  an ordered factor with levels 2 < 3 < 4 < 1 < 8 < 5 < 6 < 7 < 11 < 9 < 10 < 12 < 13 < 15 < 14 < 16 identifying the rat whose weight is measured.

Diet  a factor with levels 1 to 3 indicating the diet that the rat receives.

Details

Hand and Crowder (1996) describe data on the body weights of rats measured over 64 days. These data also appear in Table 2.4 of Crowder and Hand (1990). The body weights of the rats (in grams) are measured on day 1 and every seven days thereafter until day 64, with an extra measurement on day 44. The experiment started several weeks before “day 1.” There are three groups of rats, each on a different diet.

Source


Description

The Cefamandole data frame has 84 rows and 3 columns.

Format

This data frame contains the following columns:

- **Subject**  a factor giving the subject from which the sample was drawn.
- **Time**  a numeric vector giving the time at which the sample was drawn (minutes post-injection).
- **conc**  a numeric vector giving the observed plasma concentration of cefamandole (mcg/ml).

Details

Davidian and Giltinan (1995, 1.1, p. 2) describe data obtained during a pilot study to investigate the pharmacokinetics of the drug cefamandole. Plasma concentrations of the drug were measured on six healthy volunteers at 14 time points following an intravenous dose of 15 mg/kg body weight of cefamandole.

Source


Examples

```r
plot(Cefamandole)
fm1 <- nlsList(SSbiexp, data = Cefamandole)
summary(fm1)
```

---

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all "pdMat", "corStruct" and "varFunc" classes, "reStruct", and "modelStruct".

`coefficients<-' is an alias for `coef<-'.

Usage

```r
coeff(object, ...) <- value
coefficients(object, ...) <- value
```
coef.corStruct

Arguments

object any object representing a fitted model, or, by default, any object with a coef component.

... some methods for this generic function may require additional arguments.

value a value to be assigned to the coefficients associated with object.

Value

will depend on the method function; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

ccoef

corStruct

Description

This method function extracts the coefficients associated with the correlation structure represented by object.

Usage

## S3 method for class 'corStruct'
c coef(object, unconstrained, ...)
## S3 replacement method for class 'corStruct'
c coef(object, ...) <- value

Arguments

object an object inheriting from class "corStruct", representing a correlation structure.

unconstrained a logical value. If TRUE the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If FALSE the coefficients are returned in "natural", possibly constrained, form. Defaults to TRUE.

value a vector with the replacement values for the coefficients associated with object. It must be a vector with the same length of coef(object) and must be given in unconstrained form.

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the coefficients corresponding to object.
SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of object to value. Object must be initialized (using Initialize) before new values can be assigned to its coefficients.

Author(s)

José Pinheiro and Douglas Bates

References


See Also

corAR1, corARMA, corCAR1, corCompSymm, corExp, corGaus, corLin, corRatio, corSpatial, corSpher, corSymm, Initialize

Examples

cst1 <- corARMA(p = 1, q = 1)
coef(cst1)

Description

The estimated coefficients for the nonlinear model represented by object are extracted.

Usage

## S3 method for class 'gnls'
coef(object, ...)

Arguments

object an object inheriting from class "gnls", representing a generalized nonlinear least squares fitted model.

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the estimated coefficients for the nonlinear model represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls
Examples

```r
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
weights = varPower())
coef(fm1)
```

### Description

The estimated coefficients at level \( i \) are obtained by adding together the fixed effects estimates and the corresponding random effects estimates at grouping levels less or equal to \( i \). The resulting estimates are returned as a data frame, with rows corresponding to groups and columns to coefficients. Optionally, the returned data frame may be augmented with covariates summarized over groups.

### Usage

```r
## S3 method for class 'lme'
coef(object, augFrame, level, data, which, FUN,
     omitGroupingFactor, subset, ...)
```

### Arguments

- `object`: an object inheriting from class "lme", representing a fitted linear mixed-effects model.
- `augFrame`: an optional logical value. If TRUE, the returned data frame is augmented with variables defined in data; else, if FALSE, only the coefficients are returned. Defaults to FALSE.
- `level`: an optional positive integer giving the level of grouping to be used in extracting the coefficients from an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.
- `data`: an optional data frame with the variables to be used for augmenting the returned data frame when `augFrame = TRUE`. Defaults to the data frame used to fit `object`.
- `which`: an optional positive integer or character vector specifying which columns of `data` should be used in the augmentation of the returned data frame. Defaults to all columns in `data`.
- `FUN`: an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If `FUN` is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If `FUN` is a list of functions, the names in the list should designate classes of variables in the frame such as `ordered`, `factor`, or `numeric`. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are `mean` for numeric factors, and `Mode` for both `factor` and `ordered`. The `Mode` function, defined internally in `gsummary`, returns the modal or most popular value of the variable. It is different from the `mode` function that returns the S-language mode of the variable.
The coefficients of each \texttt{lm} object in the object list are extracted and organized into a data frame, with rows corresponding to the \texttt{lm} components and columns corresponding to the coefficients. Optionally, the returned data frame may be augmented with covariates summarized over the groups associated with the \texttt{lm} components.

### Usage

```r
## S3 method for class 'lmList'
coef(object, augFrame, data, which, FUN, 
     omitGroupingFactor, ...) 
```

### Examples

```r
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject) 
coef(fm1) 
coef(fm1, augFrame = TRUE)
```
Arguments

object an object inheriting from class "lmList", representing a list of lm objects with a common model.

augFrame an optional logical value. If TRUE, the returned data frame is augmented with variables defined in the data frame used to produce object; else, if FALSE, only the coefficients are returned. Defaults to FALSE.

data an optional data frame with the variables to be used for augmenting the returned data frame when augFrame = TRUE. Defaults to the data frame used to fit object.

which an optional positive integer or character vector specifying which columns of the data frame used to produce object should be used in the augmentation of the returned data frame. Defaults to all variables in the data.

FUN an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing the data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as ordered, factor, or numeric. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

omitGroupingFactor an optional logical value. When TRUE the grouping factor itself will be omitted from the group-wise summary of data but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to FALSE.

... some methods for this generic require additional arguments. None are used in this method.

Value

a data frame inheriting from class "coef.lmList" with the estimated coefficients for each "lm" component of object and, optionally, other covariates summarized over the groups corresponding to the "lm" components. The returned object also inherits from classes "ranef.lmList" and "data.frame".

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

lmList, fixed.effects.lmList, ranef.lmList, plot.ranef.lmList, gsummary
Examples

```r
fm1 <- lmList(distance ~ age|Subject, data = Orthodont)
coef(fm1)
coef(fm1, augFrame = TRUE)
```

---

**Extract modelStruct Object Coefficients**

**Description**

This method function extracts the coefficients associated with each component of the `modelStruct` list.

**Usage**

```r
## S3 method for class 'modelStruct'
coef(object, unconstrained, ...)
## S3 replacement method for class 'modelStruct'
coef(object, ...) <- value
```

**Arguments**

- `object`: an object inheriting from class "modelStruct", representing a list of model components, such as "corStruct" and "varFunc" objects.
- `unconstrained`: a logical value. If TRUE the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If FALSE the coefficients are returned in "natural", possibly constrained, form. Defaults to TRUE.
- `value`: a vector with the replacement values for the coefficients associated with `object`. It must be a vector with the same length of `coef(object)` and must be given in unconstrained form.
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

- a vector with all coefficients corresponding to the components of `object`.

**SIDE EFFECTS**

On the left side of an assignment, sets the values of the coefficients of `object` to `value`. Object must be initialized (using `Initialize`) before new values can be assigned to its coefficients.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`Initialize`
Examples

```r
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),
                   corStruct = corAR1(0.3))
coef(lms1)
```

Description

This method function extracts the coefficients associated with the positive-definite matrix represented by `object`.

Usage

```r
## S3 method for class 'pdMat'
coef(object, unconstrained, ...)
## S3 replacement method for class 'pdMat'
coef(object, ...) <- value
```

Arguments

- `object`: an object inheriting from class "pdMat", representing a positive-definite matrix.
- `unconstrained`: a logical value. If `TRUE` the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If `FALSE` the upper triangular elements of the positive-definite matrix represented by `object` are returned. Defaults to `TRUE`.
- `value`: a vector with the replacement values for the coefficients associated with `object`. It must be a vector with the same length of `coef(object)` and must be given in unconstrained form.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the coefficients corresponding to `object`.

SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of `object` to `value`.

Author(s)

José Pinheiro and Douglas Bates

References

coef.reStruct

See Also

pdMat

Examples

coe(pdSymm(diag(3)))

des

Description

This method function extracts the coefficients associated with the positive-definite matrix represented by object.

Usage

## S3 method for class 'reStruct'
coef(object, unconstrained, ...)
## S3 replacement method for class 'reStruct'
coef(object, ...) <- value

des

Arguments

object

an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.

unconstrained

da logical value. If TRUE the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If FALSE the coefficients are returned in "natural", possibly constrained, form. Defaults to TRUE.

value

a vector with the replacement values for the coefficients associated with object. It must be a vector with the same length of coef(object) and must be given in unconstrained form.

... some methods for this generic require additional arguments. None are used in this method.

des

Value

a vector with the coefficients corresponding to object.

SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of object to value.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

coe.pdMat, reStruct, pdMat
Examples

```r
rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
                     B = pdDiag(2 * diag(4), form = ~Educ))
coef(rs1)
```

**Description**

This method function extracts the coefficients associated with the variance function structure represented by `object`.

**Usage**

```r
## S3 method for class 'varFunc'
coef(object, unconstrained, allCoef, ...)
## S3 replacement method for class 'varIdent'
coef(object, ...) <- value
```

**Arguments**

- `object`: an object inheriting from class "varFunc" representing a variance function structure.
- `unconstrained`: a logical value. If TRUE the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If FALSE the coefficients are returned in "natural", generally constrained form. Defaults to TRUE.
- `allCoef`: a logical value. If FALSE only the coefficients which may vary during the optimization are returned. If TRUE all coefficients are returned. Defaults to FALSE.
- `value`: a vector with the replacement values for the coefficients associated with `object`. It must be have the same length of `coef(object)` and must be given in unconstrained form. `object` must be initialized before new values can be assigned to its coefficients.
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the coefficients corresponding to `object`.

**SIDE EFFECTS**

On the left side of an assignment, sets the values of the coefficients of `object` to `value`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

`varFunc`
Example:
```r
vf1 <- varPower(1)
coef(vf1)

coef(vf1) <- 2
```

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Currently, only a `groupedData` method is available.

**Usage**

```r
collapse(object, ...)
```

**Arguments**

- `object`:
  an object to be collapsed, usually a data frame.

- `...`:
  some methods for the generic may require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

- `collapse.groupedData`

**Examples**

```r
## see the method function documentation
```
Description

If `object` has a single grouping factor, it is returned unchanged. Else, it is summarized by the values of the `displayLevel` grouping factor (or the combination of its values and the values of the covariate indicated in `preserve`, if any is present). The collapsed data is used to produce a new `groupedData` object, with grouping factor given by the `displayLevel` factor.

Usage

```r
## S3 method for class 'groupedData'
collapse(object, collapseLevel, displayLevel,
          outer, inner, preserve, FUN, subset, ...)
```

Arguments

- `object`: an object inheriting from class `groupedData`, generally with multiple grouping factors.
- `collapseLevel`: an optional positive integer or character string indicating the grouping level to use when collapsing the data. Level values increase from outermost to innermost grouping. Default is the highest or innermost level of grouping.
- `displayLevel`: an optional positive integer or character string indicating the grouping level to use as the grouping factor for the collapsed data. Default is `collapseLevel`.
- `outer`: an optional logical value or one-sided formula, indicating covariates that are outer to the `displayLevel` grouping factor. If equal to `TRUE`, the `displayLevel` element `attr(object, "outer")` is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to `NULL`, meaning that no outer covariates are to be used.
- `inner`: an optional logical value or one-sided formula, indicating a covariate that is inner to the `displayLevel` grouping factor. If equal to `TRUE`, `attr(object, "outer")` is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to `NULL`, meaning that no inner covariate is present.
- `preserve`: an optional one-sided formula indicating a covariate whose levels should be preserved when collapsing the data according to the `collapseLevel` grouping factor. The collapsing factor is obtained by pasting together the levels of the `collapseLevel` grouping factor and the values of the covariate to be preserved. Default is `NULL`, meaning that no covariates need to be preserved.
- `FUN`: an optional summary function or a list of summary functions to be used for collapsing the data. The function or functions are applied only to variables in `object` that vary within the groups defined by `collapseLevel`. Invariant variables are always summarized by group using the unique value that they assume within that group. If `FUN` is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If `FUN` is a list of functions, the names in the list should designate classes of variables.
in the data such as ordered, factor, or numeric. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

subset an optional named list. Names can be either positive integers representing grouping levels, or names of grouping factors. Each element in the list is a vector indicating the levels of the corresponding grouping factor to be preserved in the collapsed data. Default is NULL, meaning that all levels are used.

... some methods for this generic require additional arguments. None are used in this method.

Value

a groupedData object with a single grouping factor given by the displayLevel grouping factor, resulting from collapsing object over the levels of the collapseLevel grouping factor.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
groupedData, plot.nlGroupedData

Examples

# collapsing by Dog
collapse(Pixel, collapse = 1) # same as collapse(Pixel, collapse = "Dog")

compareFits

Compare Fitted Objects

Description
The columns in object1 and object2 are put together in matrices which allow direct comparison of the individual elements for each object. Missing columns in either object are replaced by NAs.

Usage

compareFits(object1, object2, which)

Arguments

object1,object2
data frames, or matrices, with the same row names, but possibly different column names. These will usually correspond to coefficients from fitted objects with a grouping structure (e.g. lme and lmList objects).

which an optional integer or character vector indicating which columns in object1 and object2 are to be used in the returned object. Defaults to all columns.
Value

a three-dimensional array, with the third dimension given by the number of unique column names in either object1 or object2. To each column name there corresponds a matrix with as many rows as the rows in object1 and two columns, corresponding to object1 and object2. The returned object inherits from class comparefits.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

plot.compareFits, pairs.compareFits, comparePred, coef, random.effects

Examples

```r
fm1 <- lmList(Orthodont)
fm2 <- lme(fm1)
(cF12 <- compareFits(coef(fm1), coef(fm2)))
```

Description

Predicted values are obtained at the specified values of primary for each object. If either object1 or object2 have a grouping structure (i.e. getGroups(object) is not NULL), predicted values are obtained for each group. When both objects determine groups, the group levels must be the same. If other covariates besides primary are used in the prediction model, their group-wise averages (numeric covariates) or most frequent values (categorical covariates) are used to obtain the predicted values. The original observations are also included in the returned object.

Usage

```r
comparePred(object1, object2, primary, minimum, maximum,
          length.out, level, ...)
```

Arguments

- **object1, object2**: fitted model objects, from which predictions can be extracted using the predict method.
- **primary**: an optional one-sided formula specifying the primary covariate to be used to generate the augmented predictions. By default, if a covariate can be extracted from the data used to generate the objects (using getCovariate), it will be used as primary.
- **minimum**: an optional lower limit for the primary covariate. Defaults to min(primary), after primary is evaluated in the data used in fitting object1.
- **maximum**: an optional upper limit for the primary covariate. Defaults to max(primary), after primary is evaluated in the data used in fitting object1.
length.out  an optional integer with the number of primary covariate values at which to evaluate the predictions. Defaults to 51.

level    an optional integer specifying the desired prediction level. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Only one level can be specified. Defaults to the innermost level.

...    some methods for the generic may require additional arguments.

Value

a data frame with four columns representing, respectively, the values of the primary covariate, the groups (if object does not have a grouping structure, all elements will be 1), the predicted or observed values, and the type of value in the third column: the objects’ names are used to classify the predicted values and original is used for the observed values. The returned object inherits from classes comparePred and augPred.

Note

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: g1s, lme, and lmList.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

augPred, getGroups

Examples

fm1 <- lme(distance ~ age * Sex, data = Orthodont, random = ~ age)
fm2 <- update(fm1, distance ~ age)
comparePred(fm1, fm2, length.out = 2)

corAR1  AR(1) Correlation Structure

description

This function is a constructor for the corAR1 class, representing an autocorrelation structure of order 1. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

corAR1(value, form, fixed)
corAR1

Arguments

value  
the value of the lag 1 autocorrelation, which must be between -1 and 1. Defaults to 0 (no autocorrelation).

form  
a one sided formula of the form \( \sim t \), or \( \sim t | g \), specifying a time covariate \( t \) and, optionally, a grouping factor \( g \). A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to \( \sim 1 \), which corresponds to using the order of the observations in the data as a covariate, and no groups.

fixed  
an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corAR1, representing an autocorrelation structure of order 1.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

ACF.lme, corARMA, corClasses, Dim.corSpatial, Initialize.corStruct, summary.corStruct

Examples

## covariate is observation order and grouping factor is Mare

cs1 <- corAR1(0.2, form = ~ 1 | Mare)

# Pinheiro and Bates, p. 236

cs1AR1 <- corAR1(0.8, form = ~ 1 | Subject)

cs1AR1. <- Initialize(cs1AR1, data = Orthodont)

corMatrix(cs1AR1.)

# Pinheiro and Bates, p. 240

fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                   data = Ovary, random = pdDiag(~sin(2*pi*Time)))

fm2Ovar.lme <- update(fm1Ovar.lme, correlation = corAR1())

# Pinheiro and Bates, pp. 255-258: use in gls

fm1Dial.gls <-
gls(rate ~ (pressure + I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
     data = Dialyzer)

fm2Dial.gls <- update(fm1Dial.gls,
weights = varPower(form = ~ pressure))
fm3Dial.gls <- update(fm2Dial.gls, 
corr = corAR1(0.771, form = ~ 1 | Subject))

# Pinheiro and Bates use in nlme:
# from p. 240 needed on p. 396
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                   data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm5Ovar.lme <- update(fm1Ovar.lme, 
corr = corARMA(p = 1, q = 1))

# p. 396
fm1Ovar.nlme <- nlme(follicles~A+B*sin(2*pi*w*Time)+C*cos(2*pi*w*Time),
                      data=Ovary, fixed=A+B+C+w~1, 
                      random=pdDiag(A+B+w~1),
                      start=c(fixef(fm5Ovar.lme), 1) )

# p. 397
fm2Ovar.nlme <- update(fm1Ovar.nlme, 
corr=corAR1(0.311) )

---

corARMA

ARMA(p,q) Correlation Structure

Description

This function is a constructor for the corARMA class, representing an autocorrelation-moving average correlation structure of order (p, q). Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

corARMA(value, form, p, q, fixed)

Arguments

value

a vector with the values of the autoregressive and moving average parameters, which must have length p + q and all elements between -1 and 1. Defaults to a vector of zeros, corresponding to uncorrelated observations.

form

a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.

p, q

non-negative integers specifying respectively the autoregressive order and the moving average order of the ARMA structure. Both default to 0.

fixed

an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.
corARMA

Value

an object of class corARMA, representing an autocorrelation-moving average correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

corAR1, corClasses Initialize.corStruct, summary.corStruct

Examples

```r
## ARMA(1,2) structure, with observation order as a covariate and
## Mare as grouping factor
cs1 <- corARMA(c(0.2, 0.3, -0.1), form = ~ 1 | Mare, p = 1, q = 2)

# Pinheiro and Bates, p. 237
cs1ARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cs1ARMA <- Initialize(cs1ARMA, data = Orthodont)
corMatrix(cs1ARMA)

cs2ARMA <- corARMA(c(0.8, 0.4), form = ~ 1 | Subject, p=1, q=1)
cs2ARMA <- Initialize(cs2ARMA, data = Orthodont)
corMatrix(cs2ARMA)

# Pinheiro and Bates use in nlme:
# from p. 240 needed on p. 396
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm5Ovar.lme <- update(fm1Ovar.lme,
corr = corARMA(p = 1, q = 1))

# p. 396
fm1Ovar.nlme <- nlme(follicles~A+B*sin(2*pi*w*Time)+C*cos(2*pi*w*Time),
data=Ovary, fixed=A+B+C+w~1,
random=pdDiag(A+B+w~1),
start=c(fixef(fm5Ovar.lme), 1) )
# p. 397
fm3Ovar.nlme <- update(fm1Ovar.nlme,
corr=corARMA(p=0, q=2) )
```
Continuous AR(1) Correlation Structure

Description
This function is a constructor for the corCAR1 class, representing an autocorrelation structure of order 1, with a continuous time covariate. Objects created using this constructor must be later initialized using the appropriate Initialize method.

Usage
corCAR1(value, form, fixed)

Arguments

value the correlation between two observations one unit of time apart. Must be between 0 and 1. Defaults to 0.2.

form a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. Covariates for this correlation structure need not be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.

fixed an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value
an object of class corCAR1, representing an autocorrelation structure of order 1, with a continuous time covariate.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also
corClasses, Initialize.corStruct, summary.corStruct
Examples

```r
# covariate is Time and grouping factor is Mare
cs1 <- corCAR1(0.2, form = ~ Time | Mare)

# Pinheiro and Bates, pp. 240, 243
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm4Ovar.lme <- update(fm1Ovar.lme, correlation = corCAR1(form = ~Time))
```

---

### corClasses

**Correlation Structure Classes**

**Description**

Standard classes of correlation structures (corStruct) available in the nlme package.

**Value**

Available standard classes:

- `corAR1`: autoregressive process of order 1.
- `corARMA`: autoregressive moving average process, with arbitrary orders for the autoregressive and moving average components.
- `corCAR1`: continuous autoregressive process (AR(1) process for a continuous time covariate).
- `corCompSymm`: compound symmetry structure corresponding to a constant correlation.
- `corExp`: exponential spatial correlation.
- `corGaus`: Gaussian spatial correlation.
- `corLin`: linear spatial correlation.
- `corRatio`: Rational quadratics spatial correlation.
- `corSpher`: spherical spatial correlation.
- `corSymm`: general correlation matrix, with no additional structure.

**Note**

Users may define their own corStruct classes by specifying a constructor function and, at a minimum, methods for the functions corMatrix and coef. For examples of these functions, see the methods for classes corSymm and corAR1.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**

corCompSymm

Description

This function is a constructor for the corCompSymm class, representing a compound symmetry structure corresponding to uniform correlation. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

```r
corCompSymm(value, form, fixed)
```

Arguments

- **value**: the correlation between any two correlated observations. Defaults to 0.
- **form**: a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
- **fixed**: an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

An object of class corCompSymm, representing a compound symmetry correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

corClasses, Initialize.corStruct, summary.corStruct
**Examples**

```r
## covariate is observation order and grouping factor is Subject
cs1 <- corCompSymm(0.5, form = ~ 1 | Subject)

# Pinheiro and Bates, pp. 222-225
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
                 random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p. 225
cs1CompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cs2CompSymm <- corCompSymm(value = 0.3, form = ~ age | Subject)
cs1CompSymm <- Initialize(cs1CompSymm, data = Orthodont)
corMatrix(cs1CompSymm)

## Print/Summary methods for the empty case:
(cCS <- corCompSymm()) # Uninitialized correlation struct..
summary(cCS) # (ditto)
```

---

**corExp**

*Exponential Correlation Structure*

**Description**

This function is a constructor for the "corExp" class, representing an exponential spatial correlation structure. Letting \( d \) denote the range and \( n \) denote the nugget effect, the correlation between two observations a distance \( r \) apart is \( \exp(-r/d) \) when no nugget effect is present and \( (1-n) \exp(-r/d) \) when a nugget effect is assumed. Objects created using this constructor must later be initialized using the appropriate Initialize method.

**Usage**

```r
corExp(value, form, nugget, metric, fixed)
```

**Arguments**

- **value**: an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the exponential correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.

- **form**: a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget  an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.

metric   an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

fixed    an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class "corExp", also inheriting from class "corSpatial", representing an exponential spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

corClasses, Initialize.corStruct, summary.corStruct, dist

Examples

sp1 <- corExp(form = ~ x + y + z)
# Pinheiro and Bates, p. 238
spatDat <- data.frame(x = (0:4)/4, y = (0:4)/4)
cs1Exp <- corExp(1, form = ~ x + y)
cs1Exp <- Initialize(cs1Exp, spatDat)
corMatrix(cs1Exp)
cs2Exp <- corExp(1, form = ~ x + y, metric = "man")
cs2Exp <- Initialize(cs2Exp, spatDat)
corMatrix(cs2Exp)
cs3Exp <- corExp(c(1, 0.2), form = ~ x + y, nugget = TRUE)
cs3Exp <- Initialize(cs3Exp, spatDat)
corMatrix(cs3Exp)
# example lme(..., corExp ...)


# Pinheiro and Bates, pp. 222-247
# p. 222
options(contrasts = c("contr.treatment", "contr.poly"))
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
    random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p. 246
fm3BW.lme <- update(fm2BW.lme,
    correlation = corExp(form = ~ Time))
# p. 247
fm4BW.lme <-
    update(fm3BW.lme, correlation = corExp(form = ~ Time,
        nugget = TRUE))
anova(fm3BW.lme, fm4BW.lme)

---

corFactor

**Factor of a Correlation Matrix**

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all corStruct classes.

**Usage**

```r
corFactor(object, ...)
```

**Arguments**

- `object`  
an object from which a correlation matrix can be extracted.
- `...`  
some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`corFactor.corStruct, recalc.corStruct`

**Examples**

```r
## see the method function documentation
```
corFactor.corStruct  

**Factor of a corStruct Object Matrix**

**Description**

This method function extracts a transpose inverse square-root factor, or a series of transpose inverse square-root factors, of the correlation matrix, or list of correlation matrices, represented by `object`. Letting $\Sigma$ denote a correlation matrix, a square-root factor of $\Sigma$ is any square matrix $L$ such that $\Sigma = L' L$. This method extracts $L^{-t}$.

**Usage**

```r
## S3 method for class 'corStruct'
corFactor(object, ...)
```

**Arguments**

- `object`: an object inheriting from class "corStruct" representing a correlation structure, which must have been initialized (using Initialize).
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

If the correlation structure does not include a grouping factor, the returned value will be a vector with a transpose inverse square-root factor of the correlation matrix associated with `object` stacked column-wise. If the correlation structure includes a grouping factor, the returned value will be a vector with transpose inverse square-root factors of the correlation matrices for each group, stacked by group and stacked column-wise within each group.

**Note**

This method function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The `corMatrix` method function can be used to obtain transpose inverse square-root factors in matrix form.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

- `corFactor`
- `corMatrix.corStruct`
- `recalc.corStruct`
- `Initialize.corStruct`

**Examples**

```r
cs1 <- corAR1(form = ~1 | Subject)
cs1 <- Initialize(cs1, data = Orthodont)
corFactor(cs1)
```
**corGaus**

**Gaussian Correlation Structure**

**Description**

This function is a constructor for the `corGaus` class, representing a Gaussian spatial correlation structure. Letting \( d \) denote the range and \( n \) denote the nugget effect, the correlation between two observations a distance \( r \) apart is \( \exp(- (r/d)^2) \) when no nugget effect is present and \( (1 - n) \exp(- (r/d)^2) \) when a nugget effect is assumed. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```r
corGaus(value, form, nugget, metric, fixed)
```

**Arguments**

- `value` an optional vector with the parameter values in constrained form. If `nugget` is `FALSE`, `value` can have only one element, corresponding to the "range" of the Gaussian correlation structure, which must be greater than zero. If `nugget` is `TRUE`, meaning that a nugget effect is present, `value` can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to `numeric(0)`, which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.

- `form` a one sided formula of the form `~ S1+...+Sp` or `~ S1+...+Sp | g`, specifying spatial covariates `S1` through `Sp` and, optionally, a grouping factor `g`. When a grouping factor is present in `form`, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to `~ 1`, which corresponds to using the order of the observations in the data as a covariate, and no groups.

- `nugget` an optional logical value indicating whether a nugget effect is present. Defaults to `FALSE`.

- `metric` an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

- `fixed` an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to `FALSE`, in which case the coefficients are allowed to vary.

**Value**

An object of class `corGaus`, also inheriting from class `corSpatial`, representing a Gaussian spatial correlation structure.
corLin

Linear Correlation Structure

description

This function is a constructor for the corLin class, representing a linear spatial correlation structure. Letting \( d \) denote the range and \( n \) denote the nugget effect, the correlation between two observations a distance \( r < d \) apart is \( 1 - (r/d) \) when no nugget effect is present and \( (1 - n)(1 - (r/d)) \) when a nugget effect is assumed. If \( r \geq d \) the correlation is zero. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

corLin(value, form, nugget, metric, fixed)
Arguments

**value**
an optional vector with the parameter values in constrained form. If **nugget** is FALSE, **value** can have only one element, corresponding to the "range" of the linear correlation structure, which must be greater than zero. If **nugget** is TRUE, meaning that a nugget effect is present, **value** can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.

**form**
a one sided formula of the form $\sim S_1+\ldots+S_p$, or $\sim S_1+\ldots+S_p \mid g$, specifying spatial covariates $S_1$ through $S_p$ and, optionally, a grouping factor $g$. When a grouping factor is present in **form**, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$, which corresponds to using the order of the observations in the data as a covariate, and no groups.

**nugget**
an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.

**metric**
an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

**fixed**
an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corLin, also inheriting from class corSpatial, representing a linear spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

Initialize.corStruct, summary.corStruct, dist
Examples

```r
sp1 <- corLin(form = ~ x + y)

# example lme(..., corLin ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
    random = ~ Time)

# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())

# p 246
fm3BW.lme <- update(fm2BW.lme,
    correlation = corExp(form = ~ Time))

# p. 249
fm7BW.lme <- update(fm3BW.lme, correlation = corLin(form = ~ Time))
```

---

**corMatrix**

*Extract Correlation Matrix*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all `corStruct` classes.

**Usage**

```r
corMatrix(object, ...)
```

**Arguments**

- `object`:
  - an object for which a correlation matrix can be extracted.
- `...`:
  - some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`corMatrix.corStruct`, `corMatrix.pdMat`

**Examples**

```r
## see the method function documentation
```
Description

This method function extracts the correlation matrix (or its transpose inverse square-root factor), or list of correlation matrices (or their transpose inverse square-root factors) corresponding to covariate and object. Letting $\Sigma$ denote a correlation matrix, a square-root factor of $\Sigma$ is any square matrix $L$ such that $\Sigma = L'L$. When $corr = FALSE$, this method extracts $L^{-1}$.

Usage

```r
## S3 method for class 'corStruct'
corMatrix(object, covariate, corr, ...)
```

Arguments

- `object` an object inheriting from class "corStruct" representing a correlation structure.
- `covariate` an optional covariate vector (matrix), or list of covariate vectors (matrices), at which values the correlation matrix, or list of correlation matrices, are to be evaluated. Defaults to `getCovariate(object)`.
- `corr` a logical value. If TRUE the function returns the correlation matrix, or list of correlation matrices, represented by object. If FALSE the function returns a transpose inverse square-root of the correlation matrix, or a list of transpose inverse square-root factors of the correlation matrices.
- `...` some methods for this generic require additional arguments. None are used in this method.

Value

If covariate is a vector (matrix), the returned value will be an array with the corresponding correlation matrix (or its transpose inverse square-root factor). If the covariate is a list of vectors (matrices), the returned value will be a list with the correlation matrices (or their transpose inverse square-root factors) corresponding to each component of covariate.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

corFactor.corStruct, Initialize.corStruct
**Examples**

```r
cs1 <- corAR1(0.3)
corMatrix(cs1, covariate = 1:4)
corMatrix(cs1, covariate = 1:4, corr = FALSE)

# Pinheiro and Bates, p. 225
cs1CompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cs1CompSymm <- Initialize(cs1CompSymm, data = Orthodont)
corMatrix(cs1CompSymm)

# Pinheiro and Bates, p. 226
cs1Symm <- corSymm(value = c(0.2, 0.1, -0.1, 0, 0.2, 0),
                   form = ~ 1 | Subject)
cs1Symm <- Initialize(cs1Symm, data = Orthodont)
corMatrix(cs1Symm)

# Pinheiro and Bates, p. 236
cs1AR1 <- corAR1(0.8, form = ~ 1 | Subject)
cs1AR1 <- Initialize(cs1AR1, data = Orthodont)
corMatrix(cs1AR1)

# Pinheiro and Bates, p. 237
cs1ARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cs1ARMA <- Initialize(cs1ARMA, data = Orthodont)
corMatrix(cs1ARMA)

# Pinheiro and Bates, p. 238
spatDat <- data.frame(x = (0:4)/4, y = (0:4)/4)
cs1Exp <- corExp(1, form = ~ x + y)
cs1Exp <- Initialize(cs1Exp, spatDat)
corMatrix(cs1Exp)
```

**Description**

The correlation matrix corresponding to the positive-definite matrix represented by object is obtained.

**Usage**

```r
## S3 method for class 'pdMat'
corMatrix(object, ...)
```

**Arguments**

- `object`: an object inheriting from class "pdMat", representing a positive definite matrix.
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

the correlation matrix corresponding to the positive-definite matrix represented by object.
corMatrix.reStruct

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
as.matrix.pdMat, pdMatrix

Examples

```r
pd1 <- pdSymm(diag(1:4))
corMatrix(pd1)
```

corMatrix.reStruct Extract Correlation Matrix from Components of an reStruct Object

Description
This method function extracts the correlation matrices corresponding to the pdMat elements of object.

Usage
```r
## S3 method for class 'reStruct'
corMatrix(object, ...)
```

Arguments

- `object` an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
- `...` some methods for this generic require additional arguments. None are used in this method.

Value
a list with components given by the correlation matrices corresponding to the elements of object.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
as.matrix.reStruct, corMatrix, reStruct, pdMat

Examples

```r
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
corMatrix(rs1)
```
corNatural

General correlation in natural parameterization

Description

This function is a constructor for the corNatural class, representing a general correlation structure in the “natural” parameterization, which is described under pdNatural. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

corNatural(value, form, fixed)

Arguments

value an optional vector with the parameter values. Default is numeric(0), which results in a vector of zeros of appropriate dimension being assigned to the parameters when object is initialized (corresponding to an identity correlation structure).

form a one sided formula of the form \(~ t\), or \(~ t \mid g\), specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to \(~ 1\), which corresponds to using the order of the observations in the data as a covariate, and no groups.

fixed an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corNatural representing a general correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Initialize.corNatural, pdNatural, summary.corNatural

Examples

## covariate is observation order and grouping factor is Subject
cs1 <- corNatural(form = ~ 1 | Subject)
corRatio

Rational Quadratic Correlation Structure

Description

This function is a constructor for the corRatio class, representing a rational quadratic spatial correlation structure. Letting $d$ denote the range and $n$ denote the nugget effect, the correlation between two observations a distance $r$ apart is $1/(1 + (r/d)^2)$ when no nugget effect is present and $(1 - n)/(1 + (r/d)^2)$ when a nugget effect is assumed. Objects created using this constructor need to be later initialized using the appropriate Initialize method.

Usage

corRatio(value, form, nugget, metric, fixed)

Arguments

- **value**: an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the rational quadratic correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.

- **form**: a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.

- **nugget**: an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.

- **metric**: an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

- **fixed**: an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corRatio, also inheriting from class corSpatial, representing a rational quadratic spatial correlation structure.
corSpatial

Spatial Correlation Structure

Description

This function is a constructor for the corSpatial class, representing a spatial correlation structure. This class is "virtual", having four "real" classes, corresponding to specific spatial correlation structures, associated with it: corExp, corGaus, corLin, corRatio, and corSpher. The returned object will inherit from one of these "real" classes, determined by the type argument, and from the "virtual" corSpatial class. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

Initialize.corStruct, summary.corStruct, dist

Examples

sp1 <- corRatio(form = ~ x + y + z)

# example lme(..., corRatio ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
               random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
               correlation = corExp(form = ~ Time))
# p. 249
fm5BW.lme <- update(fm3BW.lme, correlation =
               corRatio(form = ~ Time))

# example gls(..., corRatio ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 263
fm3Wheat2 <- update(fm1Wheat2, corr =
               corRatio(c(12.5, 0.2),
               form = ~ latitude + longitude,
               nugget = TRUE))
Usage

corSpatial(value, form, nugget, type, metric, fixed)

Arguments

value an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the spatial correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.

form a one sided formula of the form ~ S1+...+Sp, or ~ S1+...+Sp | g, specifying spatial covariates S1 through Sp and, optionally, a grouping factor g. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.

nugget an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.

type an optional character string specifying the desired type of correlation structure. Available types include "spherical", "exponential", "gaussian", "linear", and "rational". See the documentation on the functions corSpher, corExp, corGaus, corLin, and corRatio for a description of these correlation structures. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "spherical".

metric an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

fixed an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class determined by the type argument and also inheriting from class corSpatial, representing a spatial correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

corSpher


See Also

corExp, corGaus, corLin, corRatio, corSpher, Initialize.corStruct, summary.corStruct, dist

Examples

spl <- corSpatial(form = ~ x + y + z, type = "g", metric = "man")

---

corSpher

Spherical Correlation Structure

Description

This function is a constructor for the corSpher class, representing a spherical spatial correlation structure. Letting \( d \) denote the range and \( n \) denote the nugget effect, the correlation between two observations a distance \( r < d \) apart is \( 1 - 1.5(r/d) + 0.5(r/d)^3 \) when no nugget effect is present and \((1 - n)(1 - 1.5(r/d) + 0.5(r/d)^3)\) when a nugget effect is assumed. If \( r \geq d \) the correlation is zero. Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

corSpher(value, form, nugget, metric, fixed)

Arguments

value

an optional vector with the parameter values in constrained form. If nugget is FALSE, value can have only one element, corresponding to the "range" of the spherical correlation structure, which must be greater than zero. If nugget is TRUE, meaning that a nugget effect is present, value can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to numeric(0), which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when object is initialized.

form

a one sided formula of the form \(~ S1+...+Sp\), or \(~ S1+...+Sp | g\), specifying spatial covariates \( S1 \) through \( Sp \) and, optionally, a grouping factor \( g \). When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to \(~ 1\), which corresponds to using the order of the observations in the data as a covariate, and no groups.

nugget

an optional logical value indicating whether a nugget effect is present. Defaults to FALSE.
metric
an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

fixed
an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value
an object of class corSpher, also inheriting from class corSpatial, representing a spherical spatial correlation structure.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also
Initialize.corStruct, summary.corStruct, dist

Examples
sp1 <- corSpher(form = ~ x + y)
# example lme(..., corSpher ...)  
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight, 
random = ~ Time)
# p. 223  
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme, 
    correlation = corExp(form = ~ Time))
# p. 249
fm6BW.lme <- update(fm3BW.lme, 
    correlation = corSpher(form = ~ Time))

# example gls(..., corSpher ...)  
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 262
fm2Wheat2 <- update(fm1Wheat2, corr = 
    corSpher(c(28, 0.2),
    form = ~ latitude + longitude, nugget = TRUE))
corSymm  General Correlation Structure

Description
This function is a constructor for the corSymm class, representing a general correlation structure. The internal representation of this structure, in terms of unconstrained parameters, uses the spherical parametrization defined in Pinheiro and Bates (1996). Objects created using this constructor must later be initialized using the appropriate Initialize method.

Usage

corSymm(value, form, fixed)

Arguments

value  an optional vector with the parameter values. Default is numeric(0), which results in a vector of zeros of appropriate dimension being assigned to the parameters when object is initialized (corresponding to an identity correlation structure).

form  a one sided formula of the form ~ t, or ~ t | g, specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in form, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to ~ 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.

fixed  an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

Value

an object of class corSymm representing a general correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

Initialize.corSymm, summary.corSymm
Examples

```r
## covariate is observation order and grouping factor is Subject
cs1 <- corSymm(form = ~ 1 | Subject)

# Pinheiro and Bates, p. 225
cs1CompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cs1CompSymm <- Initialize(cs1CompSymm, data = Orthodont)
corMatrix(cs1CompSymm)

# Pinheiro and Bates, p. 226
cs1Symm <- corSymm(value =
c(0.2, 0.1, -0.1, 0, 0.2, 0),
form = ~ 1 | Subject)
cs1Symm <- Initialize(cs1Symm, data = Orthodont)
corMatrix(cs1Symm)

# example gls(..., corSpher ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 262
fm2Wheat2 <- update(fm1Wheat2, corr =
corSpher(c(28, 0.2),
form = ~ latitude + longitude, nugget = TRUE))

# example gls(..., corSymm ...)
# Pinheiro and Bates, p. 251
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
correlation = corSymm(form = ~ 1 | Subject),
weights = varIdent(form = ~ 1 | age))
```

### Covariate

**Assign Covariate Values**

<table>
<thead>
<tr>
<th>Covariate</th>
<th>Assign Covariate Values</th>
</tr>
</thead>
</table>

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all "varFunc" classes.

**Usage**

```r
covariate(object) <- value
```

**Arguments**

- `object` any object with a covariate component.
- `value` a value to be assigned to the covariate associated with object.

**Value**

will depend on the method function; see the appropriate documentation.
Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
getcovariate

Examples
## see the method function documentation

covariate(object) <- value

Arguments

object an object inheriting from class "varFunc", representing a variance function structure.
value a value to be assigned to the covariate associated with object.

Value

a varFunc object similar to object, but with its covariate attribute replaced by value.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
getcovariate.varFunc

Examples
vf1 <- varPower(1.1, form = ~age)
covariate(vf1) <- Orthodont["age"]
**Dialyzer**

*High-Flux Hemodialyzer*

**Description**

The Dialyzer data frame has 140 rows and 5 columns.

**Format**

This data frame contains the following columns:

- **Subject** an ordered factor with levels 10 < 8 < 6 < 3 < 5 < 7 < 1 < 4 < 17 < 20 < 11 < 12 < 16 < 13 < 14 < 18 < 15 < 19 giving the unique identifier for each subject.
- **QB** a factor with levels 200 and 300 giving the bovine blood flow rate (dL/min).
- **pressure** a numeric vector giving the transmembrane pressure (dmHg).
- **rate** the hemodialyzer ultrafiltration rate (mL/hr).
- **index** index of observation within subject—1 through 7.

**Details**

Vonesh and Carter (1992) describe data measured on high-flux hemodialyzers to assess their *in vivo* ultrafiltration characteristics. The ultrafiltration rates (in mL/hr) of 20 high-flux dialyzers were measured at seven different transmembrane pressures (in dmHg). The *in vitro* evaluation of the dialyzers used bovine blood at flow rates of either 200~dl/min or 300~dl/min. The data, are also analyzed in Littell, Milliken, Stroup, and Wolfinger (1996).

**Source**


**Dim**

*Extract Dimensions from an Object*

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: "corSpatial", "corStruct", "pdCompSymm", "pdDiag", "pdIdent", "pdMat", and "pdSymm".

**Usage**

```r
Dim(object, ...)
```
Arguments

object any object for which dimensions can be extracted.

... some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Note

If dim allowed more than one argument, there would be no need for this generic function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Dim.pdMat, Dim.corStruct

Examples

### see the method function documentation

```r

```

---

### Dim.corSpatial Dimensions of a corSpatial Object

Description

if groups is missing, it returns the Dim attribute of object; otherwise, calculates the dimensions associated with the grouping factor.

Usage

```r

## S3 method for class 'corSpatial'
Dim(object, groups, ...)

```

Arguments

object an object inheriting from class "corSpatial", representing a spatial correlation structure.

groups an optional factor defining the grouping of the observations; observations within a group are correlated and observations in different groups are uncorrelated.

... further arguments to be passed to or from methods.
Value

a list with components:

N  length of groups
M  number of groups
spClass  an integer representing the spatial correlation class; 0 = user defined class, 1 = corSpher, 2 = corExp, 3 = corGaus, 4 = corLin
sumLenSq  sum of the squares of the number of observations per group
len  an integer vector with the number of observations per group
start  an integer vector with the starting position for the distance vectors in each group, beginning from zero

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Dim, Dim.corStruct

Examples

Dim(corGaus(), getGroups(Orthodont))
cs1ARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cs1ARMA <- Initialize(cs1ARMA, data = Orthodont)
Dim(cs1ARMA)

---

Dim.corStruct

Dimensions of a corStruct Object

Description

if groups is missing, it returns the Dim attribute of object; otherwise, calculates the dimensions associated with the grouping factor.

Usage

## S3 method for class 'corStruct'
Dim(object, groups, ...)

Arguments

object  an object inheriting from class "corStruct", representing a correlation structure.
groups  an optional factor defining the grouping of the observations; observations within a group are correlated and observations in different groups are uncorrelated.
...  some methods for this generic require additional arguments. None are used in this method.
Value

a list with components:

- **N**: length of groups
- **M**: number of groups
- **maxLen**: maximum number of observations in a group
- **sumLenSq**: sum of the squares of the number of observations per group
- **len**: an integer vector with the number of observations per group
- **start**: an integer vector with the starting position for the observations in each group, beginning from zero

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Dim, Dim.corSpatial

Examples

Dim(corAR1(), getGroups(Orthodont))

---

Dim.pdMat  Dimensions of a pdMat Object

Description

This method function returns the dimensions of the matrix represented by object.

Usage

```r
## S3 method for class 'pdMat'
Dim(object, ...)
```

Arguments

- **object**: an object inheriting from class "pdMat", representing a positive-definite matrix.
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value

an integer vector with the number of rows and columns of the matrix represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
Earthquake

See Also

Dim

Examples

Dim(pdSymm(diag(3)))

<table>
<thead>
<tr>
<th>Earthquake</th>
<th>Earthquake Intensity</th>
</tr>
</thead>
</table>

Description

The Earthquake data frame has 182 rows and 5 columns.

Format

This data frame contains the following columns:

- **Quake** an ordered factor with levels 20 < 16 < 14 < 10 < 3 < 8 < 23 < 22 < 6 < 13 < 7 < 21 < 18 < 15 < 4 < 12 < 19 < 5 < 9 < 1 < 2 < 17 < 11 indicating the earthquake on which the measurements were made.
- **Richter** a numeric vector giving the intensity of the earthquake on the Richter scale.
- **distance** the distance from the seismological measuring station to the epicenter of the earthquake (km).
- **soil** a factor with levels 0 and 1 giving the soil condition at the measuring station, either soil or rock.
- **accel** maximum horizontal acceleration observed (g).

Details

Measurements recorded at available seismometer locations for 23 large earthquakes in western North America between 1940 and 1980. They were originally given in Joyner and Boore (1981); are mentioned in Brillinger (1987); and are analyzed in Davidian and Giltinan (1995).

Source


ergoStool

Description

The ergoStool data frame has 36 rows and 3 columns.

Format

This data frame contains the following columns:

- **effort**: a numeric vector giving the effort (Borg scale) required to arise from a stool.
- **Type**: a factor with levels T1, T2, T3, and T4 giving the stool type.
- **Subject**: an ordered factor giving a unique identifier for the subject in the experiment.

Details

Devore (2000) cites data from an article in *Ergometrics* (1993, pp. 519-535) on “The Effects of a Pneumatic Stool and a One-Legged Stool on Lower Limb Joint Load and Muscular Activity.”

Source


Examples

```r
fm1 <- lme(effort ~ Type, data = ergoStool, random = ~ 1 | Subject)
anova( fm1 )
```

Fatigue

Description

The Fatigue data frame has 262 rows and 3 columns.

Format

This data frame contains the following columns:

- **Path**: an ordered factor with levels 1 < 2 < 3 < 4 < 5 < 6 < 7 < 8 < 9 < 10 < 11 < 12 < 13 < 14 < 15 < 16 < 17 < 18 < 19 < 20 < 21 giving the test path (or test unit) number. The order is in terms of increasing failure time or decreasing terminal crack length.
- **cycles**: number of test cycles at which the measurement is made (millions of cycles).
- **relLength**: relative crack length (dimensionless).
Details

These data are given in Lu and Meeker (1993) where they state “We obtained the data in Table 1 visually from figure 4.5.2 on page 242 of Bogdanoff and Kozin (1985).” The data represent the growth of cracks in metal for 21 test units. An initial notch of length 0.90 inches was made on each unit which then was subjected to several thousand test cycles. After every 10,000 test cycles the crack length was measured. Testing was stopped if the crack length exceeded 1.60 inches, defined as a failure, or at 120,000 cycles.

Source


---

### fdHess

#### Finite difference Hessian

**Description**

Evaluate an approximate Hessian and gradient of a scalar function using finite differences.

**Usage**

```r
dfHess(pars, fun, ..., 
   .relStep = .Machine$double.eps^(1/3), minAbsPar = 0)
```

**Arguments**

- `pars` the numeric values of the parameters at which to evaluate the function `fun` and its derivatives.
- `fun` a function depending on the parameters `pars` that returns a numeric scalar.
- `...` Optional additional arguments to `fun`.
- `.relStep` The relative step size to use in the finite differences. It defaults to the cube root of `.Machine$double.eps`
- `minAbsPar` The minimum magnitude of a parameter value that is considered non-zero. It defaults to zero meaning that any non-zero value will be considered different from zero.

**Details**

This function uses a second-order response surface design known as a “Koschal design” to determine the parameter values at which the function is evaluated.

**Value**

A list with components

- `mean` the value of function `fun` evaluated at the parameter values `pars`
- `gradient` an approximate gradient (of length `length(pars)`).
- `Hessian` a matrix whose upper triangle contains an approximate Hessian.
fitted.glsStruct

Calculate glsStruct Fitted Values

Description

The fitted values for the linear model represented by object are extracted.

Usage

## S3 method for class 'glsStruct'
fitted(object, glsFit, ...)

Arguments

- object: an object inheriting from class "glsStruct", representing a list of linear model components, such as corStruct and "varFunc" objects.
- glsFit: an optional list with components logLik (log-likelihood), beta (coefficients), sigma (standard deviation for error term), varBeta (coefficients’ covariance matrix), fitted (fitted values), and residuals (residuals). Defaults to attr(object, "glsFit").
- ...: some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the fitted values for the linear model represented by object.

Note

This method function is generally only used inside gls and fitted.gls.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, residuals.glsStruct
fitted.gnlsStruct

Calculate gnlsStruct Fitted Values

Description

The fitted values for the nonlinear model represented by object are extracted.

Usage

## S3 method for class 'gnlsStruct'
fitted(object, ...)

Arguments

object an object inheriting from class "gnlsStruct", representing a list of model components, such as corStruct and varFunc objects, and attributes specifying the underlying nonlinear model and the response variable.

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the fitted values for the nonlinear model represented by object.

Note

This method function is generally only used inside gnls and fitted.gnls.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls, residuals.gnlsStruct

---

fitted.lme

Extract lme Fitted Values

Description

The fitted values at level $i$ are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to $i$. The resulting values estimate the best linear unbiased predictions (BLUPs) at level $i$.

Usage

## S3 method for class 'lme'
fitted(object, level, asList, ...)

---
Arguments

object an object inheriting from class "lme", representing a fitted linear mixed-effects model.

level an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from object. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.

asList an optional logical value. If TRUE and a single value is given in level, the returned object is a list with the fitted values split by groups; else the returned value is either a vector or a data frame, according to the length of level. Defaults to FALSE.

... some methods for this generic require additional arguments. None are used in this method.

Value

If a single level of grouping is specified in level, the returned value is either a list with the fitted values split by groups (asList = TRUE) or a vector with the fitted values (asList = FALSE); else, when multiple grouping levels are specified in level, the returned object is a data frame with columns given by the fitted values at different levels and the grouping factors. For a vector or data frame result the napredict method is applied.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

lme, residuals.lme

Examples

fml <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
fitted(fml, level = 0:1)

fitted.lmeStruct Calculate lmeStruct Fitted Values

Description

The fitted values at level \( i \) are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to \( i \). The resulting values estimate the best linear unbiased predictions (BLUPs) at level \( i \).
Usage

```r
## S3 method for class 'lmeStruct'
fitted(object, level, conLin, lmeFit, ...)
```

Arguments

- `object` an object inheriting from class "lmeStruct", representing a list of linear mixed-effects model components, such as reStruct, corStruct, and varFunc objects.
- `level` an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from `object`. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
- `conLin` an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying lme model. Defaults to `attr(object, "conLin")`.
- `lmeFit` an optional list with components `beta` and `b` containing respectively the fixed effects estimates and the random effects estimates to be used to calculate the fitted values. Defaults to `attr(object, "lmeFit")`.
- `...` some methods for this generic accept other optional arguments.

Value

If a single level of grouping is specified in `level`, the returned value is a vector with the fitted values at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the fitted values at different levels.

Note

This method function is generally only used inside `lme` and `fitted.lme`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- `lme`, `fitted.lme`, `residuals.lmeStruct`

---

### fitted.lmList

#### Extract lmList Fitted Values

Description

The fitted values are extracted from each `lm` component of `object` and arranged into a list with as many components as `object`, or combined into a single vector.

Usage

```r
## S3 method for class 'lmList'
fitted(object, subset, asList, ...)
```
Arguments

object an object inheriting from class "lmList", representing a list of \texttt{lm} objects with a common model.

subset an optional character or integer vector naming the \texttt{lm} components of \texttt{object} from which the fitted values are to be extracted. Default is \texttt{NULL}, in which case all components are used.

asList an optional logical value. If \texttt{TRUE}, the returned object is a list with the fitted values split by groups; else the returned value is a vector. Defaults to \texttt{FALSE}.

... some methods for this generic require additional arguments. None are used in this method.

Value

a list with components given by the fitted values of each \texttt{lm} component of \texttt{object}, or a vector with the fitted values for all \texttt{lm} components of \texttt{object}.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

\texttt{lmList}, \texttt{residuals.lmList}

Examples

fml <- \texttt{lmList(distance ~ age | Subject, Orthodont)}
fitted(fml)

---

\textbf{fitted.nlmeStruct} \hspace{1cm} \textit{Calculate nlmeStruct Fitted Values}

Description

The fitted values at level \textit{i} are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to \textit{i} and evaluating the model function at the resulting estimated parameters. The resulting values estimate the predictions at level \textit{i}.

Usage

\texttt{## S3 method for class 'nlmeStruct'}
fitted(object, level, conLin, ...)

fixed.effects

Arguments

object an object inheriting from class "nlmeStruct", representing a list of mixed-effects model components, such as reStruct, corStruct, and varFunc objects, plus attributes specifying the underlying nonlinear model and the response variable.

level an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from object. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.

conLin an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying nlme model. Defaults to attr(object, "conLin").

... additional arguments that could be given to this method. None are used.

Value

if a single level of grouping is specified in level, the returned value is a vector with the fitted values at the desired level; else, when multiple grouping levels are specified in level, the returned object is a matrix with columns given by the fitted values at different levels.

Note

This method function is generally only used inside nlme and fitted.nlme.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

nlme, residuals.nlmeStruct

---

fixed.effects

Extract Fixed Effects

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include lmList and lm.

Usage

fixed.effects(object, ...)
fixef(object, ...)
Arguments

object any fitted model object from which fixed effects estimates can be extracted.

... some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

References


See Also

fixef.lmList

Examples

## see the method function documentation

fixef.lmList

Extract lmList Fixed Effects

Description

The average of the coefficients corresponding to the lm components of object is calculated.

Usage

## S3 method for class 'lmList'
fixef(object, ...)

Arguments

object an object inheriting from class "lmList", representing a list of lm objects with a common model.

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the average of the individual lm coefficients in object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, random.effects.lmList
Examples

```r
fm1 <- lmList(distance ~ age | Subject, Orthodont)
fixed.effects(fm1)
```

---

**Description**

The `formula` attributes of the `pdMat` elements of `x` are extracted and returned as a list, in case `asList=TRUE`, or converted to a single one-sided formula when `asList=FALSE`. If the `pdMat` elements do not have a `formula` attribute, a `NULL` value is returned.

**Usage**

```r
## S3 method for class 'pdBlocked'
formula(x, asList, ...)
```

**Arguments**

- `x`: an object inheriting from class "pdBlocked", representing a positive definite block diagonal matrix.
- `asList`: an optional logical value. If `TRUE`, a list with the formulas for the individual block diagonal elements of `x` is returned; else, if `FALSE`, a one-sided formula combining all individual formulas is returned. Defaults to `FALSE`.
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

A list of one-sided formulas, or a single one-sided formula, or `NULL`.

**Author(s)**

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

**See Also**

`pdBlocked`, `pdMat`

**Examples**

```r
pd1 <- pdBlocked(list(~ age, ~ Sex - 1))
formula(pd1)
formula(pd1, asList = TRUE)
```
**formula.pdMat**

**Extract pdMat Formula**

**Description**

This method function extracts the formula associated with a pdMat object, in which the column and row names are specified.

**Usage**

```r
## S3 method for class 'pdMat'
formula(x, asList, ...)
```

**Arguments**

- `x`: an object inheriting from class "pdMat", representing a positive definite matrix.
- `asList`: logical. Should the asList argument be applied to each of the components? Never used.
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

- if `x` has a `formula` attribute, its value is returned, else NULL is returned.

**Note**

Because factors may be present in `formula(x)`, the pdMat object needs to have access to a data frame where the variables named in the formula can be evaluated, before it can resolve its row and column names from the formula.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

- `pdMat`

**Examples**

```r
pd1 <- pdSymm(~Sex*age)
formula(pd1)
```
Description

This method function extracts a formula from each of the components of x, returning a list of formulas.

Usage

```r
## S3 method for class 'reStruct'
formula(x, asList, ...)
```

Arguments

- `x`: an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
- `asList`: logical. Should the asList argument be applied to each of the components?
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

a list with the formulas of each component of x.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

formula

Examples

```r
rs1 <- reStruct(list(A = pdDiag(diag(2), ~age), B = ~1))
formula(rs1)
```

---

### gapply

Apply a Function by Groups

**Description**

Applies the function to the distinct sets of rows of the data frame defined by groups.

**Usage**

```r
gapply(object, which, FUN, form, level, groups, ...)
```
Arguments

object an object to which the function will be applied - usually a groupedData object or a data.frame. Must inherit from class "data.frame".

which an optional character or positive integer vector specifying which columns of object should be used with FUN. Defaults to all columns in object.

FUN function to apply to the distinct sets of rows of the data frame object defined by the values of groups.

form an optional one-sided formula that defines the groups. When this formula is given the right-hand side is evaluated in object, converted to a factor if necessary, and the unique levels are used to define the groups. Defaults to formula(object).

level an optional positive integer giving the level of grouping to be used in an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.

groups an optional factor that will be used to split the rows into groups. Defaults to getGroups(object, form, level).

... optional additional arguments to the summary function FUN. Often it is helpful to specify na.rm = TRUE.

Value

Returns a data frame with as many rows as there are levels in the groups argument.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

gsummary

Examples

```r
## Find number of non-missing "conc" observations for each Subject
gapply( Phenobarb, FUN = function(x) sum(!is.na(x$conc)) )

# Pinheiro and Bates, p. 127
table( gapply(Quinidine, "conc", function(x) sum(!is.na(x))) )
changeRecords <- gapply( Quinidine, FUN = function(frm)
  any(is.na(frm["conc"])) & is.na(frm["dose"]) )
```
Gasoline

### Description

The Gasoline data frame has 32 rows and 6 columns.

### Format

This data frame contains the following columns:

- **yield**: a numeric vector giving the percentage of crude oil converted to gasoline after distillation and fractionation
- **endpoint**: a numeric vector giving the temperature (degrees F) at which all the gasoline is vaporized
- **Sample**: an ordered factor giving the inferred crude oil sample number
- **API**: a numeric vector giving the crude oil gravity (degrees API)
- **vapor**: a numeric vector giving the vapor pressure of the crude oil (lbf/in²)
- **ASTM**: a numeric vector giving the crude oil 10% point ASTM—the temperature at which 10% of the crude oil has become vapor.

### Details

Prater (1955) provides data on crude oil properties and gasoline yields. Atkinson (1985) uses these data to illustrate the use of diagnostics in multiple regression analysis. Three of the covariates—API, vapor, and ASTM—measure characteristics of the crude oil used to produce the gasoline. The other covariate — endpoint—is a characteristic of the refining process. Daniel and Wood (1980) notice that the covariates characterizing the crude oil occur in only ten distinct groups and conclude that the data represent responses measured on ten different crude oil samples.

### Source


---

getCovariate

### Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include corStruct, corSpatial, data.frame, and varFunc.
getCovariate.corStruct

Usage

getCovariate(object, form, data)

Arguments

object any object with a covariate component
form an optional one-sided formula specifying the covariate(s) to be extracted. Defaults to formula(object).
data a data frame in which to evaluate the variables defined in form.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

getcovariate.corStruct, getcovariate.data.frame, getcovariate.varFunc, getcovariateFormula

eXamples

## see the method function documentation

---

getCovariate.corStruct

Extract corStruct Object Covariate

Description

This method function extracts the covariate(s) associated with object.

Usage

## S3 method for class 'corStruct'
getCovariate(object, form, data)

Arguments

object an object inheriting from class corStruct representing a correlation structure.
form this argument is included to make the method function compatible with the generic. It will be assigned the value of formula(object) and should not be modified.
data an optional data frame in which to evaluate the variables defined in form, in case object is not initialized and the covariate needs to be evaluated.
Value
when the correlation structure does not include a grouping factor, the returned value will be a vector or a matrix with the covariate(s) associated with object. If a grouping factor is present, the returned value will be a list of vectors or matrices with the covariate(s) corresponding to each grouping level.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also
getCovariate

Examples
cs1 <- corAR1(form = ~ 1 | Subject)
getcovariate(cs1, data = Orthodont)

getcovariate.data.frame
Extract Data Frame Covariate

Description
The right hand side of form, stripped of any conditioning expression (i.e. an expression following a | operator), is evaluated in object.

Usage
## S3 method for class 'data.frame'
getcovariate(object, form, data)

Arguments
object an object inheriting from class data.frame.
form an optional formula specifying the covariate to be evaluated in object. Defaults to formula(object).
data some methods for this generic require a separate data frame. Not used in this method.

Value
the value of the right hand side of form, stripped of any conditional expression, evaluated in object.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
See Also

getCovariateFormula

Examples

getcovariate(Orthodont)

getcovariate.varFunc  Extract varFunc Covariate

Description

This method function extracts the covariate(s) associated with the variance function represented by object, if any is present.

Usage

## S3 method for class 'varFunc'
getcovariate(object, form, data)

Arguments

object an object inheriting from class varFunc, representing a variance function structure.
form an optional formula specifying the covariate to be evaluated in object. Defaults to formula(object).
data some methods for this generic require a data object. Not used in this method.

Value

if object has a covariate attribute, its value is returned; else NULL is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

covariate<- .varFunc

Examples

vf1 <- varPower(1.1, form = ~age)
covariate(vf1) <- Orthodont[["age"]]
getcovariate(vf1)
getCovariateFormula  Extract Covariates Formula

Description
The right hand side of formula(object), without any conditioning expressions (i.e. any expressions after a | operator) is returned as a one-sided formula.

Usage
getCovariateFormula(object)

Arguments
object any object from which a formula can be extracted.

Value
a one-sided formula describing the covariates associated with formula(object).

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
getCovariate

Examples
getCovariateFormula(y ~ x | g)
getCovariateFormula(y ~ x)

data
Extract Data from an Object

Description
This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include gls, lme, and lmList.

Usage
getData(object)

Arguments
object an object from which a data.frame can be extracted, generally a fitted model object.
Value
will depend on the method function used; see the appropriate documentation.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
glsl, getData.lme, getData.lmList

Examples
## see the method function documentation

```
glsl <s gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), data = Ovary,
correlation = corAR1(form = ~ 1 | Mare))
getData(fm1)
```
getData.lme

Extract lme Object Data

Description

If present in the calling sequence used to produce object, the data frame used to fit the model is obtained.

Usage

```r
## S3 method for class 'lme'
getData(object)
```

Arguments

- `object` an object inheriting from class `lme`, representing a linear mixed-effects fitted model.

Value

If a data argument is present in the calling sequence that produced object, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced object) is returned; else, `NULL` is returned.

Note that as from version 3.1-102, this only omits rows omitted in the fit if `na.action = na.omit`, and does not omit at all if `na.action = na.exclude`. That is generally what is wanted for plotting, the main use of this function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lme`, `getData`

Examples

```r
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), data = Ovary,
            random = ~ sin(2*pi*Time))
getData(fm1)
```
**getData.lmList**

*Extract lmList Object Data*

**Description**

If present in the calling sequence used to produce object, the data frame used to fit the model is obtained.

**Usage**

```r
## S3 method for class 'lmList'
getData(object)
```

**Arguments**

- `object`: an object inheriting from class `lmList`, representing a list of `lm` objects with a common model.

**Value**

if a data argument is present in the calling sequence that produced `object`, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced `object`) is returned; else, `NULL` is returned.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`lmList`, `getData`

**Examples**

```r
fm1 <- lmList(distance ~ age | Subject, Orthodont)
getData(fm1)
```

---

**getGroups**

*Extract Grouping Factors from an Object*

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `corStruct`, `data.frame`, `gls`, `lme`, `lmList`, and `varFunc`.

**Usage**

```r
groups <- getGroups(object, form, level, data, sep)
```
**Arguments**

- **object**: any object
- **form**: an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the | operator). Defaults to `formula(object)`.
- **level**: a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting.
- **data**: a data frame in which to interpret the variables named in `form`. Optional for most methods.
- **sep**: character, the separator to use between group levels when multiple levels are collapsed. The default is '/'.

**Value**

Will depend on the method function used; see the appropriate documentation.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**


**See Also**

- `getGroupsFormula`
- `getGroups.data.frame`
- `getGroups.gls`
- `getGroups.lmList`
- `getGroups.lme`

**Examples**

```r
## see the method function documentation
```

---

**Description**

This method function extracts the grouping factor associated with `object`, if any is present.

**Usage**

```r
## S3 method for class 'corStruct'
getGroups(object, form, level, data, sep)
```
Arguments

- **object**: an object inheriting from class `corStruct` representing a correlation structure.
- **form**: this argument is included to make the method function compatible with the generic. It will be assigned the value of `formula(object)` and should not be modified.
- **level**: this argument is included to make the method function compatible with the generic and is not used.
- **data**: an optional data frame in which to evaluate the variables defined in `form`, in case `object` is not initialized and the grouping factor needs to be evaluated.
- **sep**: character, the separator to use between group levels when multiple levels are collapsed. The default is `/`.

Value

- if a grouping factor is present in the correlation structure represented by `object`, the function returns the corresponding factor vector; else the function returns NULL.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- `getGroups`

Examples

```r
cs1 <- corAR1(form = ~ 1 | Subject)
groups <- getGroups(cs1, data = Orthodont)
```

Description

Each variable named in the expression after the `|` operator on the right hand side of `form` is evaluated in `object`. If more than one variable is indicated in `level` they are combined into a data frame; else the selected variable is returned as a vector. When multiple grouping levels are defined in `form` and `level > 1`, the levels of the returned factor are obtained by pasting together the levels of the grouping factors of level greater or equal to `level`, to ensure their uniqueness.

Usage

```r
## S3 method for class 'data.frame'
groups <- getGroups(object, form, level, data, sep)
```
Arguments

- **object**: an object inheriting from class `data.frame`.
- **form**: an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the `|` operator). Defaults to `formula(object)`.
- **level**: a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. Defaults to all levels of nesting.
- **data**: unused
- **sep**: character, the separator to use between group levels when multiple levels are collapsed. The default is `/`.

Value

either a data frame with columns given by the grouping factors indicated in `level`, from outer to inner, or, when a single level is requested, a factor representing the selected grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

`getGroupsFormula`

Examples

```r
getGroups(Pixel)
getGroups(Pixel, level = 2)
```

Description

If present, the grouping factor associated to the correlation structure for the linear model represented by `object` is extracted.

Usage

```r
## S3 method for class 'gls'
getGroups(object, form, level, data, sep)
```
Arguments

object  
an object inheriting from class `gls`, representing a generalized least squares fitted linear model.

form  
an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the `|` operator). Defaults to `formula(object)`. Not used.

level  
a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.

data  
a data frame in which to interpret the variables named in `form`. Optional for most methods. Not used.

sep  
character, the separator to use between group levels when multiple levels are collapsed. The default is `'/'`. Not used.

Value

if the linear model represented by `object` incorporates a correlation structure and the corresponding `corStruct` object has a grouping factor, a vector with the group values is returned; else, `NULL` is returned.

Author(s)

José Pinheiro and Douglas Bates `<bates@stat.wisc.edu>`

See Also

gls, corClasses

Examples

```r
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary, 
correlation = corAR1(form = ~ 1 | Mare))
getGroups(fm1)
```

---

**getGroups.lme**  
*Extract lme Object Groups*

Description

The grouping factors corresponding to the linear mixed-effects model represented by `object` are extracted. If more than one level is indicated in `level`, the corresponding grouping factors are combined into a data frame; else the selected grouping factor is returned as a vector.

Usage

```r
## S3 method for class 'lme'
getGroups(object, form, level, data, sep)
```
getGroups.lmList

Arguments

object an object inheriting from class `lme`, representing a fitted linear mixed-effects model.
form this argument is included to make the method function compatible with the generic and is ignored in this method.
level an optional integer vector giving the level(s) of grouping to be extracted from object. Defaults to the highest or innermost level of grouping.
data unused
sep character, the separator to use between group levels when multiple levels are collapsed. The default is `"/"`.

Value

either a data frame with columns given by the grouping factors indicated in `level`, or, when a single level is requested, a factor representing the selected grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lme`

Examples

```r
fm1 <- lme(pixel ~ day + day^2, Pixel,
      random = list(Dog = ~day, Side = ~1))
getGroups(fm1, level = 1:2)
```

groups.1mList Extract lmList Object Groups

Description

The grouping factor determining the partitioning of the observations used to produce the `lm` components of object is extracted.

Usage

```r
## S3 method for class 'lmList'
getGroups(object, form, level, data, sep)
```
Arguments

object  
an object inheriting from class \texttt{lmList}, representing a list of \texttt{lm} objects with a common model.

form  
an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the | operator). Defaults to \texttt{formula(object)}. Not used.

level  
a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.

data  
a data frame in which to interpret the variables named in \texttt{form}. Optional for most methods. Not used.

sep  
character, the separator to use between group levels when multiple levels are collapsed. The default is '/'. Not used.

Value

a vector with the grouping factor corresponding to the \texttt{lm} components of \texttt{object}.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

\texttt{lmList}

Examples

```r
fm1 <- lmList(distance ~ age | Subject, Orthodont)
groups(fm1)
```

---

getGroups.varFunc  

\textit{Extract varFunc Groups}

Description

This method function extracts the grouping factor associated with the variance function represented by \texttt{object}, if any is present.

Usage

```r
## S3 method for class 'varFunc'
groups(object, form, level, data, sep)
```
Arguments

object  an object inheriting from class varFunc, representing a variance function structure.
form    an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the | operator). Defaults to formula(object). Not used.
level   a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.
data    a data frame in which to interpret the variables named in form. Optional for most methods. Not used.
sep     character, the separator to use between group levels when multiple levels are collapsed. The default is '/'. Not used.

Value

if object has a groups attribute, its value is returned; else NULL is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

Examples

vf1 <- varPower(form = ~ age | Sex)
vf1 <- Initialize(vf1, Orthodont)
getGroups(vf1)

getGroupsFormula  Extract Grouping Formula

Description

The conditioning expression associated with formula(object) (i.e. the expression after the | operator) is returned either as a named list of one-sided formulas, or a single one-sided formula, depending on the value of asList. The components of the returned list are ordered from outermost to innermost level and are named after the grouping factor expression.

Usage

getGroupsFormula(object, asList, sep)

Arguments

object any object from which a formula can be extracted.
asList an optional logical value. If TRUE the returned value will be a list of formulas; else, if FALSE the returned value will be a one-sided formula. Defaults to FALSE.
sep character, the separator to use between group levels when multiple levels are collapsed. The default is '/'.

getGroupsFormula  Extract Grouping Formula
getResponse

Extract Response Variable from an Object

Description
This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include data.frame, gls, lme, and lmList.

Usage
getResponse(object, form)

Arguments
- object: any object
- form: an optional two-sided formula. Defaults to formula(object).

Value
will depend on the method function used; see the appropriate documentation.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
getResponseFormula

Examples
getResponse(Orthodont)
getResponseFormula  

Extract Formula Specifying Response Variable

Description

The left hand side of formula(object) is returned as a one-sided formula.

Usage

getResponseFormula(object)

Arguments

object  
any object from which a formula can be extracted.

Value

a one-sided formula with the response variable associated with formula(object).

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

groupBy, getResponse

Examples

getResponseFormula(y ~ x | g)

getVarCov  

Extract variance-covariance matrix

Description

Extract the variance-covariance matrix from a fitted model, such as a mixed-effects model.

Usage

gVarCov(obj, ...)  
## S3 method for class 'lme'
gVarCov(obj, individuals,
       type = c("random.effects", "conditional", "marginal"), ...)
## S3 method for class 'gls'
gVarCov(obj, individual = 1, ...)


Arguments

obj A fitted model. Methods are available for models fit by `lme` and by `gls`.

individuals For models fit by `lme` a vector of levels of the grouping factor can be specified for the conditional or marginal variance-covariance matrices.

individual For models fit by `gls` the only type of variance-covariance matrix provided is the marginal variance-covariance of the responses by group. The optional argument `individual` specifies the group of responses.

type For models fit by `lme` the `type` argument specifies the type of variance-covariance matrix, either "random.effects" for the random-effects variance-covariance (the default), or "conditional" for the conditional. variance-covariance of the responses or "marginal" for the the marginal variance-covariance of the responses.

... Optional arguments for some methods, as described above

Value

A variance-covariance matrix or a list of variance-covariance matrices.

Author(s)

Mary Lindstrom <lindstro@biostat.wisc.edu>

See Also

`lme`, `gls`

Examples

```r
fm1 <- lme(distance ~ age, data = Orthodont, subset = Sex == "Female")
getVarCov(fm1)
getVarCov(fm1, individual = "F01", type = "marginal")
getVarCov(fm1, type = "conditional")
fm2 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
getVarCov(fm2)
```

Description

This function fits a linear model using generalized least squares. The errors are allowed to be correlated and/or have unequal variances.

Usage

gls(model, data, correlation, weights, subset, method, na.action, control, verbose)

# S3 method for class 'gls'
update(object, model., ..., evaluate = TRUE)
Arguments

object: an object inheriting from class "gls", representing a generalized least squares fitted linear model.

model: a two-sided linear formula object describing the model, with the response on the left of a ~ operator and the terms, separated by + operators, on the right.

model. Changes to the model – see update.formula for details.

data: an optional data frame containing the variables named in model, correlation, weights, and subset. By default the variables are taken from the environment from which gls is called.

correlation: an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. If a grouping variable is to be used, it must be specified in the form argument to the corStruct constructor. Defaults to NULL, corresponding to uncorrelated errors.

weights: an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic errors.

subset: an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

method: a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".

na.action: a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes gls to print an error message and terminate if there are any incomplete observations.

control: a list of control values for the estimation algorithm to replace the default values returned by the function glsControl. Defaults to an empty list.

verbose: an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.

... some methods for this generic require additional arguments. None are used in this method.

evaluate: If TRUE evaluate the new call else return the call.

Details

offset terms in model are an error since 3.1-157 (2022-03): previously they were silently ignored.

Value

an object of class "gls" representing the linear model fit. Generic functions such as print, plot, and summary have methods to show the results of the fit. See glsObject for the components of the fit. The functions resid, coef and fitted, can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
References


See Also

`corClasses`, `glsControl`, `glsObject`, `glsStruct`, `plot.gls`, `predict.gls`, `qqnorm.gls`, `residuals.gls`, `summary.gls`, `varClasses`, `varFunc`

Examples

```r
# AR(1) errors within each Mare
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
# variance increases as a power of the absolute fitted values
fm2 <- update(fm1, weights = varPower())
```

### glsControl

**Control Values for gls Fit**

**Description**

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the control argument to the gls function.

**Usage**

```r
glsControl(maxIter, msMaxIter, tolerance, msTol, msVerbose, singular.ok, returnObject = FALSE, apVar, .relStep, opt = c("nlminb", "optim"), optimMethod, minAbsParApVar, natural, sigma = NULL)
```
Arguments

maxIter  maximum number of iterations for the gls optimization algorithm. Default is 50.
msMaxIter  maximum number of iterations for the optimization step inside the gls optimization. Default is 50.
tolerance  tolerance for the convergence criterion in the gls algorithm. Default is 1e-6.
msTol  tolerance for the convergence criterion of the first outer iteration when optim is used. Default is 1e-7.
msVerbose  a logical value passed as the trace control value to the chosen optimizer (see documentation on that function). Default is FALSE.
singular.ok  a logical value indicating whether non-estimable coefficients (resulting from linear dependencies among the columns of the regression matrix) should be allowed. Default is FALSE.
returnObject  a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is FALSE.
apVar  a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is TRUE.
opt  the optimizer to be used, either "nlminb" (the current default) or "optim" (the previous default).
optimMethod  character - the optimization method to be used with the optim optimizer. The default is "BFGS". An alternative is "L-BFGS-B".
minAbsParApVar  numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
natural  logical. Should the natural parameterization be used for the approximate variance calculations? Default is TRUE.
sigma  optionally a positive number to fix the residual error at. If NULL, as by default, or 0, sigma is estimated.

Value

a list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the sigma option: Siem Heisterkamp and Bert van Willigen.

See Also

gls

Examples

# decrease the maximum number of iterations and request tracing
glsControl(msMaxIter = 20, msVerbose = TRUE)
glsObject

Fitted gls Object

Description

An object returned by the `gls` function, inheriting from class "gls" and representing a generalized least squares fitted linear model. Objects of this class have methods for the generic functions `anova`, `coef`, `fitted`, `formula`, `getGroups`, `getResponse`, `intervals`, `logLik`, `plot`, `predict`, `print`, `residuals`, `summary`, and `update`.

Value

The following components must be included in a legitimate "gls" object.

- `apVar` an approximate covariance matrix for the variance-covariance coefficients. If `apVar = FALSE` in the list of control values used in the call to `gls`, this component is equal to `NULL`.
- `call` a list containing an image of the `gls` call that produced the object.
- `coefficients` a vector with the estimated linear model coefficients.
- `contrasts` a list of the contrast matrices used to represent factors in the model formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the model, this component will be an empty list.
- `dims` a list with basic dimensions used in the model fit, including the components `N` - the number of observations in the data and `p` - the number of coefficients in the linear model.
- `fitted` a vector with the fitted values.
- `modelStruct` an object inheriting from class `glsStruct`, representing a list of linear model components, such as `corStruct` and `varFunc` objects.
- `groups` a vector with the correlation structure grouping factor, if any is present.
- `logLik` the log-likelihood at convergence.
- `method` the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.
- `numIter` the number of iterations used in the iterative algorithm.
- `residuals` a vector with the residuals.
- `sigma` the estimated residual standard error.
- `varBeta` an approximate covariance matrix of the coefficients estimates.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`gls`, `glsStruct`
glsStruct

*Generalized Least Squares Structure*

**Description**

A generalized least squares structure is a list of model components representing different sets of parameters in the linear model. A `glsStruct` may contain `corStruct` and `varFunc` objects. NULL arguments are not included in the `glsStruct` list.

**Usage**

```r
glsStruct(corStruct, varStruct)
```

**Arguments**

- `corStruct` an optional `corStruct` object, representing a correlation structure. Default is NULL.
- `varStruct` an optional `varFunc` object, representing a variance function structure. Default is NULL.

**Value**

a list of model variance-covariance components determining the parameters to be estimated for the associated linear model.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

corClasses, gls, residuals.glsStruct, varFunc

**Examples**

```r
gls1 <- glsStruct(corAR1(), varPower())
```

---

**Glucose**

*Glucose levels over time*

**Description**

The Glucose data frame has 378 rows and 4 columns.

**Format**

This data frame contains the following columns:

- **Subject** an ordered factor with levels 6 < 2 < 3 < 5 < 1 < 4
- **Time** a numeric vector
- **conc** a numeric vector of glucose levels
- **Meal** an ordered factor with levels 2am < 6am < 10am < 2pm < 6pm < 10pm
Source

---

**Glucose2**

*Glucose Levels Following Alcohol Ingestion*

Description
The Glucose2 data frame has 196 rows and 4 columns.

Format
This data frame contains the following columns:

- **Subject** a factor with levels 1 to 7 identifying the subject whose glucose level is measured.
- **Date** a factor with levels 1 2 indicating the occasion in which the experiment was conducted.
- **Time** a numeric vector giving the time since alcohol ingestion (in min/10).
- **glucose** a numeric vector giving the blood glucose level (in mg/dl).

Details
Hand and Crowder (Table A.14, pp. 180-181, 1996) describe data on the blood glucose levels measured at 14 time points over 5 hours for 7 volunteers who took alcohol at time 0. The same experiment was repeated on a second date with the same subjects but with a dietary additive used for all subjects.

Source

---

**gnlS**

*Fit Nonlinear Model Using Generalized Least Squares*

Description
This function fits a nonlinear model using generalized least squares. The errors are allowed to be correlated and/or have unequal variances.

Usage
gnlS(model, data, params, start, correlation, weights, subset, na.action, naPattern, control, verbose)
Arguments

model a two-sided formula object describing the model, with the response on the left of a \(~\) operator and a nonlinear expression involving parameters and covariates on the right. If data is given, all names used in the formula should be defined as parameters or variables in the data frame.

data an optional data frame containing the variables named in model, correlation, weights, subset, and naPattern. By default the variables are taken from the environment from which gnls is called.

params an optional two-sided linear formula of the form p1+...+pn~x1+...+xm, or list of two-sided formulas of the form p1~x1+...+xm, with possibly different models for each parameter. The p1,...,pn represent parameters included on the right hand side of model and x1+...+xm define a linear model for the parameters (when the left hand side of the formula contains several parameters, they are all assumed to follow the same linear model described by the right hand side expression). A 1 on the right hand side of the formula(s) indicates a single fixed effects for the corresponding parameter(s). By default, the parameters are obtained from the names of start.

start an optional named list, or numeric vector, with the initial values for the parameters in model. It can be omitted when a selfStarting function is used in model, in which case the starting estimates will be obtained from a single call to the nls function.

correlation an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. If a grouping variable is to be used, it must be specified in the form argument to the corStruct constructor. Defaults to NULL, corresponding to uncorrelated errors.

weights an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic errors.

subset an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

na.action a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes gnls to print an error message and terminate if there are any incomplete observations.

naPattern an expression or formula object, specifying which returned values are to be regarded as missing.

control a list of control values for the estimation algorithm to replace the default values returned by the function gnlsControl. Defaults to an empty list.

verbose an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.

Value

an object of class gnls, also inheriting from class gls, representing the nonlinear model fit. Generic functions such as print, plot and summary have methods to show the results of the fit.
gni9lsObject for the components of the fit. The functions resid, coef, and fitted can be used to extract some of its components.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also
corClasses, gnl8Control, gnl8Object, gnl8Struct, predict.gnl8, varClasses, varFunc

Examples
# variance increases with a power of the absolute fitted values
fm1 <- gnl8(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean, 
weights = varPower())
summary(fm1)

---

gni9lsControl

### Control Values for gnl8 Fit

**Description**

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the control argument to the gnl8 function.
Usage

```
gnlsControl(maxIter = 50, nlsMaxIter = 7, msMaxIter = 50, minScale = 0.001,  
tolerance = 1e-6, nlsTol = 0.001, msTol = 1e-7,  
returnObject = FALSE, msVerbose = FALSE,  
apVar = TRUE, .relStep =,  
opt = c("nlminb", "optim"), optimMethod = "BFGS",  
minAbsParApVar = 0.05, sigma = NULL)
```

Arguments

- `maxIter` maximum number of iterations for the `gnls` optimization algorithm. Default is 50.
- `nlsMaxIter` maximum number of iterations for the `nls` optimization step inside the `gnls` optimization. Default is 7.
- `msMaxIter` maximum number of iterations for the optimization step inside the `gnls` optimization. Default is 50.
- `minScale` minimum factor by which to shrink the default step size in an attempt to decrease the sum of squares in the `nls` step. Default 0.001.
- `tolerance` tolerance for the convergence criterion in the `gnls` algorithm. Default is 1e-6.
- `nlsTol` tolerance for the convergence criterion in `nls` step. Default is 1e-3.
- `msTol` tolerance for the convergence criterion of the first outer iteration when `optim` is used. Default is 1e-7.
- `returnObject` a logical value indicating whether the fitted object should be returned with a `warning` (instead of an error via `stop()`) when the maximum number of iterations is reached without convergence of the algorithm.
- `msVerbose` a logical value passed as the `trace` argument to the optimizer chosen by `opt`; see documentation on that. Default is `FALSE`.
- `apVar` a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is `TRUE`.
- `.relStep` relative step for numerical derivatives calculations. Default is `.Machine$double.eps^{(1/3)}` (about 6e-6).
- `opt` the optimizer to be used, either "nlminb" (the current default) or "optim" (the previous default).
- `optimMethod` character - the optimization method to be used with the `optim` optimizer. The default is "BFGS". An alternative is "L-BFGS-B".
- `minAbsParApVar` numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
- `sigma` optionally a positive number to fix the residual error at. If `NULL`, as by default, or 0, `sigma` is estimated.

Value

a list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the `sigma` option: Siem Heisterkamp and Bert van Willigen.
See Also

`gnls`

Examples

```r
# decrease the maximum number of iterations and request tracing
gnlsControl(msMaxIter = 20, msVerbose = TRUE)
```

Fitted `gnls` Object

Description

An object returned by the `gnls` function, inheriting from class "gnls" and also from class "gls", and representing a generalized nonlinear least squares fitted model. Objects of this class have methods for the generic functions `anova`, `coef`, `fitted`, `formula`, `getGroups`, `getResponse`, `intervals`, `logLik`, `plot`, `predict`, `print`, `residuals`, `summary`, and `update`.

Value

The following components must be included in a legitimate "gnls" object.

- `apVar`: an approximate covariance matrix for the variance-covariance coefficients. If `apVar = FALSE` in the control values used in the call to `gnls`, this component is equal to `NULL`.
- `call`: a list containing an image of the `gnls` call that produced the object.
- `coefficients`: a vector with the estimated nonlinear model coefficients.
- `contrasts`: a list of the contrast matrices used to represent factors in the model formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the model, this component will be an empty list.
- `dims`: a list with basic dimensions used in the model fit, including the components `N` - the number of observations used in the fit and `p` - the number of coefficients in the nonlinear model.
- `fitted`: a vector with the fitted values.
- `modelStruct`: an object inheriting from class `gnlsStruct`, representing a list of model components, such as `corStruct` and `varFunc` objects.
- `groups`: a vector with the correlation structure grouping factor, if any is present.
- `logLik`: the log-likelihood at convergence.
- `numIter`: the number of iterations used in the iterative algorithm.
- `plist`.
- `pmap`.
- `residuals`: a vector with the residuals.
- `sigma`: the estimated residual standard error.
- `varBeta`: an approximate covariance matrix of the coefficients estimates.
Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
gnls, gnlsStruct

Description
A generalized nonlinear least squares structure is a list of model components representing different sets of parameters in the nonlinear model. A gnlsStruct may contain corStruct and varFunc objects. NULL arguments are not included in the gnlsStruct list.

Usage
gnlsStruct(corStruct, varStruct)

Arguments
corStruct an optional corStruct object, representing a correlation structure. Default is NULL.
varStruct an optional varFunc object, representing a variance function structure. Default is NULL.

Value
a list of model variance-covariance components determining the parameters to be estimated for the associated nonlinear model.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
gnls, corClasses, residuals.gnlsStruct, varFunc

Examples
gnls1 <- gnlsStruct(corAR1(), varPower())
groupedData

Construct a groupedData Object

Description

An object of the groupedData class is constructed from the formula and data by attaching the formula as an attribute of the data, along with any of outer, inner, labels, and units that are given. If order.groups is TRUE the grouping factor is converted to an ordered factor with the ordering determined by FUN. Depending on the number of grouping levels and the type of primary covariate, the returned object will be of one of three classes: nfnGroupedData - numeric covariate, single level of nesting; nffGroupedData - factor covariate, single level of nesting; and nmGroupedData - multiple levels of nesting. Several modeling and plotting functions can use the formula stored with a groupedData object to construct default plots and models.

Usage

```r
groupedData(formula, data, order.groups, FUN, outer, inner, labels, units)
## S3 method for class 'groupedData'
update(object, formula, data, order.groups, FUN, outer, inner, labels, units, ...)
```

Arguments

- **object**: an object inheriting from class groupedData.
- **formula**: a formula of the form resp ~ cov | group where resp is the response, cov is the primary covariate, and group is the grouping factor. The expression 1 can be used for the primary covariate when there is no other suitable candidate. Multiple nested grouping factors can be listed separated by the / symbol as in fact1/fact2. In an expression like this the fact2 factor is nested within the fact1 factor.
- **data**: a data frame in which the expressions in formula can be evaluated. The resulting groupedData object will consist of the same data values in the same order but with additional attributes.
- **order.groups**: an optional logical value, or list of logical values, indicating if the grouping factors should be converted to ordered factors according to the function FUN applied to the response from each group. If multiple levels of grouping are present, this argument can be either a single logical value (which will be repeated for all grouping levels) or a list of logical values. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). Ordering within a level of grouping is done within the levels of the grouping factors which are outer to it. Changing the grouping factor to an ordered factor does not affect the ordering of the rows in the data frame but it does affect the order of the panels in a trellis display of the data or models fitted to the data. Defaults to TRUE.
- **FUN**: an optional summary function that will be applied to the values of the response for each level of the grouping factor, when order.groups = TRUE, to determine the ordering. Defaults to the max function.
an optional one-sided formula, or list of one-sided formulas, indicating covariates that are outer to the grouping factor(s). If multiple levels of grouping are present, this argument can be either a single one-sided formula, or a list of one-sided formulas. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. When plotting a groupedData object, the argument outer = TRUE causes the panels to be determined by the outer formula. The points within the panels are associated by level of the grouping factor. Defaults to NULL, meaning that no outer covariates are present.

an optional one-sided formula, or list of one-sided formulas, indicating covariates that are inner to the grouping factor(s). If multiple levels of grouping are present, this argument can be either a single one-sided formula, or a list of one-sided formulas. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). An inner covariate can change within the sets of rows defined by the grouping factor. An inner formula can be used to associate points in a plot of a groupedData object. Defaults to NULL, meaning that no inner covariates are present.

an optional list of character strings giving labels for the response and the primary covariate. The label for the primary covariate is named x and that for the response is named y. Either label can be omitted.

an optional list of character strings giving the units for the response and the primary covariate. The units string for the primary covariate is named x and that for the response is named y. Either units string can be omitted.

some methods for this generic require additional arguments. None are used in this method.

an object of one of the classes nfnGroupedData, nffGroupedData, or nmGroupedData, and also inheriting from classes groupedData and data.frame.

Douglas Bates and José Pinheiro


formula, gapply, gsummary, lme, plot.nffGroupedData, plot.nfnGroupedData, plot.nmGroupedData, reStruct
Examples

Orth.new <- # create a new copy of the groupedData object
groupedData( distance ~ age | Subject,
data = as.data.frame( Orthodont ),
FUN = mean,
outer = ~ Sex,
labels = list( x = "Age",
y = "Distance from pituitary to pterygomaxillary fissure" ),
units = list( x = "(yr)", y = "(mm)" )
)  # trellis plot by Subject
plot( Orth.new )  # extractor for the formula
gsummary( Orth.new )  # apply summary by Subject
fm1 <- lme( Orth.new )  # fixed and groups formulae extracted from object
Orthodont2 <- update(Orthodont, FUN = mean)

---

gsummary  
Summarize by Groups

Description

Provide a summary of the variables in a data frame by groups of rows. This is most useful with a groupedData object to examine the variables by group.

Usage

gsummary(object, FUN, omitGroupingFactor, form, level,
groups, invariantsOnly, ...)

Arguments

object  
an object to be summarized - usually a groupedData object or a data.frame.

FUN  
an optional summary function or a list of summary functions to be applied to each variable in the frame. The function or functions are applied only to variables in object that vary within the groups defined by groups. Invariant variables are always summarized by group using the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as ordered, factor, or numeric. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

omitGroupingFactor  
an optional logical value. When TRUE the grouping factor itself will be omitted from the group-wise summary but the levels of the grouping factor will continue to be used as the row names for the data frame that is produced by the summary. Defaults to FALSE.
form

an optional one-sided formula that defines the groups. When this formula is given, the right-hand side is evaluated in object, converted to a factor if necessary, and the unique levels are used to define the groups. Defaults to `formula(object)`.

level

an optional positive integer giving the level of grouping to be used in an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.

groups

an optional factor that will be used to split the rows into groups. Defaults to `getGroups(object, form, level)`.

invariantsOnly

an optional logical value. When `TRUE` only those covariates that are invariant within each group will be summarized. The summary value for the group is always the unique value taken on by that covariate within the group. The columns in the summary are of the same class as the corresponding columns in `object`. By definition, the grouping factor itself must be an invariant. When combined with `omitGroupingFactor = TRUE`, this option can be used to discover is there are invariant covariates in the data frame. Defaults to `FALSE`.

optional additional arguments to the summary functions that are invoked on the variables by group. Often it is helpful to specify `na.rm = TRUE`.

Value

A `data.frame` with one row for each level of the grouping factor. The number of columns is at most the number of columns in `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

`summary`, `groupedData`, `getGroups`

Examples

gsummary(Orthodont)  # default summary by Subject
## gsummary with invariantsOnly = TRUE and omitGroupingFactor = TRUE
## determines whether there are covariates like Sex that are invariant
## within the repeated observations on the same Subject.
gsummary(Orthodont, inv = TRUE, omit = TRUE)
**Gun**

*Methods for firing naval guns*

**Description**

The Gun data frame has 36 rows and 4 columns.

**Format**

This data frame contains the following columns:

- **rounds** a numeric vector
- **Method** a factor with levels M1 M2
- **Team** an ordered factor with levels T1S < T3S < T2S < T1A < T2A < T3A < T1H < T3H < T2H
- **Physique** an ordered factor with levels Slight < Average < Heavy

**Details**

Hicks (p.180, 1993) reports data from an experiment on methods for firing naval guns. Gunners of three different physiques (slight, average, and heavy) tested two firing methods. Both methods were tested twice by each of nine teams of three gunners with identical physique. The response was the number of rounds fired per minute.

**Source**


**IGF**

*Radioimmunoassay of IGF-I Protein*

**Description**

The IGF data frame has 237 rows and 3 columns.

**Format**

This data frame contains the following columns:

- **Lot** an ordered factor giving the radioactive tracer lot.
- **age** a numeric vector giving the age (in days) of the radioactive tracer.
- **conc** a numeric vector giving the estimated concentration of IGF-I protein (ng/ml)

**Details**

Davidian and Giltinan (1995) describe data obtained during quality control radioimmunoassays for ten different lots of radioactive tracer used to calibrate the Insulin-like Growth Factor (IGF-I) protein concentration measurements.
Initialize

Source


Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: corStruct, lmeStruct, reStruct, and varFunc.

Usage

Initialize(object, data, ...)

Arguments

object any object requiring initialization, e.g. "plug-in" structures such as corStruct and varFunc objects.

data a data frame to be used in the initialization procedure.

... some methods for this generic function require additional arguments.

Value

an initialized object with the same class as object. Changes introduced by the initialization procedure will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

Initialize.corStruct, Initialize.lmeStruct, Initialize.glsStruct, Initialize.varFunc, isInitialized

Examples

## see the method function documentation
Initialize.corStruct  Initialize corStruct Object

Description

This method initializes object by evaluating its associated covariate(s) and grouping factor, if any is present, in data, calculating various dimensions and constants used by optimization algorithms involving corStruct objects (see the appropriate Dim method documentation), and assigning initial values for the coefficients in object, if none were present.

Usage

## S3 method for class 'corStruct'
Initialize(object, data, ...)

Arguments

object  an object inheriting from class "corStruct" representing a correlation structure.
data  a data frame in which to evaluate the variables defined in formula(object).
...  this argument is included to make this method compatible with the generic.

Value

an initialized object with the same class as object representing a correlation structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

Dim.corStruct

Examples

cs1 <- corAR1(form = ~ 1 | Subject)
cs1 <- Initialize(cs1, data = Orthodont)
### Initialize.glsStruct

#### Initialize a glsStruct Object

**Description**

The individual linear model components of the glsStruct list are initialized.

**Usage**

```r
## S3 method for class 'glsStruct'
Initialize(object, data, control, ...)
```

**Arguments**

- `object`: an object inheriting from class "glsStruct", representing a list of linear model components, such as corStruct and varFunc objects.
- `data`: a data frame in which to evaluate the variables defined in formula(object).
- `control`: an optional list with control parameters for the initialization and optimization algorithms used in gls. Defaults to list(singular.ok = FALSE), implying that linear dependencies are not allowed in the model.
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

a glsStruct object similar to object, but with initialized model components.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

gls, Initialize.corStruct, Initialize.varFunc, Initialize

---

### Initialize.lmeStruct

#### Initialize an lmeStruct Object

**Description**

The individual linear mixed-effects model components of the lmeStruct list are initialized.

**Usage**

```r
## S3 method for class 'lmeStruct'
Initialize(object, data, groups, conLin, control, ...)
```
Initialize.reStruct

Arguments

- **object**
  - an object inheriting from class "lmeStruct", representing a list of linear mixed-effects model components, such as reStruct, corStruct, and varFunc objects.

- **data**
  - a data frame in which to evaluate the variables defined in formula(object).

- **groups**
  - a data frame with the grouping factors corresponding to the lme model associated with object as columns, sorted from innermost to outermost grouping level.

- **conLin**
  - an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "loglik", corresponding to the log-likelihood of the underlying lme model. Defaults to attr(object, "conLin").

- **control**
  - an optional list with control parameters for the initialization and optimization algorithms used in lme. Defaults to list(niterEM=20, gradHess=TRUE), implying that 20 EM iterations are to be used in the derivation of initial estimates for the coefficients of the reStruct component of object and, if possible, numerical gradient vectors and Hessian matrices for the log-likelihood function are to be used in the optimization algorithm.

- **...**
  - some methods for this generic require additional arguments. None are used in this method.

Value

an lmeStruct object similar to object, but with initialized model components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, Initialize.reStruct, Initialize.corStruct, Initialize.varFunc, Initialize

---

**Description**

Initial estimates for the parameters in the pdMat objects forming object, which have not yet been initialized, are obtained using the methodology described in Bates and Pinheiro (1998). These estimates may be refined using a series of EM iterations, as described in Bates and Pinheiro (1998). The number of EM iterations to be used is defined in control.

**Usage**

## S3 method for class 'reStruct'
Initialize(object, data, conLin, control, ...)

Initialize varFunc Object

Description

This method initializes object by evaluating its associated covariate(s) and grouping factor, if any is present, in data; determining if the covariate(s) need to be updated when the values of the coefficients associated with object change; initializing the log-likelihood and the weights associated with object; and assigning initial values for the coefficients in object, if none were present. The covariate(s) will only be initialized if no update is needed when coef(object) changes.

Usage

```r
## S3 method for class 'varFunc'
Initialize(object, data, ...)
```

Arguments

- **object**: an object inheriting from class "varFunc", representing a variance function structure.
- **data**: a data frame in which to evaluate the variables named in formula(object).
- **...**: this argument is included to make this method compatible with the generic.

Value

an reStruct object similar to object, but with all pdMat components initialized.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

reStruct, pdMat, Initialize
Value

an initialized object with the same class as `object` representing a variance function structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`Initialize`

Examples

```r
vf1 <- varPower( form = ~ age | Sex )
vf1 <- Initialize( vf1, Orthodont )
```

## see the method documentation

### intervals

#### Confidence Intervals on Coefficients

Description

Confidence intervals on the parameters associated with the model represented by `object` are obtained. This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls`, `lme`, and `lmList`.

Usage

```
intervals(object, level, ...)
```

Arguments

- `object`: a fitted model object from which parameter estimates can be extracted.
- `level`: an optional numeric value for the interval confidence level. Defaults to 0.95.
- `...`: some methods for the generic may require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

`intervals.lme`, `intervals.lmList`, `intervals.gls`

Examples

```r
## see the method documentation
```
Description

Approximate confidence intervals for the parameters in the linear model represented by object are obtained, using a normal approximation to the distribution of the (restricted) maximum likelihood estimators (the estimators are assumed to have a normal distribution centered at the true parameter values and with covariance matrix equal to the negative inverse Hessian matrix of the (restricted) log-likelihood evaluated at the estimated parameters). Confidence intervals are obtained in an unconstrained scale first, using the normal approximation, and, if necessary, transformed to the constrained scale.

Usage

## S3 method for class 'gls'
intervals(object, level, which, ...)

Arguments

object an object inheriting from class "gls", representing a generalized least squares fitted linear model.
level an optional numeric value for the interval confidence level. Defaults to 0.95.
which an optional character string specifying the subset of parameters for which to construct the confidence intervals. Possible values are "all" for all parameters, "var-cov" for the variance-covariance parameters only, and "coef" for the linear model coefficients only. Defaults to "all".

Value

a list with components given by data frames with rows corresponding to parameters and columns lower, est., and upper representing respectively lower confidence limits, the estimated values, and upper confidence limits for the parameters. Possible components are:

coeff linear model coefficients, only present when which is not equal to "var-cov".
corStruct correlation parameters, only present when which is not equal to "coef" and a correlation structure is used in object.
varFunc variance function parameters, only present when which is not equal to "coef" and a variance function structure is used in object.
sigma residual standard error.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also
gls, intervals, print.intervals.gls

Examples

fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
correlation = corAR1(form = ~ 1 | Mare))
intervals(fm1)

intervals.lme

Confidence Intervals on lme Parameters

Description

Approximate confidence intervals for the parameters in the linear mixed-effects model represented
by object are obtained, using a normal approximation to the distribution of the (restricted) maxim-
imum likelihood estimators (the estimators are assumed to have a normal distribution centered at the
ture parameter values and with covariance matrix equal to the negative inverse Hessian matrix of the
(restricted) log-likelihood evaluated at the estimated parameters). Confidence intervals are obtained
in an unconstrained scale first, using the normal approximation, and, if necessary, transformed to
the constrained scale. The pdNatural parametrization is used for general positive-definite matrices.

Usage

## S3 method for class 'lme'
intervals(object, level = 0.95,
        which = c("all", "var-cov", "fixed"), ...)

Arguments

object an object inheriting from class "lme", representing a fitted linear mixed-effects
model.
level an optional numeric value with the confidence level for the intervals. Defaults
to 0.95.
which an optional character string specifying the subset of parameters for which to
construct the confidence intervals. Possible values are "all" for all parameters,
"var-cov" for the variance-covariance parameters only, and "fixed" for the
fixed effects only. Defaults to "all".
... some methods for this generic require additional arguments. None are used in
this method.

Value

a list with components given by data frames with rows corresponding to parameters and columns
lower, est., and upper representing respectively lower confidence limits, the estimated values,
and upper confidence limits for the parameters. Possible components are:

fixed fixed effects, only present when which is not equal to "var-cov".
reStruct random effects variance-covariance parameters, only present when which is not
equal to "fixed".
within-group correlation parameters, only present when which is not equal to "fixed" and a correlation structure is used in object.

varFunc

within-group variance function parameters, only present when which is not equal to "fixed" and a variance function structure is used in object.

sigma

within-group standard deviation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

lme, intervals, print.intervals.lme, pdNatural

Examples

fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
intervals(fm1)

Description

Confidence intervals on the linear model coefficients are obtained for each lm component of object and organized into a three dimensional array. The first dimension corresponding to the names of the object components. The second dimension is given by lower, est., and upper corresponding, respectively, to the lower confidence limit, estimated coefficient, and upper confidence limit. The third dimension is given by the coefficients names.

Usage

## S3 method for class 'lmList'
intervals(object, level = 0.95, pool = attr(object, "pool"), ...)

Arguments

object

an object inheriting from class "lmList", representing a list of lm objects with a common model.

level

an optional numeric value with the confidence level for the intervals. Defaults to 0.95.

pool

an optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is attr(object, "pool").

... some methods for this generic require additional arguments. None are used in this method.
Value

A three dimensional array with the confidence intervals and estimates for the coefficients of each `lm` component of `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

`lmList`, `intervals`, `plot.intervals.lmList`

Examples

```r
fm1 <- lmList(distance ~ age | Subject, Orthodont)
intervals(fm1)
```

Description

Check the design of the experiment or study for balance.

Usage

```r
isBalanced(object, countOnly, level)
```

Arguments

- **object**: A `groupedData` object containing a data frame and a formula that describes the roles of variables in the data frame. The object will have one or more nested grouping factors and a primary covariate.
- **countOnly**: A logical value indicating if the check for balance should only consider the number of observations at each level of the grouping factor(s). Defaults to `FALSE`.
- **level**: An optional integer vector specifying the desired prediction levels. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Defaults to the innermost level.

Details

A design is balanced with respect to the grouping factor(s) if there are the same number of observations at each distinct value of the grouping factor or each combination of distinct levels of the nested grouping factors. If `countOnly` is `FALSE` the design is also checked for balance with respect to the primary covariate, which is often the time of the observation. A design is balanced with respect to the grouping factor and the covariate if the number of observations at each distinct level (or combination of levels for nested factors) is constant and the times at which the observations are taken (in general, the values of the primary covariates) also are constant.
isInitialized

Value

TRUE or FALSE according to whether the data are balanced or not

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

table, groupedData

Examples

isBalanced(Orthodont) # should return TRUE
isBalanced(Orthodont, countOnly = TRUE) # should return TRUE
isBalanced(Pixel) # should return FALSE
isBalanced(Pixel, level = 1) # should return FALSE

isInitialized

Check if Object is Initialized

Description

Checks if object has been initialized (generally through a call to Initialize), by searching for components and attributes which are modified during initialization.

Usage

isInitialized(object)

Arguments

object any object requiring initialization.

Value

a logical value indicating whether object has been initialized.

Author(s)

José Pinheiro and Douglas Bates

See Also

Initialize

Examples

pd1 <- pdDiag(~age)
isInitialized(pd1)
Generate system matrix for LDEs

Description
Generate the system matrix for the linear differential equations determined by a compartment model.

Usage
LDEsysMat(pars, incidence)

Arguments
pars
a numeric vector of parameter values.

incidence
an integer matrix with columns named From, To, and Par. Values in the Par column must be in the range 1 to length(pars). Values in the From column must be between 1 and the number of compartments. Values in the To column must be between 0 and the number of compartments.

Details
A compartment model describes material transfer between k in a system of k compartments to a linear system of differential equations. Given a description of the system and a vector of parameter values this function returns the system matrix.

This function is intended for use in a general system for solving compartment models, as described in Bates and Watts (1988).

Value
A k by k numeric matrix.

Author(s)
Douglas Bates <bates@stat.wisc.edu>

References

Examples
# incidence matrix for a two compartment open system
incidence <-
  matrix(c(1,1,2,2,1,3,2,0), ncol = 3, byrow = TRUE,
  dimnames = list(NULL, c("Par", "From", "To")))
LDEsysMat(c(1.2, 0.3, 0.4), incidence)
Description

This generic function fits a linear mixed-effects model in the formulation described in Laird and Ware (1982) but allowing for nested random effects. The within-group errors are allowed to be correlated and/or have unequal variances.

This page describes the formula method; the methods `lme.lmList` and `lme.groupedData` are documented separately.

Usage

```r
lme(fixed, data, random, correlation, weights, subset, method,
    na.action, control, contrasts = NULL, keep.data = TRUE)
``` 

## S3 method for class 'formula'
```r
lme(fixed, data, random, correlation, weights, subset, method,
    na.action, control, contrasts = NULL, keep.data = TRUE)
``` 

## S3 method for class 'lme'
```r
update(object, fixed., ..., evaluate = TRUE)
``` 

Arguments

- **object**
  - an object inheriting from class `lme`, representing a fitted linear mixed-effects model.

- **fixed**
  - a two-sided linear formula object describing the fixed-effects part of the model, with the response on the left of a `~` operator and the terms, separated by `+` operators, on the right, an "lmList" object, or a "groupedData" object.
  - There is limited support for formulae such as `resp ~ 1` and `resp ~ 0`, and less prior to version '3.1-112'.

- **fixed.**
  - Changes to the fixed-effects formula -- see `update.formula` for details.

- **data**
  - an optional data frame containing the variables named in fixed, random, correlation, weights, and subset. By default the variables are taken from the environment from which `lme` is called.

- **random**
  - optionally, any of the following: (i) a one-sided formula of the form `~ x1 + ... + xn | g1/.../gm`, with `x1 + ... + xn` specifying the model for the random effects and `g1/.../gm` the grouping structure (`m` may be equal to 1, in which case `no /` is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form `~ x1 + ... + xn | g`, with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form `~ x1 + ... + xn`, or a `pdMat` object with a formula (i.e. a non-NULL value for `formula(object)`), or a list of such formulas or `pdMat` objects. In this case, the grouping structure formula will be derived from the data used to fit the linear mixed-effects model, which should inherit from class "groupedData"; (iv) a named list of formulas or `pdMat` objects as in (iii), with the grouping factors
as names. The order of nesting will be assumed the same as the order of the order of the elements in the list; (v) an \texttt{reStruct} object. See the documentation on \texttt{pdClasses} for a description of the available \texttt{pdMat} classes. Defaults to a formula consisting of the right hand side of \texttt{fixed}.

\textbf{correlation} an optional \texttt{corStruct} object describing the within-group correlation structure. See the documentation of \texttt{corClasses} for a description of the available \texttt{corStruct} classes. Defaults to \texttt{NULL}, corresponding to no within-group correlations.

\textbf{weights} an optional \texttt{varFunc} object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to \texttt{varFixed}, corresponding to fixed variance weights. See the documentation on \texttt{varClasses} for a description of the available \texttt{varFunc} classes. Defaults to \texttt{NULL}, corresponding to homoscedastic within-group errors.

\textbf{subset} an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

\textbf{method} a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".

\textbf{na.action} a function that indicates what should happen when the data contain NAs. The default action (\texttt{na.fail}) causes \texttt{lme} to print an error message and terminate if there are any incomplete observations.

\textbf{control} a list of control values for the estimation algorithm to replace the default values returned by the function \texttt{lmeControl}. Defaults to an empty list.

\textbf{contrasts} an optional list. See the \texttt{contrasts.arg} of \texttt{model.matrix.default}.

\textbf{keep.data} logical: should the data argument (if supplied and a data frame) be saved as part of the model object?

\textbf{...} some methods for this generic require additional arguments. None are used in this method.

\textbf{evaluate} If TRUE evaluate the new call else return the call.

\textbf{Details}

\texttt{offset} terms in \texttt{fixed} are an error since 3.1-157 (2022-03): previously they were silently ignored.

\textbf{Value}

An object of class "lme" representing the linear mixed-effects model fit. Generic functions such as \texttt{print}, \texttt{plot} and \texttt{summary} have methods to show the results of the fit. See \texttt{lmeObject} for the components of the fit. The functions \texttt{resid}, \texttt{coef}, \texttt{fitted}, \texttt{fixed.effects}, and \texttt{random.effects} can be used to extract some of its components.

\textbf{Note}

The function does not do any scaling internally: the optimization will work best when the response is scaled so its variance is of the order of one.

\textbf{Author(s)}

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
References


See Also

corClasses, lme.lmList, lme.groupedData, lmeControl, lmeObject, lmStruct, lmList, pdClasses, plot.lme, predict.lme, qqnorm.lme, residuals.lme, reStruct, simulate.lme, summary.lme, varClasses, varFunc

Examples

fm1 <- lme(distance ~ age, data = Orthodont) # random is ~ age
fm2 <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
summary(fm1)
summary(fm2)

lme.groupedData LME fit from groupedData Object

Description

The response variable and primary covariate in formula(fixed) are used to construct the fixed effects model formula. This formula and the groupedData object are passed as the fixed and data arguments to lme.formula, together with any other additional arguments in the function call. See the documentation on lme.formula for a description of that function.
Usage

## S3 method for class 'groupedData'
lme(fixed, data, random, correlation, weights,
    subset, method, na.action, control, contrasts, keep.data = TRUE)

Arguments

fixed        a data frame inheriting from class "groupedData".
data         this argument is included for consistency with the generic function. It is ignored in this method function.
random       optionally, any of the following: (i) a one-sided formula of the form ~x1+...+xn | g1/.../gm, with x1+...+xn specifying the model for the random effects and g1/.../gm the grouping structure (m may be equal to 1, in which case no / is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form ~x1+...+xn | g, with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form ~x1+...+xn, or a pdMat object with a formula (i.e. a non-NULL value for formula(object)), or a list of such formulas or pdMat objects. In this case, the grouping structure formula will be derived from the data used to fit the linear mixed-effects model, which should inherit from class groupedData; (iv) a named list of formulas or pdMat objects as in (iii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the elements in the list; (v) an reStruct object. See the documentation on pdClasses for a description of the available pdMat classes. Defaults to a formula consisting of the right hand side of fixed.
correlation  an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. Defaults to NULL, corresponding to no within-group correlations.
weights      an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic within-group errors.
subset       an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
method       a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
na.action    a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes lme to print an error message and terminate if there are any incomplete observations.
control      a list of control values for the estimation algorithm to replace the default values returned by the function lmeControl. Defaults to an empty list.
contrasts    an optional list. See the contrasts.arg of model.matrix.default.
keep.data    logical: should the data argument (if supplied and a data frame) be saved as part of the model object?
Value

an object of class \texttt{lme} representing the linear mixed-effects model fit. Generic functions such as \texttt{print}, \texttt{plot} and \texttt{summary} have methods to show the results of the fit. See \texttt{lmeObject} for the components of the fit. The functions \texttt{resid}, \texttt{coef}, \texttt{fitted}, \texttt{fixed.effects}, and \texttt{random.effects} can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

\texttt{lme}, \texttt{groupedData}, \texttt{lmeObject}

Examples

```r
fm1 <- lme(Orthodont)
summary(fm1)
```
**lme.lmList**

**LME fit from lmList Object**

**Description**

If the random effects names defined in `random` are a subset of the `lmList` object coefficient names, initial estimates for the covariance matrix of the random effects are obtained (overwriting any values given in `random`). `formula(fixed)` and the `data` argument in the calling sequence used to obtain `fixed` are passed as the `fixed` and `data` arguments to `lme.formula`, together with any other additional arguments in the function call. See the documentation on `lme.formula` for a description of that function.

**Usage**

```r
## S3 method for class 'lmList'
lme(fixed, data, random, correlation, weights, subset, method,
   na.action, control, contrasts, keep.data)
```

**Arguments**

- **fixed**: an object inheriting from class "lmList.", representing a list of `lm` fits with a common model.
- **data**: this argument is included for consistency with the generic function. It is ignored in this method function.
- **random**: an optional one-sided linear formula with no conditioning expression, or a `pdMat` object with a `formula` attribute. Multiple levels of grouping are not allowed with this method function. Defaults to a formula consisting of the right hand side of `formula(fixed)`.
- **correlation**: an optional `corStruct` object describing the within-group correlation structure. See the documentation of `corClasses` for a description of the available `corStruct` classes. Defaults to `NULL`, corresponding to no within-group correlations.
- **weights**: an optional `varFunc` object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to `varFixed`, corresponding to fixed variance weights. See the documentation on `varClasses` for a description of the available `varFunc` classes. Defaults to `NULL`, corresponding to homoscedastic within-group errors.
- **subset**: an optional expression indicating the subset of the rows of `data` that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
- **method**: a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
- **na.action**: a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes `lme` to print an error message and terminate if there are any incomplete observations.
- **control**: a list of control values for the estimation algorithm to replace the default values returned by the function `lmeControl`. Defaults to an empty list.
contrasts an optional list. See the contrasts.arg of model.matrix.default.

keep.data logical: should the data argument (if supplied and a data frame) be saved as part of the model object?

Value

an object of class lme representing the linear mixed-effects model fit. Generic functions such as print, plot and summary have methods to show the results of the fit. See lmeObject for the components of the fit. The functions resid, coef, fitted, fixed.effects, and random.effects can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

lme, lmList, lmeObject

Examples

fm1 <- lmList(Orthodont)
fm2 <- lme(fm1)
summary(fm1)
summary(fm2)
Specifying Control Values for \texttt{lme} Fit

### Description

The values supplied in the \texttt{lmeControl()} call replace the defaults, and a \texttt{list} with all settings (i.e., values for all possible arguments) is returned. The returned list is used as the \texttt{control} argument to the \texttt{lme} function.

### Usage

\begin{verbatim}
\texttt{lmeControl(maxIter = 50, msMaxIter = 50, tolerance = 1e-6, niterEM = 25, msMaxEval = 200, msTol = 1e-7, msVerbose = FALSE, returnObject = FALSE, gradHess = TRUE, apVar = TRUE, .relStep = .Machine$double.eps*(1/3), minAbsParApVar = 0.05, opt = c("nlminb", "optim"), optimMethod = "BFGS", natural = TRUE, sigma = NULL, allow.n.lt.q = FALSE, ...)}
\end{verbatim}

### Arguments

- \texttt{maxIter} maximum number of iterations for the \texttt{lme} optimization algorithm. Default is 50.
- \texttt{msMaxIter} maximum number of iterations for the optimization step inside the \texttt{lme} optimization. Default is 50.
- \texttt{tolerance} tolerance for the convergence criterion in the \texttt{lme} algorithm. Default is 1e-6.
- \texttt{niterEM} number of iterations for the EM algorithm used to refine the initial estimates of the random effects variance-covariance coefficients. Default is 25.
- \texttt{msMaxEval} maximum number of evaluations of the objective function permitted for \texttt{nlminb}. Default is 200.
- \texttt{msTol} tolerance for the convergence criterion on the first iteration when \texttt{optim} is used. Default is 1e-7.
- \texttt{msVerbose} a logical value passed as the \texttt{trace} argument to \texttt{nlminb} or \texttt{optim}. Default is \texttt{FALSE}.
- \texttt{returnObject} a logical value indicating whether the fitted object should be returned with a \texttt{warning} (instead of an error via \texttt{stop()}) when the maximum number of iterations is reached without convergence of the algorithm. Default is \texttt{FALSE}.
- \texttt{gradHess} a logical value indicating whether numerical gradient vectors and Hessian matrices of the log-likelihood function should be used in the internal optimization. This option is only available when the correlation structure (\texttt{corStruct}) and the variance function structure (\texttt{varFunc}) have no "varying" parameters and the \texttt{pdMat} classes used in the random effects structure are \texttt{pdSymm} (general positive-definite), \texttt{pdDiag} (diagonal), \texttt{pdIdent} (multiple of the identity), or \texttt{pdCompSymm} (compound symmetry). Default is \texttt{TRUE}.
- \texttt{apVar} a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is \texttt{TRUE}.
lmeObject

.Fitted lme Object

Description

An object returned by the lme function, inheriting from class "lme" and representing a fitted linear mixed-effects model. Objects of this class have methods for the generic functions anova, coef, fitted, fixed.effects, formula, getGroups, getResponse, intervals, logLik, pairs, plot, predict, print, random.effects, residuals, sigma, summary, update, and vcov.

Value

a list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the sigma option: Siem Heisterkamp and Bert van Willigen.

See Also

lme, nlminb, optim

Examples

# decrease the maximum number iterations in the ms call and
# request that information on the evolution of the ms iterations be printed
str(lCtr <- lmeControl(msMaxIter = 20, msVerbose = TRUE))
## This should always work:
do.call(lmeControl, lCtr)
Value

The following components must be included in a legitimate "lme" object.

- **apVar**: an approximate covariance matrix for the variance-covariance coefficients. If `apVar = FALSE` in the control values used in the call to `lme`, this component is `NULL`.

- **call**: a list containing an image of the `lme` call that produced the object.

- **coefficients**: a list with two components, `fixed` and `random`, where the first is a vector containing the estimated fixed effects and the second is a list of matrices with the estimated random effects for each level of grouping. For each matrix in the `random` list, the columns refer to the random effects and the rows to the groups.

- **contrasts**: a list of the contrast matrices used to represent factors in the fixed effects formula and/or random effects formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the `lme` model, this component will be an empty list.

- **dims**: a list with basic dimensions used in the `lme` fit, including the components `N` - the number of observations in the data, `Q` - the number of grouping levels, `qvec` - the number of random effects at each level from innermost to outermost (last two values are equal to zero and correspond to the fixed effects and the response), `ngrps` - the number of groups at each level from innermost to outermost (last two values are one and correspond to the fixed effects and the response), and `ncol` - the number of columns in the model matrix for each level of grouping from innermost to outermost (last two values are equal to the number of fixed effects and one).

- **fitted**: a data frame with the fitted values as columns. The leftmost column corresponds to the population fixed effects (corresponding to the fixed effects only) and successive columns from left to right correspond to increasing levels of grouping.

- **fixDF**: a list with components `X` and `terms` specifying the denominator degrees of freedom for, respectively, t-tests for the individual fixed effects and F-tests for the fixed-effects terms in the models.

- **groups**: a data frame with the grouping factors as columns. The grouping level increases from left to right.

- **logLik**: the (restricted) log-likelihood at convergence.

- **method**: the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.

- **modelStruct**: an object inheriting from class `lmeStruct`, representing a list of mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.

- **numIter**: the number of iterations used in the iterative algorithm.

- **residuals**: a data frame with the residuals as columns. The leftmost column corresponds to the population residuals and successive columns from left to right correspond to increasing levels of grouping.

- **terms**: the `terms`, including `formula`, see also `terms.object`.

- **sigma**: the estimated within-group error standard deviation.

- **varFix**: an approximate covariance matrix of the fixed effects estimates.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
**Description**

A linear mixed-effects structure is a list of model components representing different sets of parameters in the linear mixed-effects model. An lmeStruct list must contain at least a reStruct object, but may also contain corStruct and varFunc objects. NULL arguments are not included in the lmeStruct list.

**Usage**

lmeStruct(reStruct, corStruct, varStruct)

**Arguments**

- **reStruct**
  - a reStruct representing a random effects structure.

- **corStruct**
  - an optional corStruct object, representing a correlation structure. Default is NULL.

- **varStruct**
  - an optional varFunc object, representing a variance function structure. Default is NULL.

**Value**

a list of model components determining the parameters to be estimated for the associated linear mixed-effects model.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

corClasses, lme, residuals.lmeStruct, reStruct, varFunc

**Examples**

```r
lms1 <- lmeStruct(reStruct(~age), corAR1(), varPower())
```
lmList

List of lm Objects with a Common Model

Description

Data is partitioned according to the levels of the grouping factor g and individual lm fits are obtained for each data partition, using the model defined in object.

Usage

lmList(object, data, level, subset, na.action = na.fail, pool = TRUE, warn.lm = TRUE)

## S3 method for class 'formula'
lmList(object, data, level, subset, na.action = na.fail, pool = TRUE, warn.lm = TRUE)

## S3 method for class 'lmList'
update(object, formula., ..., evaluate = TRUE)

## S3 method for class 'lmList'
print(x, pool, ...)

Arguments

object

For lmList, either a linear formula object of the form y ~ x1+...+xn | g or a groupedData object. In the formula object, y represents the response, x1,...,xn the covariates, and g the grouping factor specifying the partitioning of the data according to which different lm fits should be performed. The grouping factor g may be omitted from the formula, in which case the grouping structure will be obtained from data, which must inherit from class groupedData. The method function lmList.groupedData is documented separately. For the method update.lmList, object is an object inheriting from class lmList.

formula

(used in update.lmList only) a two-sided linear formula with the common model for the individuals lm fits.

formula.

Changes to the formula – see update.formula for details.

data

a data frame in which to interpret the variables named in object.

level

an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.

subset

an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

na.action

a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes lmList to print an error message and terminate if there are any incomplete observations.

pool

an optional logical value indicating whether a pooled estimate of the residual standard error should be used in calculations of standard deviations or standard errors for summaries.
lmList.groupedData

Description

The response variable and primary covariate in formula(object) are used to construct the linear model formula. This formula and the groupedData object are passed as the object and data arguments to lmList.formula, together with any other additional arguments in the function call. See the documentation on lmList.formula for a description of that function.

Usage

## S3 method for class 'groupedData'
lmList(object, data, level, subset, na.action = na.fail, pool = TRUE, warn.lm = TRUE)

Arguments

object a data frame inheriting from class "groupedData".
data this argument is included for consistency with the generic function. It is ignored in this method function.
level an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.

Value

a list of lm objects with as many components as the number of groups defined by the grouping factor. Generic functions such as coef, fixed.effects, lme, pairs, plot, predict, random.effects, summary, and update have methods that can be applied to an lmList object.

References


See Also

lm, lme.lmList, plot.lmList, pooledSD, predict.lmList, residuals.lmList, summary.lmList

Examples

fm1 <- lmList(distance ~ age | Subject, Orthodont)
summary(fm1)
logDet

subset
an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

na.action
a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes lmList to print an error message and terminate if there are any incomplete observations.

pool, warn.lm optional logicals, see lmList.

Value
a list of lm objects with as many components as the number of groups defined by the grouping factor. Generic functions such as coef, fixed.effects, lme, pairs, plot, predict, random.effects, summary, and update have methods that can be applied to an lmList object.

See Also
groupedData, lm, lme, lmList, lmList, lmList.formula

Examples
fm1 <- lmList(Orthodont)
summary(fm1)

logDet

Extract the Logarithm of the Determinant

Description
This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: corStruct, several pdMat classes, and reStruct.

Usage
logDet(object, ...)

Arguments
object any object from which a matrix, or list of matrices, can be extracted
...
some methods for this generic function require additional arguments.

Value
will depend on the method function used; see the appropriate documentation.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
logDet.corStruct

See Also
logLik.corStruct, logDet.pdMat, logDet.reStruct

Examples
## see the method function documentation

cs1 <- corAR1(0.3)
logDet(cs1, covariate = 1:4)

Description
This method function extracts the logarithm of the determinant of a square-root factor of the correlation matrix associated with object, or the sum of the log-determinants of square-root factors of the list of correlation matrices associated with object.

Usage
## S3 method for class 'corStruct'
logDet(object, covariate, ...)

Arguments
object an object inheriting from class "corStruct", representing a correlation structure.
covariate an optional covariate vector (matrix), or list of covariate vectors (matrices), at which values the correlation matrix, or list of correlation matrices, are to be evaluated. Defaults to getCovariate(object).
... some methods for this generic require additional arguments. None are used in this method.

Value
the log-determinant of a square-root factor of the correlation matrix associated with object, or the sum of the log-determinants of square-root factors of the list of correlation matrices associated with object.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
logLik.corStruct, corMatrix.corStruct, logDet

Examples
cs1 <- corAR1(0.3)
logDet(cs1, covariate = 1:4)
logDet.pdMat

Extract Log-Determinant from a pdMat Object

Description

This method function extracts the logarithm of the determinant of a square-root factor of the positive-definite matrix represented by object.

Usage

```r
## S3 method for class 'pdMat'
logDet(object, ...)
```

Arguments

- `object`: an object inheriting from class "pdMat", representing a positive definite matrix.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

the log-determinant of a square-root factor of the positive-definite matrix represented by `object`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`pdMat`, `logDet`

Examples

```r
pd1 <- pdSymm(diag(1:3))
logDet(pd1)
```

logDet.reStruct

Extract reStruct Log-Determinants

Description

Calculates, for each of the pdMat components of object, the logarithm of the determinant of a square-root factor.

Usage

```r
## S3 method for class 'reStruct'
logDet(object, ...)
```
Arguments

object an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the log-determinants of square-root factors of the pdMat components of object.

Author(s)

José Pinheiro

See Also

reStruct, pdMat, logDet

Examples

rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
                   B = pdDiag(2 * diag(4), form = ~Educ)))
logDet(rs1)

Description

This method function extracts the component of a Gaussian log-likelihood associated with the correlation structure, which is equal to the negative of the logarithm of the determinant (or sum of the logarithms of the determinants) of the matrix (or matrices) represented by object.

Usage

## S3 method for class 'corStruct'
logLik(object, data, ...)

Arguments

object an object inheriting from class "corStruct", representing a correlation structure.
data this argument is included to make this method function compatible with other logLik methods and will be ignored.
... some methods for this generic require additional arguments. None are used in this method.

Value

the negative of the logarithm of the determinant (or sum of the logarithms of the determinants) of the correlation matrix (or matrices) represented by object.
logLik.glsStruct

Log-Likelihood of a glsStruct Object

Description

Pars is used to update the coefficients of the model components of object and the individual (restricted) log-likelihood contributions of each component are added together. The type of log-likelihood (restricted or not) is determined by the settings attribute of object.

Usage

## S3 method for class 'glsStruct'
logLik(object, Pars, conLin, ...)

Arguments

object  an object inheriting from class "glsStruct", representing a list of linear model components, such as corStruct and "varFunc" objects.

Pars  the parameter values at which the (restricted) log-likelihood is to be evaluated.

conLin  an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying linear model. Defaults to attr(object, "conLin").

...  some methods for this generic require additional arguments. None are used in this method.

Value

the (restricted) log-likelihood for the linear model described by object, evaluated at Pars.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, glsStruct, logLik.lme
logLik.gnls

Log-Likelihood of a gnls Object

Description

Returns the log-likelihood value of the nonlinear model represented by object evaluated at the estimated coefficients.

Usage

## S3 method for class 'gnls'
logLik(object, REML, ...)

Arguments

- **object**: an object inheriting from class "gnls", representing a generalized nonlinear least squares fitted model.
- **REML**: an logical value for consistency with logLik.gls, but only FALSE is accepted.
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value

the log-likelihood of the linear model represented by object evaluated at the estimated coefficients.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls, logLik.lme

Examples

fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean, weights = varPower())
logLik(fm1)

logLik.gnlsStruct

Log-Likelihood of a gnlsStruct Object

Description

Pars is used to update the coefficients of the model components of object and the individual log-likelihood contributions of each component are added together.

Usage

## S3 method for class 'gnlsStruct'
logLik(object, Pars, conLin, ...)

Arguments

object an object inheriting from class gnlsStruct, representing a list of model components, such as corStruct and varFunc objects, and attributes specifying the underlying nonlinear model and the response variable.

Pars the parameter values at which the log-likelihood is to be evaluated.

conLin an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying nonlinear model. Defaults to_attr(object, "conLin").

Value

the log-likelihood for the linear model described by object, evaluated at Pars.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnls, gnlsStruct, logLik.gnls

Description

If REML=FALSE, returns the log-likelihood value of the linear mixed-effects model represented by object evaluated at the estimated coefficients; else, the restricted log-likelihood evaluated at the estimated coefficients is returned.

Usage

## S3 method for class 'lme'
logLik(object, REML, ...)

Arguments

object an object inheriting from class "lme", representing a fitted linear mixed-effects model.

REML an optional logical value. If TRUE the restricted log-likelihood is returned, else, if FALSE, the log-likelihood is returned. Defaults to the method of estimation used, that is TRUE if and only object was fitted with method = "REML" (the default for these fitting functions).

... some methods for this generic require additional arguments. None are used in this method.
Value

the (restricted) log-likelihood of the model represented by object evaluated at the estimated coefficients.

Author(s)

José Pinheiro and Douglas Bates

References


See Also

lme, gls, logLik.corStruct, logLik.glsStruct, logLik.lmeStruct, logLik.lmList, logLik.reStruct, logLik.varFunc,

Examples

```r
fm1 <- lme(distance ~ Sex * age, Orthodont, random = ~ age, method = "ML")
logLik(fm1)
logLik(fm1, REML = TRUE)
```

logLik.lmeStruct  
*Log-Likelihood of an lmeStruct Object*

Description

Pars is used to update the coefficients of the model components of object and the individual (restricted) log-likelihood contributions of each component are added together. The type of log-likelihood (restricted or not) is determined by the settings attribute of object.

Usage

```r
## S3 method for class 'lmeStruct'
logLik(object, Pars, conLin, ...)
```

Arguments

object  
an object inheriting from class "lmeStruct", representing a list of linear mixed-effects model components, such as reStruct, corStruct, and varFunc objects.

Pars  
the parameter values at which the (restricted) log-likelihood is to be evaluated.

conLin  
an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying lme model. Defaults to attr(object, "conLin").

...  
some methods for this generic require additional arguments. None are used in this method.
Value

the (restricted) log-likelihood for the linear mixed-effects model described by object, evaluated at Pars.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, lmeStruct, logLik.lme

logLik.lmList  

Log-Likelihood of an lmList Object

Description

If pool=FALSE, the (restricted) log-likelihoods of the lm components of object are summed together. Else, the (restricted) log-likelihood of the lm fit with different coefficients for each level of the grouping factor associated with the partitioning of the object components is obtained.

Usage

## S3 method for class 'lmList'
logLik(object, REML, pool, ...)

Arguments

object an object inheriting from class "lmList", representing a list of lm objects with a common model.
REML an optional logical value. If TRUE the restricted log-likelihood is returned, else, if FALSE, the log-likelihood is returned. Defaults to FALSE.
pool an optional logical value indicating whether all lm components of object may be assumed to have the same error variance. Default is attr(object, "pool").
... some methods for this generic require additional arguments. None are used in this method.

Value

either the sum of the (restricted) log-likelihoods of each lm component in object, or the (restricted) log-likelihood for the lm fit with separate coefficients for each component of object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, logLik.lme,
Examples

```r
fm1 <- lmList(distance ~ age | Subject, Orthodont)
logLik(fm1)  # returns NA when it should not
```

logLik.reStruct  

**Calculate reStruct Log-Likelihood**

Description

Calculates the log-likelihood, or restricted log-likelihood, of the Gaussian linear mixed-effects model represented by `object` and `conLin` (assuming spherical within-group covariance structure), evaluated at `coef(object)`. The settings attribute of `object` determines whether the log-likelihood, or the restricted log-likelihood, is to be calculated. The computational methods are described in Bates and Pinheiro (1998).

Usage

```r
## S3 method for class 'reStruct'
logLik(object, conLin, ...)
```

Arguments

- `object`: an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
- `conLin`: a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

the log-likelihood, or restricted log-likelihood, of linear mixed-effects model represented by `object` and `conLin`, evaluated at `coef(object)`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- reStruct, pdMat, logLik.lme
Description

This method function extracts the component of a Gaussian log-likelihood associated with the variance function structure represented by object, which is equal to the sum of the logarithms of the corresponding weights.

Usage

```r
## S3 method for class 'varFunc'
logLik(object, data, ...)
```

Arguments

- `object` an object inheriting from class "varFunc", representing a variance function structure.
- `data` this argument is included to make this method function compatible with other logLik methods and will be ignored.
- `...` some methods for this generic require additional arguments. None are used in this method.

Value

the sum of the logarithms of the weights corresponding to the variance function structure represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- `logLik.lme`

Examples

```r
vf1 <- varPower(form = ~age)
vf1 <- Initialize(vf1, Orthodont)
coef(vf1) <- 0.1
logLik(vf1)
```
Machines

Productivity Scores for Machines and Workers

Description

The Machines data frame has 54 rows and 3 columns.

Format

This data frame contains the following columns:

- **Worker**: an ordered factor giving the unique identifier for the worker.
- **Machine**: a factor with levels A, B, and C identifying the machine brand.
- **score**: a productivity score.

Details

Data on an experiment to compare three brands of machines used in an industrial process are presented in Milliken and Johnson (p. 285, 1992). Six workers were chosen randomly among the employees of a factory to operate each machine three times. The response is an overall productivity score taking into account the number and quality of components produced.

Source


MathAchieve

Mathematics achievement scores

Description

The Math Achieve data frame has 7185 rows and 6 columns.

Format

This data frame contains the following columns:

- **School**: an ordered factor identifying the school that the student attends
- **Minority**: a factor with levels No Yes indicating if the student is a member of a minority racial group.
- **Sex**: a factor with levels Male Female
- **SES**: a numeric vector of socio-economic status.
- **MathAch**: a numeric vector of mathematics achievement scores.
- **MEANSES**: a numeric vector of the mean SES for the school.
Details

Each row in this data frame contains the data for one student.

Examples

summary(MathAchieve)

Matrix

Assign Matrix Values

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include pdMat, pdBlocked, and reStruct.

Usage

matrix(object) <- value

Arguments

object any object to which as.matrix can be applied.
value a matrix, or list of matrices, with the same dimensions as as.matrix(object) with the new values to be assigned to the matrix associated with object.
Value

will depend on the method function; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

as.matrix, also for examples, matrix<-.pdMat, matrix<-.reStruct.

Description

The positive-definite matrix represented by object is replaced by value. If the original matrix had row and/or column names, the corresponding names for value can either be NULL, or a permutation of the original names.

Usage

## S3 replacement method for class 'pdMat'
matrix(object) <- value
## S3 replacement method for class 'pdBlocked'
matrix(object) <- value

Arguments

object an object inheriting from class "pdMat", representing a positive definite matrix.
value a matrix with the new values to be assigned to the positive-definite matrix represented by object. Must have the same dimensions as as.matrix(object).

Value

a pdMat or pdBlocked object similar to object, but with its coefficients modified to produce the matrix in value.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

pdMat,"matrix<-

Examples

class(pd1 <- pdSymm(diag(3))) # "pdSymm" "pdMat"
matrix(pd1) <- diag(1:3)
pd1
Matrix.reStruct Assign reStruct Matrices

Description
The individual matrices in value are assigned to each pdMat component of object, in the order they are listed. The new matrices must have the same dimensions as the matrices they are meant to replace.

Usage
### S3 replacement method for class 'reStruct'
matrix(object) <- value

Arguments
- **object**: an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
- **value**: a matrix, or list of matrices, with the new values to be assigned to the matrices associated with the pdMat components of object.

Value
an reStruct object similar to object, but with the coefficients of the individual pdMat components modified to produce the matrices listed in value.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
reStruct, pdMat,"matrix<-"

Examples
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
matrix(rs1) <- list(diag(2), 3)

Meat Tenderness of meat

Description
The Meat data frame has 30 rows and 4 columns.
**Milk**

**Format**

This data frame contains the following columns:

- **Storage** an ordered factor specifying the storage treatment - 1 (0 days), 2 (1 day), 3 (2 days), 4 (4 days), 5 (9 days), and 6 (18 days)
- **score** a numeric vector giving the tenderness score of beef roast.
- **Block** an ordered factor identifying the muscle from which the roast was extracted with levels II < V < I < III < IV
- **Pair** an ordered factor giving the unique identifier for each pair of beef roasts with levels II-1 < ... < IV-1

**Details**

Cochran and Cox (section 11.51, 1957) describe data from an experiment conducted at Iowa State College (Paul, 1943) to compare the effects of length of cold storage on the tenderness of beef roasts. Six storage periods ranging from 0 to 18 days were used. Thirty roasts were scored by four judges on a scale from 0 to 10, with the score increasing with tenderness. The response was the sum of all four scores. Left and right roasts from the same animal were grouped into pairs, which were further grouped into five blocks, according to the muscle from which they were extracted. Different storage periods were applied to each roast within a pair according to a balanced incomplete block design.

**Source**


---

**Milk**

**Format**

This data frame contains the following columns:

- **protein** a numeric vector giving the protein content of the milk.
- **Time** a numeric vector giving the time since calving (weeks).
- **Cow** an ordered factor giving a unique identifier for each cow.
- **Diet** a factor with levels barley, barley+lupins, and lupins identifying the diet for each cow.

**Details**

Diggle, Liang, and Zeger (1994) describe data on the protein content of cows’ milk in the weeks following calving. The cattle are grouped according to whether they are fed a diet with barley alone, with barley and lupins, or with lupins alone.

**Source**

Description

The model matrices for each element of `formula(object)`, calculated using data, are bound together column-wise. When multiple grouping levels are present (i.e. when `length(object) > 1`), the individual model matrices are combined from innermost (at the leftmost position) to outermost (at the rightmost position).

Usage

```r
## S3 method for class 'reStruct'
model.matrix(object, data, contrast, ...)
```

Arguments

- `object`: an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of `pdMat` objects.
- `data`: a data frame in which to evaluate the variables defined in `formula(object)`.
- `contrast`: an optional named list specifying the contrasts to be used for representing the factor variables in `data`. The components names should match the names of the variables in `data` for which the contrasts are to be specified. The components of this list will be used as the `contrasts` attribute of the corresponding factor. If missing, the default contrast specification is used.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

A matrix obtained by binding together, column-wise, the model matrices for each element of `formula(object)`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`model.matrix`, `contrasts`, `reStruct`, `formula.reStruct`

Examples

```r
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
model.matrix(rs1, Pixel)
```
Muscle

Contraction of heart muscle sections

Description

The Muscle data frame has 60 rows and 3 columns.

Format

This data frame contains the following columns:

- **Strip** an ordered factor indicating the strip of muscle being measured.
- **conc** a numeric vector giving the concentration of CaCl\(_2\)
- **length** a numeric vector giving the shortening of the heart muscle strip.

Details

Baumann and Waldvogel (1963) describe data on the shortening of heart muscle strips dipped in a CaCl\(_2\) solution. The muscle strips are taken from the left auricle of a rat’s heart.

Source


Names

Names Associated with an Object

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `formula`, `modelStruct`, `pdBlocked`, `pdMat`, and `reStruct`.

Usage

`Names(object, ...)`

Arguments

- **object** any object for which names can be extracted and/or assigned.
- **...** some methods for this generic function require additional arguments.
- **value** names to be assigned to object.

Value

will depend on the method function used; see the appropriate documentation.
SIDE EFFECTS

On the left side of an assignment, sets the names associated with object to value, which must have an appropriate length.

Note

If names were generic, there would be no need for this generic function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

Names.formula, Names.pdMat

Examples

## see the method function documentation

---

Names.formula Extract Names from a formula

Description

This method function returns the names of the terms corresponding to the right hand side of object (treated as a linear formula), obtained as the column names of the corresponding model.matrix.

Usage

## S3 method for class 'formula'
Names(object, data, exclude, ...)

Arguments

object an object inheriting from class “formula”.

data an optional data frame containing the variables specified in object. By default the variables are taken from the environment from which Names.formula is called.

exclude an optional character vector with names to be excluded from the returned value. Default is c("pi",".").

... some methods for this generic require additional arguments. None are used in this method.

Value

a character vector with the column names of the model.matrix corresponding to the right hand side of object which are not listed in excluded.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
See Also

`model.matrix`, `terms`, `Names`

Examples

```r
Names(distance ~ Sex * age, data = Orthodont)
```

---

**Names.pdBlocked**

### Names of a pdBlocked Object

**Description**

This method function extracts the first element of the `Dimnames` attribute, which contains the column names, for each block diagonal element in the matrix represented by `object`.

**Usage**

```r
## S3 method for class 'pdBlocked'
Names(object, asList, ...)
```

**Arguments**

- `object`: an object inheriting from class "pdBlocked" representing a positive-definite matrix with block diagonal structure
- `asList`: a logical value. If `TRUE` a list with the names for each block diagonal element is returned. If `FALSE` a character vector with all column names is returned. Defaults to `FALSE`.
- `...`: some methods for this generic require additional arguments. None are used in this method.

**Value**

- if `asList` is FALSE, a character vector with column names of the matrix represented by `object`;
- otherwise, if `asList` is TRUE, a list with components given by the column names of the individual block diagonal elements in the matrix represented by `object`.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`Names`, `Names.pdMat`

**Examples**

```r
pd1 <- pdBlocked(list(~Sex - 1, ~age - 1), data = Orthodont)
Names(pd1)
```
Names.pdMat

Names of a pdMat Object

Description

This method function returns the first element of the Dimnames attribute of object, which contains the column names of the matrix represented by object.

Usage

```r
## S3 method for class 'pdMat'
Names(object, ...)
## S3 replacement method for class 'pdMat'
Names(object, ...) <- value
```

Arguments

- `object`: an object inheriting from class "pdMat", representing a positive-definite matrix.
- `value`: a character vector with the replacement values for the column and row names of the matrix represented by `object`. It must have length equal to the dimension of the matrix represented by `object` and, if names have been previously assigned to `object`, it must correspond to a permutation of the original names.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

- if `object` has a Dimnames attribute then the first element of this attribute is returned; otherwise `NULL`.

SIDE EFFECTS

- On the left side of an assignment, sets the Dimnames attribute of `object` to `list(value, value)`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- `Names`, `Names.pdBlocked`

Examples

```r
pd1 <- pdSymm(~age, data = Orthodont)
Names(pd1)
```
Names.reStruct

Names of an reStruct Object

Description

This method function extracts the column names of each of the positive-definite matrices represented the pdMat elements of object.

Usage

```r
## S3 method for class 'reStruct'
Names(object, ...)
## S3 replacement method for class 'reStruct'
Names(object, ...) <- value
```

Arguments

- `object`: an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
- `value`: a list of character vectors with the replacement values for the names of the individual pdMat objects that form object. It must have the same length as `object`.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

a list containing the column names of each of the positive-definite matrices represented by the pdMat elements of object.

SIDE EFFECTS

On the left side of an assignment, sets the Names of the pdMat elements of object to the corresponding element of value.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`reStruct`, `pdMat`, `Names.pdMat`

Examples

```r
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
Names(rs1)
```
needUpdate

Description
This function is generic; method functions can be written to handle specific classes of objects. By default, it tries to extract a needUpdate attribute of object. If this is NULL or FALSE it returns FALSE; else it returns TRUE. Updating of objects usually takes place in iterative algorithms in which auxiliary quantities associated with the object, and not being optimized over, may change.

Usage

needUpdate(object)

Arguments

object any object

Value

a logical value indicating whether object needs to be updated.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

needUpdate.modelStruct

Examples

vf1 <- varExp()
vf1 <- Initialize(vf1, data = Orthodont)
needUpdate(vf1)

needUpdate.modelStruct

Description
This method function checks if any of the elements of object needs to be updated. Updating of objects usually takes place in iterative algorithms in which auxiliary quantities associated with the object, and not being optimized over, may change.

Usage

## S3 method for class 'modelStruct'
needUpdate(object)
Nitrendipene

Arguments

object an object inheriting from class "modelStruct", representing a list of model components, such as corStruct and varFunc objects.

Value

a logical value indicating whether any element of object needs to be updated.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

needUpdate

Examples

lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)), varStruct = varPower(form = ~age))
needUpdate(lms1)

Nitrendipene Assay of nitrendipene

Description

The Nitrendipene data frame has 89 rows and 4 columns.

Format

This data frame contains the following columns:

activity a numeric vector
NIF a numeric vector
Tissue an ordered factor with levels 2 < 1 < 3 < 4
log.NIF a numeric vector

Source

nlme Nonlinear Mixed-Effects Models

Description

This generic function fits a nonlinear mixed-effects model in the formulation described in Lindstrom and Bates (1990) but allowing for nested random effects. The within-group errors are allowed to be correlated and/or have unequal variances.

Usage

nlme(model, data, fixed, random, groups, start, correlation, weights, subset, method, na.action, naPattern, control, verbose)

Arguments

model a nonlinear model formula, with the response on the left of a ~ operator and
an expression involving parameters and covariates on the right, or an nlsList object. If data is given, all names used in the formula should be defined as parameters or variables in the data frame. The method function nlme.nlsList is documented separately.

data an optional data frame containing the variables named in model, fixed, random, correlation, weights, subset, and naPattern. By default the variables are taken from the environment from which nlme is called.

fixed a two-sided linear formula of the form f1+...+fn~x1+...+xm, or a list of two-sided formulas of the form f1~x1+...+xm, with possibly different models for different parameters. The f1,...,fn are the names of parameters included on the right hand side of model and the x1+...+xm expressions define linear models for these parameters (when the left hand side of the formula contains several parameters, they all are assumed to follow the same linear model, described by the right hand side expression). A 1 on the right hand side of the formula(s) indicates a single fixed effects for the corresponding parameter(s).

random optionally, any of the following: (i) a two-sided formula of the form r1+...+rn~x1+...+xm | g1/.../gQ, with r1,...,rn naming parameters included on the right hand side of model, x1+...+xm specifying the random-effects model for these parameters and g1/.../gQ the grouping structure (Q may be equal to 1, in which case no / is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a two-sided formula of the form r1+...+rn~x1+...+xm, a list of two-sided formulas of the form r1~x1+...+xm, with possibly different random-effects models for different parameters, a pdMat object with a two-sided formula, or list of two-sided formulas (i.e. a non-NULL value for formula(random)), or a list of pdMat objects with two-sided formulas, or lists of two-sided formulas. In this case, the grouping structure formula will be given in groups, or derived from the data used to fit the nonlinear mixed-effects model, which should inherit from class groupedData; (iii) a named list of formulas, lists of formulas, or pdMat objects.
objects as in (ii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the elements in the list; (iv) an reStruct object. See the documentation on pdClasses for a description of the available pdMat classes. Defaults to fixed, resulting in all fixed effects having also random effects.

groups
an optional one-sided formula of the form ~g1 (single level of nesting) or ~g1/.../gQ (multiple levels of nesting), specifying the partitions of the data over which the random effects vary. g1,...,gQ must evaluate to factors in data. The order of nesting, when multiple levels are present, is taken from left to right (i.e. g1 is the first level, g2 the second, etc.).

start
an optional numeric vector, or list of initial estimates for the fixed effects and random effects. If declared as a numeric vector, it is converted internally to a list with a single component fixed, given by the vector. The fixed component is required, unless the model function inherits from class selfStart, in which case initial values will be derived from a call to nlsList. An optional random component is used to specify initial values for the random effects and should consist of a matrix, or a list of matrices with length equal to the number of grouping levels. Each matrix should have as many rows as the number of groups at the corresponding level and as many columns as the number of random effects in that level.

correlation
an optional corStruct object describing the within-group correlation structure. See the documentation of corClasses for a description of the available corStruct classes. Defaults to NULL, corresponding to no within-group correlations.

weights
an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to varFixed, corresponding to fixed variance weights. See the documentation on varClasses for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic within-group errors.

subset
an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

method
a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "ML".

na.action
a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes nlme to print an error message and terminate if there are any incomplete observations.

naPattern
an expression or formula object, specifying which returned values are to be regarded as missing.

control
a list of control values for the estimation algorithm to replace the default values returned by the function nlmControl. Defaults to an empty list.

verbose
an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.

Value
an object of class nlme representing the nonlinear mixed-effects model fit. Generic functions such as print, plot and summary have methods to show the results of the fit. See nlmeObject for the components of the fit. The functions resid, coef, fitted, fixed.effects, and random.effects can be used to extract some of its components.
Note

The function does not do any scaling internally: the optimization will work best when the response is scaled so its variance is of the order of one.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

For the different correlation structures, variance functions and links, see 'References' in lme.

See Also

nlmeControl, nlme.nlsList, nlmeObject, nlstList, nlmeStruct, pdClasses, reStruct, varFunc, corClasses, varClasses

Examples

```r
fm1 <- nlme(height ~ SSasymp(age, Asym, R0, lrc),
  data = Loblolly,
  fixed = Asym + R0 + lrc ~ 1,
  random = Asym ~ 1,
  start = c(Asym = 103, R0 = -8.5, lrc = -3.3))
summary(fm1)
fm2 <- update(fm1, random = pdDiag(Asym + lrc ~ 1))
summary(fm2)
```

nlme.nlsList

NLME fit from nlsList Object

Description

If the random effects names defined in random are a subset of the lmList object coefficient names, initial estimates for the covariance matrix of the random effects are obtained (overwriting any values given in random). formula(fixed) and the data argument in the calling sequence used to obtain fixed are passed as the fixed and data arguments to nlme.formula, together with any other additional arguments in the function call. See the documentation on nlme.formula for a description of that function.

Usage

```r
## S3 method for class 'nlsList'
nlme(model, data, fixed, random, groups, start, correlation, weights,
    subset, method, na.action, naPattern, control, verbose)
```
Arguments

model an object inheriting from class "nlsList", representing a list of nls fits with a common model.
data this argument is included for consistency with the generic function. It is ignored in this method function.
fixed this argument is included for consistency with the generic function. It is ignored in this method function.
random an optional one-sided linear formula with no conditioning expression, or a pdMat object with a formula attribute. Multiple levels of grouping are not allowed with this method function. Defaults to a formula consisting of the right hand side of formula(fixed).
groups an optional one-sided formula of the form `~g1` (single level of nesting) or `~g1/.../gQ` (multiple levels of nesting), specifying the partitions of the data over which the random effects vary. `g1, ..., gQ` must evaluate to factors in data. The order of nesting, when multiple levels are present, is taken from left to right (i.e. `g1` is the first level, `g2` the second, etc.).
start an optional numeric vector, or list of initial estimates for the fixed effects and random effects. If declared as a numeric vector, it is converted internally to a list with a single component fixed, given by the vector. The fixed component is required, unless the model function inherits from class `selfStart`, in which case initial values will be derived from a call to `nlsList`. An optional random component is used to specify initial values for the random effects and should consist of a matrix, or a list of matrices with length equal to the number of grouping levels. Each matrix should have as many rows as the number of groups at the corresponding level and as many columns as the number of random effects in that level.
correlation an optional corStruct object describing the within-group correlation structure. See the documentation of `corClasses` for a description of the available corStruct classes. Defaults to NULL, corresponding to no within-group correlations.
weights an optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to `varFixed`, corresponding to fixed variance weights. See the documentation on `varClasses` for a description of the available varFunc classes. Defaults to NULL, corresponding to homoscedastic within-group errors.
subset an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
method a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "ML".
na.action a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes nlm to print an error message and terminate if there are any incomplete observations.
naPattern an expression or formula object, specifying which returned values are to be regarded as missing.
control a list of control values for the estimation algorithm to replace the default values returned by the function `nlmeControl`. Defaults to an empty list.
verbose an optional logical value. If TRUE information on the evolution of the iterative algorithm is printed. Default is FALSE.
Value

an object of class `nlme` representing the linear mixed-effects model fit. Generic functions such as `print`, `plot` and `summary` have methods to show the results of the fit. See `nlmeObject` for the components of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, and `random.effects` can be used to extract some of its components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

`nlme`, `lmList`, `nlmeObject`

Examples

```r
fm1 <- nlsList(SSasymp, data = Loblolly)
fm2 <- nlme(fm1, random = Asym ~ 1)
summary(fm1)
summary(fm2)
```
nlmeControl

Control Values for nlme Fit

Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the control argument to the nlme function.

Usage

nlmeControl(maxIter, pnlsMaxIter, msMaxIter, minScale,
             tolerance, niterEM, pnls Tol, msTol,
             returnObject, msVerbose, msWarnNoConv,
             gradHess, apVar, .relStep, minAbsParApVar = 0.05,
             opt = c("nlminb", "nlm"), natural = TRUE, sigma = NULL, ...)

Arguments

maxIter   maximum number of iterations for the nlme optimization algorithm. Default is 50.

pnlsMaxIter   maximum number of iterations for the PNLS optimization step inside the nlme optimization. Default is 7.

msMaxIter   maximum number of iterations for nlminb (iter.max) or the nlm (iterlim, from the 10-th step) optimization step inside the nlme optimization. Default is 50 (which may be too small for e.g. for overparametrized cases).

minScale   minimum factor by which to shrink the default step size in an attempt to decrease the sum of squares in the PNLS step. Default 0.001.

tolerance   tolerance for the convergence criterion in the nlme algorithm. Default is 1e-6.

niterEM   number of iterations for the EM algorithm used to refine the initial estimates of the random effects variance-covariance coefficients. Default is 25.

pnls Tol   tolerance for the convergence criterion in PNLS step. Default is 1e-3.

msTol   tolerance for the convergence criterion in nlm, passed as the gradtol argument to the function (see documentation on nlm). Default is 1e-7.

returnObject   a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is FALSE.

msVerbose   a logical value passed as the trace to nlminb(..., control= list(trace = *, ..)) or as argument print.level to nlm(). Default is FALSE.

msWarnNoConv   logical indicating if a warning should be signalled whenever the minimization (by opt) in the LME step does not converge; defaults to TRUE.

gradHess   a logical value indicating whether numerical gradient vectors and Hessian matrices of the log-likelihood function should be used in the nlm optimization. This option is only available when the correlation structure (corStruct) and the variance function structure (varFunc) have no "varying" parameters and the pdMat classes used in the random effects structure are pdSymm (general positive-definite), pdDiag (diagonal), pdIdent (multiple of the identity), or pdCompSymm (compound symmetry). Default is TRUE.
apVar

A logical value indicating whether the approximate covariance matrix of the
variance-covariance parameters should be calculated. Default is TRUE.

.relStep

Relative step for numerical derivatives calculations. Default is
.Machine$double.eps^(1/3).

minAbsParApVar

Numeric value - minimum absolute parameter value in the approximate variance
calculation. The default is 0.05.

opt

The optimizer to be used, either "nlminb" (the default) or "nlm".

natural

A logical value indicating whether the pdNatural parametrization should be
used for general positive-definite matrices (pdSymm) in reStruct, when the ap-
proximate covariance matrix of the estimators is calculated. Default is TRUE.

sigma

Optionally a positive number to fix the residual error at. If NULL, as by default,
or 0, sigma is estimated.

Value

A list with components for each of the possible arguments.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>; the sigma option: Siem Heisterkamp
and Bert van Willigen.

See Also

nlme, nlm, optim, nlmeStruct

Examples

# decrease the maximum number of iterations and request tracing
nlmeControl(msMaxIter = 20, msVerbose = TRUE)
The following components must be included in a legitimate "nlme" object.

- **apVar**: an approximate covariance matrix for the variance-covariance coefficients. If apVar = FALSE in the control values used in the call to nlme, this component is NULL.

- **call**: a list containing an image of the nlme call that produced the object.

- **coefficients**: a list with two components, fixed and random, where the first is a vector containing the estimated fixed effects and the second is a list of matrices with the estimated random effects for each level of grouping. For each matrix in the random list, the columns refer to the random effects and the rows to the groups.

- **contrasts**: a list of the contrast matrices used to represent factors in the fixed effects formula and/or random effects formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the nlme model, this component will be an empty list.

- **dims**: a list with basic dimensions used in the nlme fit, including the components N - the number of observations in the data, Q - the number of grouping levels, qvec - the number of random effects at each level from innermost to outermost (last two values are equal to zero and correspond to the fixed effects and the response), ngrps - the number of groups at each level from innermost to outermost (last two values are one and correspond to the fixed effects and the response), and ncol - the number of columns in the model matrix for each level of grouping from innermost to outermost (last two values are equal to the number of fixed effects and one).

- **fitted**: a data frame with the fitted values as columns. The leftmost column corresponds to the population fixed effects (corresponding to the fixed effects only) and successive columns from left to right correspond to increasing levels of grouping.

- **fixDF**: a list with components X and terms specifying the denominator degrees of freedom for, respectively, t-tests for the individual fixed effects and F-tests for the fixed-effects terms in the models.

- **groups**: a data frame with the grouping factors as columns. The grouping level increases from left to right.

- **logLik**: the (restricted) log-likelihood at convergence.

- **map**: a list with components fmap, rmap, rmapRel, and bmap, specifying various mappings for the fixed and random effects, used to generate predictions from the fitted object.

- **method**: the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.

- **modelStruct**: an object inheriting from class nlmeStruct, representing a list of mixed-effects model components, such as reStruct, corStruct, and varFunc objects.

- **numIter**: the number of iterations used in the iterative algorithm.

- **residuals**: a data frame with the residuals as columns. The leftmost column corresponds to the population residuals and successive columns from left to right correspond to increasing levels of grouping.

- **sigma**: the estimated within-group error standard deviation.

- **varFix**: an approximate covariance matrix of the fixed effects estimates.
nlmeStruct

Description

A nonlinear mixed-effects structure is a list of model components representing different sets of parameters in the nonlinear mixed-effects model. An nlmeStruct list must contain at least a reStruct object, but may also contain corStruct and varFunc objects. NULL arguments are not included in the nlmeStruct list.

Usage

nlmeStruct(reStruct, corStruct, varStruct)

Arguments

reStruct  a reStruct representing a random effects structure.
corStruct an optional corStruct object, representing a correlation structure. Default is NULL.
varStruct an optional varFunc object, representing a variance function structure. Default is NULL.

Value

a list of model components determining the parameters to be estimated for the associated nonlinear mixed-effects model.

Examples

nlms1 <- nlmeStruct(reStruct(~age), corAR1(), varPower())

nlmeStruct Nonlinear Mixed-Effects Structure

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

corClasses, nlme, residuals.nlmeStruct, reStruct, varFunc
**nlsList**

*List of nls Objects with a Common Model*

**Description**

Data is partitioned according to the levels of the grouping factor defined in `model` and individual nls fits are obtained for each data partition, using the model defined in `model`.

**Usage**

```r
nlsList(model, data, start, control, level, subset,
     na.action = na.fail, pool = TRUE, warn.nls = NA)
```

```r
## S3 method for class 'formula'
nlsList(model, data, start, control, level, subset,
     na.action = na.fail, pool = TRUE, warn.nls = NA)
```

```r
## S3 method for class 'nlsList'
update(object, model., ..., evaluate = TRUE)
```

**Arguments**

- `object` an object inheriting from class `nlsList`, representing a list of fitted nls objects.
- `model` either a nonlinear model formula, with the response on the left of a `~` operator and an expression involving parameters, covariates, and a grouping factor separated by the `|` operator on the right, or a selfStart function. The method function `nlsList.selfStart` is documented separately.
- `model.` changes to the model – see `update.formula` for details.
- `data` a data frame in which to interpret the variables named in `model`.
- `start` an optional named list with initial values for the parameters to be estimated in `model`. It is passed as the `start` argument to each nls call and is required when the nonlinear function in `model` does not inherit from class selfStart.
- `control` a list of control values passed as the `control` argument to `nls`. Defaults to an empty list.
- `level` an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
- `subset` an optional expression indicating the subset of the rows of `data` that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
- `na.action` a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes `nlsList` to print an error message and terminate if there are any incomplete observations.
- `pool` an optional logical value that is preserved as an attribute of the returned value. This will be used as the default for pool in calculations of standard deviations or standard errors for summaries.
- `warn.nls` logical indicating if `nls()` errors (all of which are caught by `tryCatch`) should be signalled as a “summarizing” warning.
... some methods for this generic require additional arguments. None are used in this method.

evaluate If TRUE evaluate the new call else return the call.

Details

As nls(.) is called on each sub group, and convergence of these may be problematic, these calls happen with error catching.

Since nlme version 3.1-127 (2016-04), all the errors are caught (via tryCatch) and if present, a “summarizing” warning is stored as attribute of the resulting “nlsList” object and signalled unless suppressed by warn.nls = FALSE or currently also when warn.nls = NA (default) and getOption("show.error.messages") is false.

nlsList() originally had used try(*) (with its default silent=FALSE) and hence all errors were printed to the console unless the global option show.error.messages was set to true. This still works, but has been deprecated.

Value

a list of nls objects with as many components as the number of groups defined by the grouping factor. Generic functions such as coef, fixed.effects, lme, pairs, plot, predict, random.effects, summary, and update have methods that can be applied to an nlsList object.

References


See Also

nls, nlme.nlsList, nlsList.selfStart, summary.nlsList

Examples

fm1 <- nlsList(uptake ~ SSasympOff(conc, Asym, lrc, c0),
  data = CO2, start = c(Asym = 30, lrc = -4.5, c0 = 52))
summary(fm1)
cfm1 <- confint(fm1) # via profiling each % FIXME: only *one* message instead of one *each*
mat.class <- class(matrix(1)) # ("matrix", "array") for R >= 4.0.0; ("matrix" in older R)
i.ok <- which(vapply(cfm1, function(r) identical(class(r), mat.class), NA))
stopifnot(length(i.ok) > 0, !anyNA(match(c(2:4, 6:9, 12), i.ok)))
## where as (some of) the others gave errors during profile re-fitting :
str(cfm1[-i.ok])

nlsList.selfStart    nlsList Fit from a selfStart Function

Description

The response variable and primary covariate in formula(data) are used together with model to construct the nonlinear model formula. This is used in the nls calls and, because a selfStarting model function can calculate initial estimates for its parameters from the data, no starting estimates need to be provided.
Usage

```r
## S3 method for class 'selfStart'
nlsList(model, data, start, control, level, subset,
        na.action = na.fail, pool = TRUE, warn.nls = NA)
```

Arguments

- `model`: a "selfStart" model function, which calculates initial estimates for the model parameters from `data`.
- `data`: a data frame in which to interpret the variables in `model`. Because no grouping factor can be specified in `model`, `data` must inherit from class "groupedData".
- `start`: an optional named list with initial values for the parameters to be estimated in `model`. It is passed as the `start` argument to each `nls` call and is required when the nonlinear function in `model` does not inherit from class `selfStart`.
- `control`: a list of control values passed as the `control` argument to `nls`. Defaults to an empty list.
- `level`: an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
- `subset`: an optional expression indicating the subset of the rows of `data` that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
- `na.action`: a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes `nlsList` to print an error message and terminate if there are any incomplete observations.
- `pool`, `warn.nls`: optional `logicals`, see `nlsList`.

Value

A list of `nls` objects with as many components as the number of groups defined by the grouping factor. A NULL value is assigned to the components corresponding to clusters for which the `nls` algorithm failed to converge. Generic functions such as `coef`, `fixed.effects`, `lme`, `pairs`, `plot`, `predict`, `random.effects`, `summary`, and `update` have methods that can be applied to an `nlsList` object.

See Also

- `selfStart`, `groupedData`, `nls`, `nlsList`, `nlme`, `nlList`, `nlsList.formula`

Examples

```r
fm1 <- nlsList(SSasympOff, CO2)
summary(fm1)
```
Oats

**Description**

The Oats data frame has 72 rows and 4 columns.

**Format**

This data frame contains the following columns:

- **Block** an ordered factor with levels VI < V < III < IV < II < I
- **Variety** a factor with levels Golden Rain Marvellous Victory
- **nitro** a numeric vector
- **yield** a numeric vector

**Details**

These data have been introduced by Yates (1935) as an example of a split-plot design. The treatment structure used in the experiment was a $3 \times 4$ full factorial, with three varieties of oats and four concentrations of nitrogen. The experimental units were arranged into six blocks, each with three whole-plots subdivided into four subplots. The varieties of oats were assigned randomly to the whole-plots and the concentrations of nitrogen to the subplots. All four concentrations of nitrogen were used on each whole-plot.

**Source**


Orthodont

**Description**

The Orthodont data frame has 108 rows and 4 columns of the change in an orthodontic measurement over time for several young subjects.

**Format**

This data frame contains the following columns:

- **distance** a numeric vector of distances from the pituitary to the pterygomaxillary fissure (mm). These distances are measured on x-ray images of the skull.
- **age** a numeric vector of ages of the subject (yr).
- **Subject** an ordered factor indicating the subject on which the measurement was made. The levels are labelled M01 to M16 for the males and F01 to F13 for the females. The ordering is by increasing average distance within sex.
- **Sex** a factor with levels Male and Female
Details

Investigators at the University of North Carolina Dental School followed the growth of 27 children (16 males, 11 females) from age 8 until age 14. Every two years they measured the distance between the pituitary and the pterygomaxillary fissure, two points that are easily identified on x-ray exposures of the side of the head.

Source


Examples

```r
formula(Orthodont)
plot(Orthodont)
```

---

### Ovary

**Counts of Ovarian Follicles**

**Description**

The Ovary data frame has 308 rows and 3 columns.

**Format**

This data frame contains the following columns:

- **Mare** an ordered factor indicating the mare on which the measurement is made.
- **Time** time in the estrus cycle. The data were recorded daily from 3 days before ovulation until 3 days after the next ovulation. The measurement times for each mare are scaled so that the ovulations for each mare occur at times 0 and 1.
- **follicles** the number of ovarian follicles greater than 10 mm in diameter.

**Details**

Pierson and Ginther (1987) report on a study of the number of large ovarian follicles detected in different mares at several times in their estrus cycles.

**Source**


Description

The Oxboys data frame has 234 rows and 4 columns.

Format

This data frame contains the following columns:

- **Subject**: an ordered factor giving a unique identifier for each boy in the experiment
- **age**: a numeric vector giving the standardized age (dimensionless)
- **height**: a numeric vector giving the height of the boy (cm)
- **Occasion**: an ordered factor - the result of converting age from a continuous variable to a count so these slightly unbalanced data can be analyzed as balanced.

Details

These data are described in Goldstein (1987) as data on the height of a selection of boys from Oxford, England versus a standardized age.

Source


Description

The Oxide data frame has 72 rows and 5 columns.

Format

This data frame contains the following columns:

- **Source**: a factor with levels 1 and 2
- **Lot**: a factor giving a unique identifier for each lot.
- **Wafer**: a factor giving a unique identifier for each wafer within a lot.
- **Site**: a factor with levels 1, 2, and 3
- **Thickness**: a numeric vector giving the thickness of the oxide layer.
**Details**

These data are described in Littell et al. (1996, p. 155) as coming “from a passive data collection study in the semiconductor industry where the objective is to estimate the variance components to determine the assignable causes of the observed variability.” The observed response is the thickness of the oxide layer on silicon wafers, measured at three different sites of each of three wafers selected from each of eight lots sampled from the population of lots.

**Source**


---

**pairs.compareFits**  
*Pairs Plot of compareFits Object*

**Description**

Scatter plots of the values being compared are generated for each pair of coefficients in \( x \). Different symbols (colors) are used for each object being compared and values corresponding to the same group are joined by a line, to facilitate comparison of fits. If only two coefficients are present, the *trellis* function `xyplot` is used; otherwise the *trellis* function `splom` is used.

**Usage**

```r
## S3 method for class 'compareFits'
pairs(x, subset, key, ...)
```

**Arguments**

- `x`: an object of class `compareFits`.
- `subset`: an optional logical or integer vector specifying which rows of `x` should be used in the plots. If missing, all rows are used.
- `key`: an optional logical value, or list. If `TRUE`, a legend is included at the top of the plot indicating which symbols (colors) correspond to which objects being compared. If `FALSE`, no legend is included. If given as a list, `key` is passed down as an argument to the *trellis* function generating the plots (`splom` or `xyplot`). Defaults to `TRUE`.
- `...`: optional arguments passed down to the *trellis* function generating the plots.

**Value**

Pairwise scatter plots of the values being compared, with different symbols (colors) used for each object under comparison.

**Author(s)**

José Pinheiro and Douglas Bates
pairs.lme

See Also
compareFits, plot.compareFits, pairs.lme, pairs.lmList, xyplot, splom

Examples

```r
eexample(compareFits) # cF12 <- compareFits(coef(lmList(Orthodont)), .. lme(*))
pairs(cF12)
```

pairs.lme  

Pairs Plot of an lme Object

Description

Diagnostic plots for the linear mixed-effects fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. The expression on the right hand side of the formula, before a `|` operator, must evaluate to a data frame with at least two columns. If the data frame has two columns, a scatter plot of the two variables is displayed (the Trellis function `xyplot` is used). Otherwise, if more than two columns are present, a scatter plot matrix with pairwise scatter plots of the columns in the data frame is displayed (the Trellis function `splom` is used).

Usage

```r
## S3 method for class 'lme'
pairs(x, form, label, id, idLabels, grid, ...)
```

Arguments

- `x`: an object inheriting from class "lme", representing a fitted linear mixed-effects model.
- `form`: an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain `x` can be referenced. In addition, `x` itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a `|` operator can be used to define separate panels in a Trellis display. The expression on the right hand side of `form`, and to the left of the `|` operator, must evaluate to a data frame with at least two columns. Default is `~ coef(.)`, corresponding to a pairs plot of the coefficients evaluated at the innermost level of nesting.
- `label`: an optional character vector of labels for the variables in the pairs plot.
- `id`: an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for an outlier test based on the Mahalanobis distances of the estimated random effects. Groups with random effects distances greater than the `1 - value` percentile of the appropriate chi-square distribution are identified in the plot using `idLabels`. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify points in the plot. If missing, no points are identified.

```r
## S3 method for class 'lme'
pairs(x, form, label, id, idLabels, grid, ...)
```
pairs.lmList

Description

Diagnostic plots for the linear model fits corresponding to the x components are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. The expression on the right hand side of the formula, before a | operator, must evaluate to a data frame with at least two columns. If the data frame has two columns, a scatter plot of the two variables is displayed (the Trellis function xyplot is used). Otherwise, if more than two columns are present, a scatter plot matrix with pairwise scatter plots of the columns in the data frame is displayed (the Trellis function splom is used).

Usage

```
## S3 method for class 'lmList'
pairs(x, form, label, id, idLabels, grid, ...)
```
pairs.lmList

Arguments

x an object inheriting from class "lmList", representing a list of lm objects with a common model.

form an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain x can be referenced. In addition, x itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. The expression on the right hand side of Form, and to the left of the | operator, must evaluate to a data frame with at least two columns. Default is ~ coef(.), corresponding to a pairs plot of the coefficients of x.

label an optional character vector of labels for the variables in the pairs plot.

id an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for an outlier test based on the Mahalanobis distances of the estimated random effects. Groups with random effects distances greater than the 1 − value percentile of the appropriate chi-square distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify points in the plot. If missing, no points are identified.

idLabels an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the points identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified points. Default is the innermost grouping factor.

grid an optional logical value indicating whether a grid should be added to plot. Default is FALSE.

... optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, pairs.lme, pairs.compareFits, xyplot, splom

Examples

fm1 <- lmList(distance ~ age | Subject, Orthodont)

# scatter plot of coefficients by gender, identifying unusual subjects
pairs(fm1, ~coef(.) | Sex, id = 0.1, adj = -0.5)

# scatter plot of estimated random effects -- "bivariate Gaussian (?)"
pairs(fm1, ~ranef(.))
Effect of Phenylbiguanide on Blood Pressure

Description

The PBG data frame has 60 rows and 5 columns.

Format

This data frame contains the following columns:

- **deltaBP**: a numeric vector
- **dose**: a numeric vector
- **Run**: an ordered factor with levels T5 < T4 < T3 < T2 < T1 < P5 < P3 < P2 < P4 < P1
- **Treatment**: a factor with levels MDL 72222 Placebo Rabbit
- **Rabbit**: an ordered factor with levels 5 < 3 < 2 < 4 < 1

Details

Data on an experiment to examine the effect of a antagonist MDL 72222 on the change in blood pressure experienced with increasing dosage of phenylbiguanide are described in Ludbrook (1994) and analyzed in Venables and Ripley (2002, section 10.3). Each of five rabbits was exposed to increasing doses of phenylbiguanide after having either a placebo or the HD5-antagonist MDL 72222 administered.

Source


Positive-Definite Block Diagonal Matrix

Description

This function is a constructor for the pdBlocked class, representing a positive-definite block-diagonal matrix. Each block-diagonal element of the underlying matrix is itself a positive-definite matrix and is represented internally as an individual pdMat object. When value is numeric(0), a list of uninitialized pdMat objects, a list of one-sided formulas, or a list of vectors of character strings, object is returned as an uninitialized pdBlocked object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is a list of initialized pdMat objects, object will be constructed from the list obtained by applying as.matrix to each of the pdMat elements of value. Finally, if value is a list of numeric vectors, they are assumed to represent the unrestricted coefficients of the block-diagonal elements of the underlying positive-definite matrix.
Usage

```r
pdBlocked(value, form, nam, data, pdClass)
```

Arguments

- **value**: an optional list with elements to be used as the value argument to other `pdMat` constructors. These include: `pdMat` objects, positive-definite matrices, one-sided linear formulas, vectors of character strings, or numeric vectors. All elements in the list must be similar (e.g., all one-sided formulas, or all numeric vectors). Defaults to `numeric(0)`, corresponding to an uninitialized object.

- **form**: an optional list of one-sided linear formulas specifying the row/column names for the block-diagonal elements of the matrix represented by `object`. Because factors may be present in `form`, the formulas need to be evaluated on a `data.frame` to resolve the names they define. This argument is ignored when `value` is a list of one-sided formulas. Defaults to `NULL`.

- **nam**: an optional list of vector of character strings specifying the row/column names for the block-diagonal elements of the matrix represented by `object`. Each of its components must have length equal to the dimension of the corresponding block-diagonal element and unreplicated elements. This argument is ignored when `value` is a list of vector of character strings. Defaults to `NULL`.

- **data**: an optional data frame in which to evaluate the variables named in `value` and `form`. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If `NULL`, no attempt is made to obtain information on any factors appearing in the formulas. Defaults to the parent frame from which the function was called.

- **pdClass**: an optional vector of character strings naming the `pdMat` classes to be assigned to the individual blocks in the underlying matrix. If a single class is specified, it is used for all block-diagonal elements. This argument will only be used when `value` is missing, or its elements are not `pdMat` objects. Defaults to "pdSymm".

Value

A `pdBlocked` object representing a positive-definite block-diagonal matrix, also inheriting from class `pdMat`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

`as.matrix.pdMat`, `coef.pdMat`, `pdClasses`, `matrix<-.pdMat`

Examples

```r
pd1 <- pdBlocked(list(diag(1:2), diag(c(0.1, 0.2, 0.3))),
                 nam = list(c("A","B"), c("a1", "a2", "a3")))
pd1
```
Positive-Definite Matrix Classes

Description

Standard classes of positive-definite matrices (pdMat) structures available in the nlme package.

Value

Available standard classes:

- **pdSymm**: general positive-definite matrix, with no additional structure
- **pdLogChol**: general positive-definite matrix, with no additional structure, using a log-Cholesky parameterization
- **pdDiag**: diagonal
- **pdIdent**: multiple of an identity
- **pdCompSymm**: compound symmetry structure (constant diagonal and constant off-diagonal elements)
- **pdBlocked**: block-diagonal matrix, with diagonal blocks of any "atomic" pdMat class
- **pdNatural**: general positive-definite matrix in natural parametrization (i.e. parametrized in terms of standard deviations and correlations). The underlying coefficients are not unrestricted, so this class should NOT be used for optimization.

Note

Users may define their own pdMat classes by specifying a constructor function and, at a minimum, methods for the functions pdConstruct, pdMatrix and coef. For examples of these functions, see the methods for classes pdSymm and pdDiag.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

pdBlocked, pdCompSymm, pdDiag, pdFactor, pdIdent, pdMat, pdMatrix, pdNatural, pdSymm, pdLogChol
Description

This function is a constructor for the pdCompSymm class, representing a positive-definite matrix with compound symmetry structure (constant diagonal and constant off-diagonal elements). The underlying matrix is represented by 2 unrestricted parameters. When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdCompSymm object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric vector of length 2, it is assumed to represent the unrestricted coefficients of the underlying positive-definite matrix.

Usage

pdCompSymm(value, form, nam, data)

Arguments

value an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector of length 2. Defaults to numeric(0), corresponding to an uninitialized object.

form an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.

nam an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.

data an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a pdCompSymm object representing a positive-definite matrix with compound symmetry structure, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

pdConstruct

See Also

as.matrix.pdMat, coef.pdMat, matrix<-.pdMat, pdClasses

Examples

pd1 <- pdCompSymm(diag(3) + 1, nam = c("A","B","C"))
pd1

pdConstruct Construct pdMat Objects

Description

This function is an alternative constructor for the pdMat class associated with object and is mostly used internally in other functions. See the documentation on the principal constructor function, generally with the same name as the pdMat class of object.

Usage

pdConstruct(object, value, form, nam, data, ...)

Arguments

object an object inheriting from class pdMat, representing a positive definite matrix.
value an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to numeric(0), corresponding to an uninitialized object.
form an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.
nam an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.
data an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.
...
optional arguments for some methods.

Value

a pdMat object representing a positive-definite matrix, inheriting from the same classes as object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
See Also

`pdCompSymm, pdDiag, pdIdent, pdNatural, pdSymm`

Examples

```r
pd1 <- pdSymm()
pdConstruct(pd1, diag(1:4))
```

---

**pdConstruct.pdBlocked Construct pdBlocked Objects**

**Description**

This function gives an alternative constructor for the `pdBlocked` class, representing a positive-definite block-diagonal matrix. Each block-diagonal element of the underlying matrix is itself a positive-definite matrix and is represented internally as an individual `pdMat` object. When `value` is `numeric(0)`, a list of uninitialized `pdMat` objects, a list of one-sided formulas, or a list of vectors of character strings, `object` is returned as an uninitialized `pdBlocked` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is a list of initialized `pdMat` objects, `object` will be constructed from the list obtained by applying `as.matrix` to each of the `pdMat` elements of `value`. Finally, if `value` is a list of numeric vectors, they are assumed to represent the unrestricted coefficients of the block-diagonal elements of the underlying positive-definite matrix.

**Usage**

```r
## S3 method for class 'pdBlocked'
pdConstruct(object, value, form, nam, data, pdClass, ...)
```

**Arguments**

- `object` an object inheriting from class "pdBlocked", representing a positive definite block-diagonal matrix.
- `value` an optional list with elements to be used as the value argument to other `pdMat` constructors. These include: `pdMat` objects, positive-definite matrices, one-sided linear formulas, vectors of character strings, or numeric vectors. All elements in the list must be similar (e.g. all one-sided formulas, or all numeric vectors). Defaults to `numeric(0)`, corresponding to an uninitialized object.
- `form` an optional list of one-sided linear formula specifying the row/column names for the block-diagonal elements of the matrix represented by `object`. Because factors may be present in `form`, the formulas needs to be evaluated on a `data.frame` to resolve the names they defines. This argument is ignored when `value` is a list of one-sided formulas. Defaults to `NULL`.
- `nam` an optional list of vector of character strings specifying the row/column names for the block-diagonal elements of the matrix represented by `object`. Each of its components must have length equal to the dimension of the corresponding block-diagonal element and unreplicated elements. This argument is ignored when `value` is a list of vector of character strings. Defaults to `NULL`.
pdDiag

data: an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

pdClass: an optional vector of character strings naming the pdMat classes to be assigned to the individual blocks in the underlying matrix. If a single class is specified, it is used for all block-diagonal elements. This argument will only be used when value is missing, or its elements are not pdMat objects. Defaults to "pdSymm".

Value

a pdBlocked object representing a positive-definite block-diagonal matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

as.matrix.pdMat, coef.pdMat, pdBlocked, pdClasses, pdConstruct, matrix<-.pdMat

Examples

pd1 <- pdBlocked(list(c("A","B"), c("a1", "a2", "a3"))
pdConstruct(pd1, list(diag(1:2), diag(c(0.1, 0.2, 0.3))))

Description

This function is a constructor for the pdDiag class, representing a diagonal positive-definite matrix. If the matrix associated with object is of dimension n, it is represented by n unrestricted parameters, given by the logarithm of the square-root of the diagonal values. When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdDiag object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric vector, it is assumed to represent the unrestricted coefficients of the underlying positive-definite matrix.

Usage

pdDiag(value, form, nam, data)
pdFactor

Square-Root Factor of a Positive-Definite Matrix

Description

A square-root factor of the positive-definite matrix represented by object is obtained. Letting \( \Sigma \) denote a positive-definite matrix, a square-root factor of \( \Sigma \) is any square matrix \( L \) such that \( \Sigma = L'L \). This function extracts \( L \).

Arguments

- **value**: an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by \(+\)), a vector of character strings, or a numeric vector of length equal to the dimension of the underlying positive-definite matrix. Defaults to `numeric(0)`, corresponding to an uninitialized object.

- **form**: an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in `form`, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when `value` is a one-sided formula. Defaults to `NULL`.

- **nam**: an optional vector of character strings specifying the row/column names for the matrix represented by `object`. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when `value` is a vector of character strings. Defaults to `NULL`.

- **data**: an optional data frame in which to evaluate the variables named in `value` and `form`. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If `NULL`, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

- A pdDiag object representing a diagonal positive-definite matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

- `as.matrix.pdMat`, `coef.pdMat`, `pdClasses`, `matrix<-.pdMat`

Examples

```r
pd1 <- pdDiag(diag(1:3), nam = c("A","B","C"))
pd1
```
Usage

\texttt{pdFactor(object)}

Arguments

\texttt{object} \hspace{1cm} \text{an object inheriting from class pdMat, representing a positive definite matrix, which must have been initialized (i.e. length(coef(object)) > 0).}

Value

\text{a vector with a square-root factor of the positive-definite matrix associated with object stacked column-wise.}

Note

This function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The \texttt{pdMatrix} function can be used to obtain square-root factors in matrix form.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

\texttt{pdMatrix}

Examples

\begin{verbatim}
pd1 <- pdCompSymm(4 * diag(3) + 1)
pdFactor(pd1)
\end{verbatim}
pdIdent

Value

a vector with square-root factors of the positive-definite matrices corresponding to the elements of object stacked column-wise.

Note

This function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The pdMatrix function can be used to obtain square-root factors in matrix form.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

dFactor, pdMatrix, reStruct, pdFactor, pdMat

Examples

rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
pdFactor(rs1)

Description

This function is a constructor for the pdIdent class, representing a multiple of the identity positive-definite matrix. The matrix associated with object is represented by 1 unrestricted parameter, given by the logarithm of the square-root of the diagonal value. When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdIdent object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric value, it is assumed to represent the unrestricted coefficient of the underlying positive-definite matrix.

Usage

pdIdent(value, form, nam, data)
Arguments

value an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric value. Defaults to numeric(0), corresponding to an uninitialized object.

form an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.

nam an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.

data an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a pdIdent object representing a multiple of the identity positive-definite matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

```r
pd1 <- pdIdent(4 * diag(3), nam = c("A","B","C"))
pd1
```
Description

This function is a constructor for the pdLogChol class, representing a general positive-definite matrix. If the matrix associated with object is of dimension $n$, it is represented by $n(n + 1)/2$ unrestricted parameters, using the log-Cholesky parametrization described in Pinheiro and Bates (1996).

- When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a character vector, object is returned as an uninitialized pdLogChol object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions.
- If value is an initialized pdMat object, object will be constructed from as.matrix(value).
- Finally, if value is a numeric vector, it is assumed to represent the unrestricted coefficients of the matrix-logarithm parametrization of the underlying positive-definite matrix.

Usage

```r
pdLogChol(value, form, nam, data)
```

Arguments

- **value**: an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to numeric(0), corresponding to an uninitialized object.
- **form**: an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.
- **nam**: an optional character vector specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a character vector. Defaults to NULL.
- **data**: an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Details

Internally, the pdLogChol representation of a symmetric positive definite matrix is a vector starting with the logarithms of the diagonal of the Choleski factorization of that matrix followed by its upper triangular portion.

Value

- a pdLogChol object representing a general positive-definite matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
References


See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

```r
(pd1 <- pdLogChol(diag(1:3), nam = c("A","B","C")))

(pd4 <- pdLogChol(1:6))
(pd4c <- chol(pd4)) # -> upper-tri matrix with off-diagonals 4 5 6
pd4c[upper.tri(pd4c)]
log(diag(pd4c)) # 1 2 3
```

**pdMat**

*Positive-Definite Matrix*

Description

This function gives an alternative way of constructing an object inheriting from the `pdMat` class named in `pdClass`, or from `data.class(object)` if `object` inherits from `pdMat`, and is mostly used internally in other functions. See the documentation on the principal constructor function, generally with the same name as the `pdMat` class of object.

Usage

```r
pdMat(value, form, nam, data, pdClass)
```

Arguments

- **value**: an optional initialization value, which can be any of the following: a `pdMat` object, a positive-definite matrix, a one-sided linear formula (with variables separated by `+`), a vector of character strings, or a numeric vector. Defaults to `numeric(0)`, corresponding to an uninitialized object.

- **form**: an optional one-sided linear formula specifying the row/column names for the matrix represented by `object`. Because factors may be present in `form`, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when `value` is a one-sided formula. Defaults to `NULL`.

- **nam**: an optional vector of character strings specifying the row/column names for the matrix represented by `object`. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when `value` is a vector of character strings. Defaults to `NULL`.

- **data**: an optional data frame in which to evaluate the variables named in `value` and `form`. It is used to obtain the levels for `factors`, which affect the dimensions and the row/column names of the underlying matrix. If `NULL`, no attempt is made to obtain information on `factors` appearing in the formulas. Defaults to the parent frame from which the function was called.
pdMatrix

pdClass

an optional character string naming the pdMat class to be assigned to the returned object. This argument will only be used when value is not a pdMat object. Defaults to "pdSymm".

Value

a pdMat object representing a positive-definite matrix, inheriting from the class named in pdClass, or from class(object), if object inherits from pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

pdClasses, pdCompSymm, pdDiag, pdIdent, pdNatural, pdSymm, reStruct, solve.pdMat, summary.pdMat

Examples

```r
pd1 <- pdMat(diag(1:4), pdClass = "pdDiag")
pd1
str(pd1)
```

---

### pdMatrix

**Extract Matrix or Square-Root Factor from a pdMat Object**

**Description**

The positive-definite matrix represented by object, or a square-root factor of it is obtained. Letting \( \Sigma \) denote a positive-definite matrix, a square-root factor of \( \Sigma \) is any square matrix \( L \) such that \( \Sigma = L' L \). This function extracts \( \Sigma \) or \( L \).

**Usage**

```r
pdMatrix(object, factor)
```

**Arguments**

- **object**: an object inheriting from class pdMat, representing a positive definite matrix.
- **factor**: an optional logical value. If TRUE, a square-root factor of the positive-definite matrix represented by object is returned; else, if FALSE, the positive-definite matrix is returned. Defaults to FALSE.

**Value**

- if factor is FALSE the positive-definite matrix represented by object is returned; else a square-root of the positive-definite matrix is returned.
pdMatrix.reStruct

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also
as.matrix.pdMat, pdClasses, pdFactor, pdMat, pdMatrix.reStruct, corMatrix

Examples
pd1 <- pdSymm(diag(1:4))
pdMatrix(pd1)

---

pdMatrix.reStruct  Extract Matrix or Square-Root Factor from Components of an reStruct Object

Description
This method function extracts the positive-definite matrices corresponding to the pdMat elements of object, or square-root factors of the positive-definite matrices.

Usage
## S3 method for class 'reStruct'
pdMatrix(object, factor)

Arguments
object an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
factor an optional logical value. If TRUE, square-root factors of the positive-definite matrices represented by the elements of object are returned; else, if FALSE, the positive-definite matrices are returned. Defaults to FALSE.

Value
a list with components given by the positive-definite matrices corresponding to the elements of object, or square-root factors of the positive-definite matrices.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References
See Also

as.matrix.reStruct, reStruct, pdMat, pdMatrix, pdMatrix.pdMat

Examples

rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
pdMatrix(rs1)

pdNatural

General Positive-Definite Matrix in Natural Parametrization

Description

This function is a constructor for the `pdNatural` class, representing a general positive-definite matrix, using a natural parametrization. If the matrix associated with `object` is of dimension \(n\), it is represented by \(n(n + 1)/2\) parameters. Letting \(\sigma_{ij}\) denote the \(ij\)-th element of the underlying positive definite matrix and \(\rho_{ij} = \sigma_{ij}/\sigma_{ii}\sqrt{\sigma_{jj}}\), \(i \neq j\) denote the associated "correlations", the "natural" parameters are given by \(\sqrt{\sigma_{ii}}\), \(i = 1, \ldots, n\) and \(\log((1 + \rho_{ij})/(1 - \rho_{ij}))\), \(i \neq j\). Note that all natural parameters are individually unrestricted, but not jointly unrestricted (meaning that not all unrestricted vectors would give positive-definite matrices). Therefore, this parametrization should NOT be used for optimization. It is mostly used for deriving approximate confidence intervals on parameters following the optimization of an objective function. When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdSymm` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric vector, it is assumed to represent the natural parameters of the underlying positive-definite matrix.

Usage

`pdNatural(value, form, nam, data)`

Arguments

- `value`:
  - an optional initialization value, which can be any of the following: a `pdMat` object, a positive-definite matrix, a one-sided linear formula (with variables separated by `+`), a vector of character strings, or a numeric vector. Defaults to `numeric(0)`, corresponding to an uninitialized object.

- `form`:
  - an optional one-sided linear formula specifying the row/column names for the matrix represented by `object`. Because factors may be present in `form`, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when `value` is a one-sided formula. Defaults to `NULL`.

- `nam`:
  - an optional vector of character strings specifying the row/column names for the matrix represented by `object`. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when `value` is a vector of character strings. Defaults to `NULL`.

- `data`:
  - an optional data frame in which to evaluate the variables named in `value` and `form`. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If `NULL`, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.
pdSymm

Value

a pdNatural object representing a general positive-definite matrix in natural parametrization, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

pdNatural(diag(1:3))

---

pdSymm General Positive-Definite Matrix

Description

This function is a constructor for the pdSymm class, representing a general positive-definite matrix. If the matrix associated with object is of dimension n, it is represented by n(n + 1)/2 unrestricted parameters, using the matrix-logarithm parametrization described in Pinheiro and Bates (1996). When value is numeric(0), an uninitialized pdMat object, a one-sided formula, or a vector of character strings, object is returned as an uninitialized pdSymm object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is an initialized pdMat object, object will be constructed from as.matrix(value). Finally, if value is a numeric vector, it is assumed to represent the unrestricted coefficients of the matrix-logarithm parametrization of the underlying positive-definite matrix.

Usage

pdSymm(value, form, nam, data)

Arguments

value an optional initialization value, which can be any of the following: a pdMat object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to numeric(0), corresponding to an uninitialized object.

form an optional one-sided linear formula specifying the row/column names for the matrix represented by object. Because factors may be present in form, the formula needs to be evaluated on a data.frame to resolve the names it defines. This argument is ignored when value is a one-sided formula. Defaults to NULL.
Phenobarb

nam: an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.

data: an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

Value

a pdSymm object representing a general positive-definite matrix, also inheriting from class pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

as.matrix.pdMat, coef.pdMat, pdClasses, matrix<-.pdMat

Examples

pd1 <- pdSymm(diag(1:3), nam = c("A","B","C"))
pd1

Phenobarb: Phenobarbitol Kinetics

Description

The Phenobarb data frame has 744 rows and 7 columns.

Format

This data frame contains the following columns:

Subject: an ordered factor identifying the infant.

Wt: a numeric vector giving the birth weight of the infant (kg).

Apgar: an ordered factor giving the 5-minute Apgar score for the infant. This is an indication of health of the newborn infant.

ApgarInd: a factor indicating whether the 5-minute Apgar score is < 5 or >= 5.

time: a numeric vector giving the time when the sample is drawn or drug administered (hr).

dose: a numeric vector giving the dose of drug administered (ug/kg).

conc: a numeric vector giving the phenobarbital concentration in the serum (ug/L).
**Details**

Data from a pharmacokinetics study of phenobarbital in neonatal infants. During the first few days of life the infants receive multiple doses of phenobarbital for prevention of seizures. At irregular intervals blood samples are drawn and serum phenobarbital concentrations are determined. The data were originally given in Grasela and Donn (1985) and are analyzed in Boeckmann, Sheiner and Beal (1994), in Davidian and Giltinan (1995), and in Littell et al. (1996).

**Source**


Grasela and Donn (1985), Neonatal population pharmacokinetics of phenobarbital derived from routine clinical data, *Developmental Pharmacology and Therapeutics*, 8, 374-383.


---

**phenoModel**

*Model function for the Phenobarb data*

**Description**

A model function for a model used with the Phenobarb data. This function uses compiled C code to improve execution speed.

**Usage**

```r
phenoModel(Subject, time, dose, lCl, lV)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Subject</td>
<td>an integer vector of subject identifiers. These should be sorted in increasing order.</td>
</tr>
<tr>
<td>time</td>
<td>numeric. A vector of the times at which the sample was drawn or the drug administered (hr).</td>
</tr>
<tr>
<td>dose</td>
<td>numeric. A vector of doses of drug administered (ug/kg).</td>
</tr>
<tr>
<td>lCl</td>
<td>numeric. A vector of values of the natural log of the clearance parameter according to Subject and time.</td>
</tr>
<tr>
<td>lV</td>
<td>numeric. A vector of values of the natural log of the effective volume of distribution according to Subject and time.</td>
</tr>
</tbody>
</table>

**Details**

See the details section of Phenobarb for a description of the model function that phenoModel evaluates.
Value

a numeric vector of predicted phenobarbital concentrations.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


---

Pixel

X-ray pixel intensities over time

Description

The Pixel data frame has 102 rows and 4 columns of data on the pixel intensities of CT scans of dogs over time.

Format

This data frame contains the following columns:

- **Dog** a factor with levels 1 to 10 designating the dog on which the scan was made
- **Side** a factor with levels L and R designating the side of the dog being scanned
- **day** a numeric vector giving the day post injection of the contrast on which the scan was made
- **pixel** a numeric vector of pixel intensities

Source


Examples

```r
fm1 <- lme(pixel ~ day + I(day^2), data = Pixel,
            random = list(Dog = ~ day, Side = ~ 1))
summary(fm1)
VarCorr(fm1)
```
Description

An `xyplot` of the autocorrelations versus the lags, with `type = "h"`, is produced. If `alpha > 0`, curves representing the critical limits for a two-sided test of level `alpha` for the autocorrelations are added to the plot.

Usage

```r
## S3 method for class 'ACF'
plot(x, alpha, xlab, ylab, grid, ...)
```

Arguments

- `x` an object inheriting from class `ACF`, consisting of a data frame with two columns named `lag` and `ACF`, representing the autocorrelation values and the corresponding lags.
- `alpha` an optional numeric value with the significance level for testing if the autocorrelations are zero. Lines corresponding to the lower and upper critical values for a test of level `alpha` are added to the plot. Default is `0`, in which case no lines are plotted.
- `xlab`, `ylab` optional character strings with the x- and y-axis labels. Default respectively to "Lag" and "Autocorrelation".
- `grid` an optional logical value indicating whether a grid should be added to plot. Default is `FALSE`.
- `...` optional arguments passed to the `xyplot` function.

Value

An `xyplot` Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`ACF`, `xyplot`

Examples

```r
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
plot(ACF(fm1, maxLag = 10), alpha = 0.01)
```
Description

A Trellis xyplot of predictions versus the primary covariate is generated, with a different panel for each value of the grouping factor. Predicted values are joined by lines, with different line types (colors) being used for each level of grouping. Original observations are represented by circles.

Usage

```r
## S3 method for class 'augPred'
plot(x, key, grid, ...)
```

Arguments

- `x`: an object of class "augPred".
- `key`: an optional logical value, or list. If TRUE, a legend is included at the top of the plot indicating which symbols (colors) correspond to which prediction levels. If FALSE, no legend is included. If given as a list, `key` is passed down as an argument to the `trellis` function generating the plots (xyplot). Defaults to TRUE.
- `grid`: an optional logical value indicating whether a grid should be added to plot. Default is FALSE.
- `...`: optional arguments passed down to the `trellis` function generating the plots.

Value

A Trellis plot of predictions versus the primary covariate, with panels determined by the grouping factor.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

augPred, xyplot

Examples

```r
fm1 <- lme(Orthodont)
plot(augPred(fm1, level = 0:1, length.out = 2))
```
Plot a compareFits Object

Description
A Trellis dotplot of the values being compared, with different rows per group, is generated, with a different panel for each coefficient. Different symbols (colors) are used for each object being compared.

Usage
## S3 method for class 'compareFits'
plot(x, subset, key, mark, ...)

Arguments
- **x**: an object of class "compareFits".
- **subset**: an optional logical or integer vector specifying which rows of x should be used in the plots. If missing, all rows are used.
- **key**: an optional logical value, or list. If TRUE, a legend is included at the top of the plot indicating which symbols (colors) correspond to which objects being compared. If FALSE, no legend is included. If given as a list, key is passed down as an argument to the trellis function generating the plots (dotplot). Defaults to TRUE.
- **mark**: an optional numeric vector, of length equal to the number of coefficients being compared, indicating where vertical lines should be drawn in the plots. If missing, no lines are drawn.
- **...**: optional arguments passed down to the trellis function generating the plots.

Value
A Trellis dotplot of the values being compared, with rows determined by the groups and panels by the coefficients.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
- `compareFits`
- `pairs.compareFits`
- `dotplot`

Examples
```r
example(compareFits) # cF12 <- compareFits(coef(lmList(Orthodont)), .. lme(*))
plot(cF12)
```
plot.gls

Plot a gls Object

Description

Diagnostic plots for the linear model fit are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If form is a one-sided formula, histograms of the variable on the right hand side of the formula, before a | operator, are displayed (the Trellis function histogram is used). If form is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function xyplot is used). Finally, if form is two-sided and its left hand side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function bwplot is used).

Usage

## S3 method for class 'gls'
plot(x, form, abline, id, idLabels, idResType, grid, ...)

Arguments

x an object inheriting from class "gls", representing a generalized least squares fitted linear model.

form an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain x can be referenced. In addition, x itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. Default is resid(., type = "p") ~ fitted(.,) corresponding to a plot of the standardized residuals versus fitted values, both evaluated at the innermost level of nesting.

abline an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.

id an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals. Observations with absolute standardized residuals greater than the 1 - value/2 quantile of the standard normal distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.

idLabels an optional vector, or one-sided formula. If given as a vector, it is converted to character mode and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character mode and used to label the identified observations. Default is the innermost grouping factor.

idResType an optional character string specifying the type of residuals to be used in identifying outliers, when id is a numeric value. If "pearson", the standardized
residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals premultiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".

grid

an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, xyplot, bwplot, histogram

Examples

fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
correlation = corAR1(form = ~ 1 | Mare))
# standardized residuals versus fitted values by Mare
plot(fm1, resid(.), type = "p") ~ fitted(.) | Mare, abline = 0)
# box-plots of residuals by Mare
plot(fm1, Mare ~ resid(.))
# observed versus fitted values by Mare
plot(fm1, follicles ~ fitted(.) | Mare, abline = c(0,1))
plot.lme

Arguments

x an object inheriting from class "intervals.lmList", representing confidence intervals and estimates for the coefficients in the lm components of the lmList object used to produce x.

xlab, ylab axis labels, each with a sensible default.

strip a function or FALSE, see dotplot() from package lattice.

... optional arguments passed to the dotplot function (see above).

Value

a Trellis plot with the confidence intervals on the coefficients of the individual lm components of the lmList that generated x.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

intervals.lmList, lmList, dotplot

Examples

fm1 <- lmList(distance ~ age | Subject, Orthodont)
plot(intervals(fm1))

plot.lme Plot an lme or nls object

Description

Diagnostic plots for the linear mixed-effects fit are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If form is a one-sided formula, histograms of the variable on the right hand side of the formula, before a | operator, are displayed (the Trellis function histogram is used). If form is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function xyplot is used). Finally, if form is two-sided and its left had side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function bwplot is used).

Usage

## S3 method for class 'lme'
plot(x, form, abline, id, idLabels, idResType, grid, ...)

## S3 method for class 'nls'
plot(x, form, abline, id, idLabels, idResType, grid, ...)
Arguments

x  an object inheriting from class "lme", representing a fitted linear mixed-effects model, or from nls, representing an fitted nonlinear least squares model.

form  an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain x can be referenced. In addition, x itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. Default is resid(., type = "p") ~ fitted(.), corresponding to a plot of the standardized residuals versus fitted values, both evaluated at the innermost level of nesting.

abline  an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.

id  an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized, or normalized residuals. Observations with absolute standardized (normalized) residuals greater than the 1 − value/2 quantile of the standard normal distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.

idLabels  an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.

idResType  an optional character string specifying the type of residuals to be used in identifying outliers, when id is a numeric value. If "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".

grid  an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.

...  optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, xyplot, bwplot, histogram
Examples

```r
# standardized residuals versus fitted values by gender
plot(fm1, resid(., type = "p") ~ fitted(.) | Sex, abline = 0)
```

# box-plots of residuals by Subject
```
plot(fm1, Subject ~ resid(.))
```

# observed versus fitted values by Subject
```
plot(fm1, distance ~ fitted(.) | Subject, abline = c(0,1))
```

---

plot.lmList

Plot an lmList Object

Description

Diagnostic plots for the linear model fits corresponding to the x components are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If `form` is a one-sided formula, histograms of the variable on the right hand side of the formula, before a `|` operator, are displayed (the Trellis function `histogram` is used). If `form` is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function `xyplot` is used). Finally, if `form` is two-sided and its left hand side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function `bwplot` is used).

Usage

```r
## S3 method for class 'lmList'
plot(x, form, abline, id, idLabels, grid, ...)
```

Arguments

- **x**: an object inheriting from class "lmList", representing a list of lm objects with a common model.
- **form**: an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain `x` can be referenced. In addition, `x` itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a `|` operator can be used to define separate panels in a Trellis display. Default is `resid(., type = "pool") ~ fitted(.)`, corresponding to a plot of the standardized residuals (using a pooled estimate for the residual standard error) versus fitted values.
- **abline**: an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
- **id**: an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals. Observations with absolute standardized residuals greater than the `1 - value/2` quantile of the standard normal distribution are identified in the plot using `idLabels`. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
plot.nffGroupedData

Description

A Trellis dot-plot of the response by group is generated. If outer variables are specified, the combination of their levels are used to determine the panels of the Trellis display. The Trellis function dotplot is used.

Usage

```r
## S3 method for class 'nffGroupedData'
plot(x, outer, inner, innerGroups, xlab, ylab, strip, panel, key,
     grid, ...)```

idLabels an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is getGroups(x).

grid an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.

Value

a diagnostic Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, predict.lm, xyplot, bwplot, histogram

Examples

```r
fm1 <- lmList(distance ~ age | Subject, Orthodont)
# standardized residuals versus fitted values by gender
plot(fm1, resid(., type = "pool") ~ fitted(.) | Sex, abline = 0, id = 0.05)
# box-plots of residuals by Subject
plot(fm1, Subject ~ resid(.))
# observed versus fitted values by Subject
plot(fm1, distance ~ fitted(.) | Subject, abline = c(0,1))
```
Arguments

- **x**: an object inheriting from class `nffGroupedData`, representing a `groupedData` object with a factor primary covariate and a single grouping level.
- **outer**: an optional logical value or one-sided formula, indicating covariates that are outer to the grouping factor, which are used to determine the panels of the Trellis plot. If equal to `TRUE`, `attr(object, "outer")` is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to `NULL`, meaning that no outer covariates are to be used.
- **inner**: an optional logical value or one-sided formula, indicating a covariate that is inner to the grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to `TRUE`, `attr(object, "inner")` is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to `NULL`, meaning that no inner covariate is present.
- **innerGroups**: an optional one-sided formula specifying a factor to be used for grouping the levels of the `inner` covariate. Different colors, or symbols, are used for each level of the `innerGroups` factor. Default is `NULL`, meaning that no `innerGroups` covariate is present.
- **xlab**: an optional character string with the label for the horizontal axis. Default is the `y` elements of `attr(object, "labels")` and `attr(object, "units")` pasted together.
- **ylab**: an optional character string with the label for the vertical axis. Default is the grouping factor name.
- **strip**: an optional function passed as the `strip` argument to the `dotplot` function. Default is `strip.default(..., style = 1)` (see `trellis.args`).
- **panel**: an optional function used to generate the individual panels in the Trellis display, passed as the `panel` argument to the `dotplot` function.
- **key**: an optional logical function or function. If `TRUE` and either `inner` or `innerGroups` are non-`NULL`, a legend for the different `inner` (`innerGroups`) levels is included at the top of the plot. If given as a function, it is passed as the key argument to the `dotplot` function. Default is `TRUE` if either `inner` or `innerGroups` are non-`NULL` and `FALSE` otherwise.
- **grid**: this argument is included for consistency with the `plot.nfnGroupedData` method calling sequence. It is ignored in this method function.
- **...**: optional arguments passed to the `dotplot` function.

Value

A Trellis dot-plot of the response by group.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

**plot.nfnGroupedData**

**Plot an nfnGroupedData Object**

**Description**

A Trellis plot of the response versus the primary covariate is generated. If outer variables are specified, the combination of their levels are used to determine the panels of the Trellis display. Otherwise, the levels of the grouping variable determine the panels. A scatter plot of the response versus the primary covariate is displayed in each panel, with observations corresponding to same inner group joined by line segments. The Trellis function `xyplot` is used.

**Usage**

```r
## S3 method for class 'nfnGroupedData'
plot(x, outer, inner, innerGroups, xlab, ylab, strip, aspect, panel,
     key, grid, ...)
```

**Arguments**

- `x`  
an object inheriting from class `nfnGroupedData`, representing a `groupedData` object with a numeric primary covariate and a single grouping level.

- `outer`  
an optional logical value or one-sided formula, indicating covariates that are outer to the grouping factor, which are used to determine the panels of the Trellis plot. If equal to `TRUE`, `attr(object, "outer")` is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to `NULL`, meaning that no outer covariates are to be used.

- `inner`  
an optional logical value or one-sided formula, indicating a covariate that is inner to the grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to `TRUE`, `attr(object, "inner")` is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to `NULL`, meaning that no inner covariate is present.

- `innerGroups`  
an optional one-sided formula specifying a factor to be used for grouping the levels of the inner covariate. Different colors, or line types, are used for each level of the `innerGroups` factor. Default is `NULL`, meaning that no `innerGroups` covariate is present.

- `xlab, ylab`  
optional character strings with the labels for the plot. Default is the corresponding elements of `attr(object, "labels")` and `attr(object, "units")` pasted together.

**See Also**

- `groupedData`
- `dotplot`

**Examples**

```r
plot(Machines)
plot(Machines, inner = TRUE)
```
strip    an optional function passed as the strip argument to the xyplot function. Default is strip.default(..., style = 1) (see trellis.args).
aspect   an optional character string indicating the aspect ratio for the plot passed as the aspect argument to the xyplot function. Default is "xy" (see trellis.args).
panel    an optional function used to generate the individual panels in the Trellis display, passed as the panel argument to the xyplot function.
key      an optional logical function or function. If TRUE and innerGroups is non-NULL, a legend for the different innerGroups levels is included at the top of the plot. If given as a function, it is passed as the key argument to the xyplot function. Default is TRUE if innerGroups is non-NULL and FALSE otherwise.
grid     an optional logical value indicating whether a grid should be added to plot. Default is TRUE.
...      optional arguments passed to the xyplot function.

Value
a Trellis plot of the response versus the primary covariate.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also
groupedData, xyplot

Examples
# different panels per Subject
plot(Orthodont)
# different panels per gender
plot(Orthodont, outer = TRUE)

plot.nmGroupedData    Plot an nmGroupedData Object

Description
The groupedData object is summarized by the values of the displayLevel grouping factor (or the combination of its values and the values of the covariate indicated in preserve, if any is present). The collapsed data is used to produce a new groupedData object, with grouping factor given by the displayLevel factor, which is plotted using the appropriate plot method for groupedData objects with single level of grouping.
Usage

## S3 method for class 'nmGroupedData'

plot(x, collapseLevel, displayLevel, outer, inner,
     preserve, FUN, subset, key, grid, ...)

Arguments

x  
an object inheriting from class nmGroupedData, representing a groupedData object with multiple grouping factors.

collapseLevel  
an optional positive integer or character string indicating the grouping level to use when collapsing the data. Level values increase from outermost to innermost grouping. Default is the highest or innermost level of grouping.

displayLevel  
an optional positive integer or character string indicating the grouping level to use for determining the panels in the Trellis display, when outer is missing. Default is collapseLevel.

outer  
an optional logical value or one-sided formula, indicating covariates that are outer to the displayLevel grouping factor, which are used to determine the panels of the Trellis plot. If equal to TRUE, the displayLevel element attr(object, "outer") is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to NULL, meaning that no outer covariates are to be used.

inner  
an optional logical value or one-sided formula, indicating a covariate that is inner to the displayLevel grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to TRUE, attr(object, "outer") is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to NULL, meaning that no inner covariate is present.

preserve  
an optional one-sided formula indicating a covariate whose levels should be preserved when collapsing the data according to the collapseLevel grouping factor. The collapsing factor is obtained by pasting together the levels of the collapseLevel grouping factor and the values of the covariate to be preserved. Default is NULL, meaning that no covariates need to be preserved.

FUN  
an optional summary function or a list of summary functions to be used for collapsing the data. The function or functions are applied only to variables in object that vary within the groups defined by collapseLevel. Invariant variables are always summarized by group using the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the data such as ordered, factor, or numeric. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

subset  
an optional named list. Names can be either positive integers representing grouping levels, or names of grouping factors. Each element in the list is a vector indicating the levels of the corresponding grouping factor to be used for plotting the data. Default is NULL, meaning that all levels are used.
key an optional logical value, or list. If TRUE, a legend is included at the top of
the plot indicating which symbols (colors) correspond to which prediction levels.
If FALSE, no legend is included. If given as a list, key is passed down as an
argument to the trellis function generating the plots (xyplot). Defaults to
TRUE.

grid an optional logical value indicating whether a grid should be added to plot. De-
default is TRUE.

Value
a Trellis display of the data collapsed over the values of the collapseLevel grouping factor and
grouped according to the displayLevel grouping factor.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References
Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G.

See Also
groupedData, collapse.groupedData, plot.nfnGroupedData, plot.nffGroupedData

Examples
# no collapsing, panels by Dog
plot(Pixel, display = "Dog", inner = ~Side)
# collapsing by Dog, preserving day
plot(Pixel, collapse = "Dog", preserve = ~day)
Arguments

- **x**: an object inheriting from class "ranef.lme", representing the estimated coefficients or estimated random effects for the lme object from which it was produced.

- **form**: an optional formula specifying the desired type of plot.
  - If given as a one-sided formula, a dotplot() of the estimated random effects (coefficients) grouped according to all combinations of the levels of the factors named in form is returned.
  - If given as a two-sided formula (or by default, NULL), an xyplot() Trellis display of the random effect (coefficient) versus the named covariates is returned. In NULL case the row names of the random effects (coefficients) are used (as covariates).

See also 'Details':

- **omitFixed**: an optional logical value indicating whether columns with values that are constant across groups should be omitted. Default is TRUE.
- **level**: an optional integer value giving the level of grouping to be used for x. Only used when x is a list with different components for each grouping level. Defaults to the highest or innermost level of grouping.
- **grid**: an optional logical value indicating whether a grid should be added to plot. Only applies to plots associated with two-sided formulas in form. Default is TRUE.
- **control**: an optional list with control values for the plot, when form is given as a two-sided formula. The control values are referenced by name in the control list and only the ones to be modified from the default need to be specified. Available values include: drawLine, a logical value indicating whether a loess smoother should be added to the scatter plots and a line connecting the medians should be added to the boxplots (default is TRUE); span.loess, used as the span argument in the call to panel.loess (default is 2/3); degree.loess, used as the degree argument in the call to panel.loess (default is 1); cex.axis, the character expansion factor for the x-axis (default is 0.8); srt.axis, the rotation factor for the x-axis (default is 0); and mgp.axis, the margin parameters for the x-axis (default is c(2, 0.5, 0)).
- **xlab, ylab**: axis labels, each with a sensible default.
- **strip**: a function or FALSE, see dotplot() from package lattice.
- **...**: optional arguments passed to the Trellis dotplot function.

Details

If form is missing, or is given as a one-sided formula, a Trellis dot-plot (via dotplot() from pkg lattice) of the random effects is generated, with a different panel for each random effect (coefficient). Rows in the dot-plot are determined by the form argument (if not missing) or by the row names of the random effects (coefficients). Single factors (~g) or crossed factors (~g1*g2) are allowed. For a single factor, its levels determine the dot-plot rows (with possibly multiple dots per row); otherwise, if form specifies a crossing of factors, the dot-plot rows are determined by all combinations of the levels of the individual factors in the formula.

If form is a two-sided formula, the left hand side must be a single random effect (coefficient) and the right hand side is formed by covariates in x separated by +. An xyplot() Trellis display is generated, with a different panel for each variable listed in the right hand side of form. Scatter plots are generated for numeric variables and boxplots are generated for categorical (Factor or ordered) variables.
plot.ranef.lmList

**Value**

A Trellis plot of the estimated random-effects (coefficients) versus covariates, or groups.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`ranef.lme, lme, dotplot`

**Examples**

```r
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
plot(ranef(fm1))
fm1RE <- ranef(fm1, aug = TRUE)
plot(fm1RE, form = ~ Sex)
plot(fm1RE, form = age ~ Sex) # "connected" boxplots
```

---

**Description**

If `form` is missing, or is given as a one-sided formula, a Trellis dot-plot of the random effects is generated, with a different panel for each random effect (coefficient). Rows in the dot-plot are determined by the `form` argument (if not missing) or by the row names of the random effects (coefficients). If a single factor is specified in `form`, its levels determine the dot-plot rows (with possibly multiple dots per row); otherwise, if `form` specifies a crossing of factors, the dot-plot rows are determined by all combinations of the levels of the individual factors in the formula. The Trellis function `dotplot` is used in this method function.

If `form` is a two-sided formula, a Trellis display is generated, with a different panel for each variable listed in the right hand side of `form`. Scatter plots are generated for numeric variables and boxplots are generated for categorical (factor or ordered) variables.

**Usage**

```r
## S3 method for class 'ranef.lmList'
plot(x, form, grid, control, ...)
```

**Arguments**

- `x`: An object inheriting from class `"ranef.lmList"`, representing the estimated coefficients or estimated random effects for the `lmList` object from which it was produced.
- `form`: An optional formula specifying the desired type of plot. If given as a one-sided formula, a dotplot of the estimated random effects (coefficients) grouped according to all combinations of the levels of the factors named in `form` is returned. Single factors (`~g`) or crossed factors (`~g1*g2`) are allowed. If given as a two-sided formula, the left hand side must be a single random effects (coefficient) and the right hand side is formed by covariates in `x` separated by `+`. A Trellis
plot.Variogram

display of the random effect (coefficient) versus the named covariates is returned in this case. Default is NULL, in which case the row names of the random effects (coefficients) are used.

grid an optional logical value indicating whether a grid should be added to plot. Only applies to plots associated with two-sided formulas in form. Default is FALSE.

control an optional list with control values for the plot, when form is given as a two-sided formula. The control values are referenced by name in the control list and only the ones to be modified from the default need to be specified. Available values include: drawLoessLine, a logical value indicating whether a loess smoother should be added to the scatter plots and a line connecting the medians should be added to the boxplots (default is TRUE); sas.1oess, used as the span argument in the call to panel.loess (default is 2/3); degree.loess, used as the degree argument in the call to panel.loess (default is 1); cex.axis, the character expansion factor for the x-axis (default is 0.8); srt.axis, the rotation factor for the x-axis (default is 0); and mgp.axis, the margin parameters for the x-axis (default is c(2, 0.5, 0)).

... optional arguments passed to the Trellis dotplot function.

Value

da Trellis plot of the estimated random-effects (coefficients) versus covariates, or groups.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
lmList, dotplot

Examples

fm1 <- lmList(distance ~ age | Subject, Orthodont)
plot(ranef(fm1))
fmlRE <- ranef(fm1, aug = TRUE)
plot(fmlRE, form = ~ Sex)
plot(fmlRE, form = age ~ Sex)

plot.Variogram  

Plot a Variogram Object

Description

an xyplot of the semi-variogram versus the distances is produced. If smooth = TRUE, a loess smoother is added to the plot. If showModel = TRUE and x includes an "modelVariog" attribute, the corresponding semi-variogram is added to the plot.

Usage

## S3 method for class 'Variogram'
plot(x, smooth, showModel, sigma, span, xlab, ylab, type, ylim, grid, ...)


Arguments

- **x**: an object inheriting from class "Variogram", consisting of a data frame with two columns named `vario` and `dist`, representing the semi-variogram values and the corresponding distances.
- **smooth**: an optional logical value controlling whether a loess smoother should be added to the plot. Defaults to `TRUE`, when `showModel` is `FALSE`.
- **showModel**: an optional logical value controlling whether the semi-variogram corresponding to an "modelVariog" attribute of `x`, if any is present, should be added to the plot. Defaults to `TRUE`, when the "modelVariog" attribute is present.
- **sigma**: an optional numeric value used as the height of a horizontal line displayed in the plot. Can be used to represent the process standard deviation. Default is `NULL`, implying that no horizontal line is drawn.
- **span**: an optional numeric value with the smoothing parameter for the loess fit. Default is 0.6.
- **xlab,ylab**: optional character strings with the x- and y-axis labels. Default respectively to "Distance" and "SemiVariogram".
- **type**: an optional character indicating the type of plot. Defaults to "p".
- **ylim**: an optional numeric vector with the limits for the y-axis. Defaults to `c(0, max(x$vario))`.
- **grid**: an optional logical value indicating whether a grid should be added to plot. Default is `FALSE`.
- **...**: optional arguments passed to the Trellis `xyplot` function.

Value

an `xyplot` Trellis plot.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`Variogram`, `xyplot`, `loess`

Examples

```r
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
plot(Variogram(fm1, form = ~ Time | Mare, maxDist = 0.7))
```

---

### pooledSD

**Extract Pooled Standard Deviation**

Description

The pooled estimated standard deviation is obtained by adding together the residual sum of squares for each non-null element of object, dividing by the sum of the corresponding residual degrees-of-freedom, and taking the square-root.
predict.gls

Usage

pooledSD(object)

Arguments

object an object inheriting from class lmList.

Value

the pooled standard deviation for the non-null elements of object, with an attribute df with the number of degrees-of-freedom used in the estimation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, lm

Examples

fm1 <- lmList(Orthodont)
pooledSD(fm1)

predict.gls

Predictions from a gls Object

Description

The predictions for the linear model represented by object are obtained at the covariate values defined in newdata.

Usage

## S3 method for class 'gls'
predict(object, newdata, na.action, ...)

Arguments

object an object inheriting from class "gls", representing a generalized least squares fitted linear model.

newdata an optional data frame to be used for obtaining the predictions. All variables used in the linear model must be present in the data frame. If missing, the fitted values are returned.

na.action a function that indicates what should happen when newdata contains NAs. The default action (na.fail) causes the function to print an error message and terminate if there are any incomplete observations.

... some methods for this generic require additional arguments. None are used in this method.
predict.gnls

Predictions from a gnls Object

Description
The predictions for the nonlinear model represented by object are obtained at the covariate values defined in newdata.

Usage
## S3 method for class 'gnls'
predict(object, newdata, na.action, naPattern, ...)

Arguments
- **object**: an object inheriting from class "gnls", representing a generalized nonlinear least squares fitted model.
- **newdata**: an optional data frame to be used for obtaining the predictions. All variables used in the nonlinear model must be present in the data frame. If missing, the fitted values are returned.
- **na.action**: a function that indicates what should happen when newdata contains NAs. The default action (na.fail) causes the function to print an error message and terminate if there are any incomplete observations.
- **naPattern**: an expression or formula object, specifying which returned values are to be regarded as missing.
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value
a vector with the predicted values.
Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
gnls

Examples
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
weights = varPower())
newSoybean <- data.frame(Time = c(10,30,50,80,100)) predict(fm1, newSoybean)

Description
The predictions at level \( i \) are obtained by adding together the population predictions (based only on
the fixed effects estimates) and the estimated contributions of the random effects to the predictions at
grouping levels less or equal to \( i \). The resulting values estimate the best linear unbiased predictions
(BLUPs) at level \( i \). If group values not included in the original grouping factors are present in
newdata, the corresponding predictions will be set to NA for levels greater or equal to the level at
which the unknown groups occur.

Usage
## S3 method for class 'lme'
predict(object, newdata, level = Q, asList = FALSE,
na.action = na.fail, ...)

Arguments
object an object inheriting from class "lme", representing a fitted linear mixed-effects
model.
newdata an optional data frame to be used for obtaining the predictions. All variables
used in the fixed and random effects models, as well as the grouping factors,
must be present in the data frame. If missing, the fitted values are returned.
level an optional integer vector giving the level(s) of grouping to be used in obtaining
the predictions. Level values increase from outermost to innermost grouping,
with level zero corresponding to the population predictions. Defaults to the
highest or innermost level of grouping.
asList an optional logical value. If TRUE and a single value is given in level, the
returned object is a list with the predictions split by groups; else the returned
value is either a vector or a data frame, according to the length of level.
na.action a function that indicates what should happen when newdata contains NAs. The
default action (na.fail) causes the function to print an error message and termi-
nate if there are any incomplete observations.
... some methods for this generic require additional arguments. None are used in
this method.
**Value**

if a single level of grouping is specified in `level`, the returned value is either a list with the predictions split by groups (`asList = TRUE`) or a vector with the predictions (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the predictions at different levels and the grouping factors.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`lme`, `fitted.lme`

**Examples**

```r
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
newOrth <- data.frame(Sex = c("Male", "Male", "Female", "Female", "Male", "Male"),
                      age = c(15, 20, 10, 12, 2, 4),
                      Subject = c("M01", "M01", "F30", "F30", "M04", "M04"))
## The 'Orthodont' data has *no* 'F30', so predict NA at level 1:
predict(fm1, newOrth, level = 0:1)
```

**predict.lmList**

*Predictions from an lmList Object*

**Description**

If the grouping factor corresponding to `object` is included in `newdata`, the data frame is partitioned according to the grouping factor levels; else, `newdata` is repeated for all `lm` components. The predictions and, optionally, the standard errors for the predictions, are obtained for each `lm` component of `object`, using the corresponding element of the partitioned `newdata`, and arranged into a list with as many components as `object`, or combined into a single vector or data frame (if `se.fit=TRUE`).

**Usage**

```r
## S3 method for class 'lmList'
predict(object, newdata, subset, pool, asList, se.fit, ...)
```

**Arguments**

- **object**: an object inheriting from class "lmList", representing a list of `lm` objects with a common model.
- **newdata**: an optional data frame to be used for obtaining the predictions. All variables used in the `object` model formula must be present in the data frame. If missing, the same data frame used to produce `object` is used.
- **subset**: an optional character or integer vector naming the `lm` components of `object` from which the predictions are to be extracted. Default is NULL, in which case all components are used.
- **asList**: an optional logical value. If TRUE, the returned object is a list with the predictions split by groups; else the returned value is a vector. Defaults to FALSE.
predict.nlme

An optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is attr(object, “pool”).

se.fit

An optional logical value indicating whether pointwise standard errors should be computed along with the predictions. Default is FALSE.

... some methods for this generic require additional arguments. None are used in this method.

Value

A list with components given by the predictions (and, optionally, the standard errors for the predictions) from each lmm component of object, a vector with the predictions from all lmm components of object, or a data frame with columns given by the predictions and their corresponding standard errors.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lmList, predict.lm

Examples

fm1 <- lmList(distance ~ age | Subject, Orthodont)
predict(fm1, se.fit = TRUE)

predict.nlme  Predictions from an nlme Object

Description

The predictions at level i are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to i and evaluating the model function at the resulting estimated parameters. If group values not included in the original grouping factors are present in newdata, the corresponding predictions will be set to NA for levels greater or equal to the level at which the unknown groups occur.

Usage

## S3 method for class 'nlme'
predict(object, newdata, level = Q, asList = FALSE,
   na.action = na.fail, naPattern = NULL, ...)

Arguments

object an object inheriting from class “nlme”, representing a fitted nonlinear mixed-effects model.

newdata an optional data frame to be used for obtaining the predictions. All variables used in the nonlinear model, the fixed and the random effects models, as well as the grouping factors, must be present in the data frame. If missing, the fitted values are returned.
level: an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping (and is object$dims$Q).

asList: an optional logical value. If TRUE and a single value is given in level, the returned object is a list with the predictions split by groups; else the returned value is either a vector or a data frame, according to the length of level.

na.action: a function that indicates what should happen when newdata contains NAs. The default action (na.fail) causes the function to print an error message and terminate if there are any incomplete observations.

naPattern: an expression or formula object, specifying which returned values are to be regarded as missing.

... some methods for this generic require additional arguments. None are used in this method.

Value

if a single level of grouping is specified in level, the returned value is either a list with the predictions split by groups (asList = TRUE) or a vector with the predictions (asList = FALSE); else, when multiple grouping levels are specified in level, the returned object is a data frame with columns given by the predictions at different levels and the grouping factors.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

nlme, fitted.lme

Examples

head(Loblolly) # groupedData w/ 'Seed' is grouping variable:
## Grouped Data: height ~ age | Seed
## height age Seed
## 1 4.51 3 301
## 15 10.89 5 301
## .. ..... . .....

fm1 <- nlme(height ~ SSasymp(age, Asym, R0, lrc), data = Loblolly,
fixed = Asym + R0 + lrc ~ 1,
random = Asym ~ 1, ## <---grouping---> Asym ~ 1 | Seed
start = c(Asym = 103, R0 = -8.5, lrc = -3.3))

fm1

age. <- seq(from = 2, to = 30, by = 2)
newLL.301 <- data.frame(age = age., Seed = 301)
newLL.329 <- data.frame(age = age., Seed = 329)
(p301 <- predict(fm1, newLL.301, level = 0:1))
(p329 <- predict(fm1, newLL.329, level = 0:1))
## Prediction are the same at level 0:
all.equal(p301[,"predict.fixed"],
p329[,"predict.fixed"],
## and differ by the 'Seed' effect at level 1:

predict.nlme
print.summary.pdMat

Description

The standard deviations and correlations associated with the positive-definite matrix represented by object (considered as a variance-covariance matrix) are printed, together with the formula and the grouping level associated object, if any are present.

Usage

## S3 method for class 'summary.pdMat'
print(x, sigma, rdig, Level, resid, ...)

Arguments

x
an object inheriting from class "summary.pdMat", generally resulting from applying summary to an object inheriting from class "pdMat".

sigma
an optional numeric value used as a multiplier for the square-root factor of the positive-definite matrix represented by object (usually the estimated within-group standard deviation from a mixed-effects model). Defaults to 1.

rdig
an optional integer value with the number of significant digits to be used in printing correlations. Defaults to 3.

Level
an optional character string with a description of the grouping level associated with object (generally corresponding to levels of grouping in a mixed-effects model). Defaults to NULL.

resid
an optional logical value. If TRUE an extra row with the "residual" standard deviation given in sigma will be included in the output. Defaults to FALSE.

... optional arguments passed to print.default; see the documentation on that method function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

summary.pdMat,pdMat

Examples

pd1 <- pdCompSymm(3 * diag(2) + 1, form = ~age + age^2, data = Orthodont)
print(summary(pd1), sigma = 1.2, resid = TRUE)
print.varFunc  

*Print a varFunc Object*

**Description**

The class and the coefficients associated with x are printed.

**Usage**

```r
## S3 method for class 'varFunc'
print(x, ...)
```

**Arguments**

- **x**
  - an object inheriting from class "varFunc", representing a variance function structure.

- **...**
  - optional arguments passed to print.default; see the documentation on that method function.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

- `summary.varFunc`

**Examples**

```r
vf1 <- varPower(0.3, form = ~age)
vf1 <- Initialize(vf1, Orthodont)
print(vf1)
```

---

**qqnorm.gls**

*Normal Plot of Residuals from a gls Object*

**Description**

Diagnostic plots for assessing the normality of residuals the generalized least squares fit are obtained. The form argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display.

**Usage**

```r
## S3 method for class 'gls'
qqnorm(y, form, abline, id, idLabels, grid, ...)
```
Arguments

- **y**: an object inheriting from class "gls", representing a generalized least squares fitted model.
- **form**: an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain y can be referenced. In addition, y itself can be referenced in the formula using the symbol ".". Conditional expressions on the right of a | operator can be used to define separate panels in a Trellis display. The expression on the right hand side of form and to the left of a | operator must evaluate to a residuals vector. Default is ~ resid(., type = "p"), corresponding to a normal plot of the standardized residuals.
- **abline**: an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
- **id**: an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals (random effects). Observations with absolute standardized residuals (random effects) greater than the 1 − value/2 quantile of the standard normal distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
- **idLabels**: an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.
- **grid**: an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.
- **...**: optional arguments passed to the Trellis plot function.

Value

a diagnostic Trellis plot for assessing normality of residuals.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, plot.gls

Examples

```r
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
correlation = corAR1(form = ~ 1 | Mare))
qqnorm(fm1, abline = c(0,1))
```
qqnorm.lme

Normal Plot of Residuals or Random Effects from an lme Object

Description

Diagnostic plots for assessing the normality of residuals and random effects in the linear mixed-effects fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display.

Usage

```r
## S3 method for class 'lme'
qqnorm(y, form, abline, id, idLabels, grid, ...)
```

Arguments

- `y`: an object inheriting from class "lme", representing a fitted linear mixed-effects model or from class "lmList", representing a list of `lm` objects, or from class "lm", representing a fitted linear model, or from class "nls", representing a nonlinear least squares fitted model.
- `form`: an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain `y` can be referenced. In addition, `y` itself can be referenced in the formula using the symbol `.`. Conditional expressions on the right of a `|` operator can be used to define separate panels in a Trellis display. The expression on the right hand side of `form` and to the left of a `|` operator must evaluate to a residuals vector, or a random effects matrix. Default is `~ resid(. , type = "p")`, corresponding to a normal plot of the standardized residuals evaluated at the innermost level of nesting.
- `abline`: an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
- `id`: an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals (random effects). Observations with absolute standardized residuals (random effects) greater than the `1 - value/2` quantile of the standard normal distribution are identified in the plot using `idLabels`. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
- `idLabels`: an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to `id`. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.
- `grid`: an optional logical value indicating whether a grid should be added to plot. Default is `FALSE`.
- `...`: optional arguments passed to the Trellis plot function.
Quinidine

Value

A diagnostic Trellis plot for assessing normality of residuals or random effects.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

lme, plot.lme

Examples

fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
## normal plot of standardized residuals by gender
qqnorm(fm1, ~ resid(.), type = "p") | Sex, abline = c(0, 1))
## normal plots of random effects
qqnorm(fm1, ~ranef(.))

Quinidine

Description

The Quinidine data frame has 1471 rows and 14 columns.

Format

This data frame contains the following columns:

Subject a factor identifying the patient on whom the data were collected.
time a numeric vector giving the time (hr) at which the drug was administered or the blood sample drawn. This is measured from the time the patient entered the study.
conc a numeric vector giving the serum quinidine concentration (mg/L).
dose a numeric vector giving the dose of drug administered (mg). Although there were two different forms of quinidine administered, the doses were adjusted for differences in salt content by conversion to milligrams of quinidine base.
interval a numeric vector giving the when the drug has been given at regular intervals for a sufficiently long period of time to assume steady state behavior, the interval is recorded.
Age a numeric vector giving the age of the subject on entry to the study (yr).
Height a numeric vector giving the height of the subject on entry to the study (in.).
Weight a numeric vector giving the body weight of the subject (kg).
Race a factor with levels Caucasian, Latin, and Black identifying the race of the subject.
Smoke a factor with levels no and yes giving smoking status at the time of the measurement.
Ethanol a factor with levels none, current, former giving ethanol (alcohol) abuse status at the time of the measurement.
Heart a factor with levels No/Mild, Moderate, and Severe indicating congestive heart failure for the subject.
Creatinine an ordered factor with levels < 50 < = 50 indicating the creatinine clearance (mg/min).
glyco a numeric vector giving the alpha-1 acid glycoprotein concentration (mg/dL). Often measured at the same time as the quinidine concentration.
Details

Verme et al. (1992) analyze routine clinical data on patients receiving the drug quinidine as a treatment for cardiac arrhythmia (atrial fibrillation or ventricular arrhythmias). All patients were receiving oral quinidine doses. At irregular intervals blood samples were drawn and serum concentrations of quinidine were determined. These data are analyzed in several publications, including Davidian and Giltinan (1995, section 9.3).

Source


---

### quinModel

**Model function for the Quinidine data**

**Description**

A model function for a model used with the Quinidine data. This function calls compiled C code.

**Usage**

```r
quinModel(Subject, time, conc, dose, interval, lV, lKa, lCl)
```

**Arguments**

- `Subject`  
  a factor identifying the patient on whom the data were collected.

- `time`  
  a numeric vector giving the time (hr) at which the drug was administered or the blood sample drawn. This is measured from the time the patient entered the study.

- `conc`  
  a numeric vector giving the serum quinidine concentration (mg/L).

- `dose`  
  a numeric vector giving the dose of drug administered (mg). Although there were two different forms of quinidine administered, the doses were adjusted for differences in salt content by conversion to milligrams of quinidine base.

- `interval`  
  a numeric vector giving the when the drug has been given at regular intervals for a sufficiently long period of time to assume steady state behavior, the interval is recorded.

- `lV`  
  numeric. A vector of values of the natural log of the effective volume of distribution according to `Subject` and `time`.

- `lKa`  
  numeric. A vector of values of the natural log of the absorption rate constant according to `Subject` and `time`.

- `lCl`  
  numeric. A vector of values of the natural log of the clearance parameter according to `Subject` and `time`. 
Details

See the details section of Quinidine for a description of the model function that quinModel evaluates.

Value

a numeric vector of predicted quinidine concentrations.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


Evaluation of Stress in Railway Rails

Description

The Rail data frame has 18 rows and 2 columns.

Format

This data frame contains the following columns:

- **Rail**: an ordered factor identifying the rail on which the measurement was made.
- **travel**: a numeric vector giving the travel time for ultrasonic head-waves in the rail (nanoseconds). The value given is the original travel time minus 36,100 nanoseconds.

Details

Devore (2000, Example 10.10, p. 427) cites data from an article in Materials Evaluation on “a study of travel time for a certain type of wave that results from longitudinal stress of rails used for railroad track.”

Source


random.effects  

**Extract Random Effects**

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `lmlist` and `lme`.

**Usage**

```r
random.effects(object, ...)  
ranef(object, ...)
```

**Arguments**

- `object` any fitted model object from which random effects estimates can be extracted.
- `...` some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**References**


**See Also**

`ranef.lmlist`, `ranef.lme`

**Examples**

## see the method function documentation

---

**ranef.lme  

**Extract lme Random Effects**

**Description**

The estimated random effects at level $i$ are represented as a data frame with rows given by the different groups at that level and columns given by the random effects. If a single level of grouping is specified, the returned object is a data frame; else, the returned object is a list of such data frames. Optionally, the returned data frame(s) may be augmented with covariates summarized over groups.

**Usage**

```r
## S3 method for class 'lme'
ranef(object, augFrame, level, data, which, FUN,  
      standard, omitGroupingFactor, subset, ...)
```
ranef.lme

Arguments

object
an object inheriting from class "lme", representing a fitted linear mixed-effects model.

augFrame
an optional logical value. If TRUE, the returned data frame is augmented with variables defined in data; else, if FALSE, only the coefficients are returned. Defaults to FALSE.

level
an optional vector of positive integers giving the levels of grouping to be used in extracting the random effects from an object with multiple nested grouping levels. Defaults to all levels of grouping.

data
an optional data frame with the variables to be used for augmenting the returned data frame when augFrame = TRUE. Defaults to the data frame used to fit object.

which
an optional positive integer vector specifying which columns of data should be used in the augmentation of the returned data frame. Defaults to all columns in data.

FUN
an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as ordered, factor, or numeric. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

standard
an optional logical value indicating whether the estimated random effects should be "standardized" (i.e. divided by the estimate of the standard deviation of that group of random effects). Defaults to FALSE.

omitGroupingFactor
an optional logical value. When TRUE the grouping factor itself will be omitted from the group-wise summary of data but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to FALSE.

subset
an optional expression indicating for which rows the random effects should be extracted.

... some methods for this generic require additional arguments. None are used in this method.

Value

a data frame, or list of data frames, with the estimated random effects at the grouping level(s) specified in level and, optionally, other covariates summarized over groups. The returned object inherits from classes random.effects.lme and data.frame.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>
ranef.lmList

Extract lmList Random Effects

Description

The difference between the individual lm components coefficients and their average is calculated.

Usage

## S3 method for class 'lmList'
ranef(object, augFrame, data, which, FUN, standard, 
   omitGroupingFactor, ...)

Arguments

object an object inheriting from class "lmList", representing a list of lm objects with a common model.

augFrame an optional logical value. If TRUE, the returned data frame is augmented with variables defined in data; else, if FALSE, only the coefficients are returned. Defaults to FALSE.

data an optional data frame with the variables to be used for augmenting the returned data frame when augFrame = TRUE. Defaults to the data frame used to fit object.

which an optional positive integer vector specifying which columns of data should be used in the augmentation of the returned data frame. Defaults to all columns in data.

FUN an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as ordered, factor, or numeric. The indicated function will be applied to any group-varying variables of that class. The default functions to be used are mean for numeric factors, and Mode for both factor and ordered. The Mode function, defined internally in gsummary, returns the modal or most popular value of the variable. It is different from the mode function that returns the S-language mode of the variable.

Examples

fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
ransf(fm1)
random.effects(fm1)  # same as above
random.effects(fm1, augFrame = TRUE)
RatPupWeight

standard  
an optional logical value indicating whether the estimated random effects should be "standardized" (i.e. divided by the corresponding estimated standard error). Defaults to FALSE.

omitGroupingFactor  
an optional logical value. When TRUE the grouping factor itself will be omitted from the group-wise summary of data but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to FALSE.

...  
some methods for this generic require additional arguments. None are used in this method.

Value  
a vector with the differences between the individual lm coefficients in object and their average.

Author(s)  
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References  

See Also  
fixed.effects.lmList, lmList, random.effects

Examples  
  fm1 <- lmList(distance ~ age | Subject, Orthodont)  
  ranef(fm1)  
  random.effects(fm1)  # same as above

RatPupWeight

The weight of rat pups

Description  
The RatPupWeight data frame has 322 rows and 5 columns.

Format  
This data frame contains the following columns:

- **weight** a numeric vector
- **sex** a factor with levels Male Female
- **Litter** an ordered factor with levels 9 < 8 < 7 < 4 < 2 < 10 < 1 < 3 < 5 < 6 < 21 < 22 < 24 < 27 < 26 < 25 < 23 < 17 < 11 < 14 < 13 < 15 < 16 < 20 < 19 < 18 < 12
- **Lsize** a numeric vector
- **Treatment** an ordered factor with levels Control < Low < High
Recalculate Condensed Linear Model Object

Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: corStruct, modelStruct, reStruct, and varFunc.

Usage

recalc(object, conLin, ...)

Arguments

object any object which induces a recalculation of the condensed linear model object conLin.
conLin a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
... some methods for this generic can take additional arguments.

Value

the recalculated condensed linear model object.

Note

This function is only used inside model fitting functions, such as lme and gls, that require recalculation of a condensed linear model object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

recalc.corStruct, recalc.modelStruct, recalc.reStruct, recalc.varFunc

Examples

## see the method function documentation
Description

This method function pre-multiplies the "Xy" component of conLin by the transpose square-root factor(s) of the correlation matrix (matrices) associated with object and adds the log-likelihood contribution of object, given by \( \logLik(object) \), to the "logLik" component of conLin.

Usage

```r
## S3 method for class 'corStruct'
recalc(object, conLin, ...)
```

Arguments

- `object`: an object inheriting from class "corStruct", representing a correlation structure.
- `conLin`: a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix \((X)\) combined with a response vector \((y)\), and "logLik", corresponding to the log-likelihood of the underlying model.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

the recalculated condensed linear model object.

Note

This method function is only used inside model fitting functions, such as `lme` and `gls`, that allow correlated error terms.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

corFactor, `logLik.corStruct`
Recalculate for a modelStruct Object

Description

This method function recalculates the condensed linear model object using each element of object sequentially from last to first.

Usage

```r
## S3 method for class 'modelStruct'
recalc(object, conLin, ...)
```

Arguments

- `object`: an object inheriting from class "modelStruct", representing a list of model components, such as `corStruct` and `varFunc` objects.
- `conLin`: an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model. Defaults to `attr(object, "conLin")`.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

the recalculated condensed linear model object.

Note

This method function is generally only used inside model fitting functions, such as `lme` and `gls`, that allow model components, such as correlated error terms and variance functions.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- `recalc.corStruct`
- `recalc.reStruct`
- `recalc.varFunc`
Recalculate for an reStruct Object

Description

The log-likelihood, or restricted log-likelihood, of the Gaussian linear mixed-effects model represented by `object` and `conLin` (assuming spherical within-group covariance structure), evaluated at `coef(object)` is calculated and added to the `logLik` component of `conLin`. The settings attribute of `object` determines whether the log-likelihood, or the restricted log-likelihood, is to be calculated. The computational methods for the (restricted) log-likelihood calculations are described in Bates and Pinheiro (1998).

Usage

```r
## S3 method for class 'reStruct'
recalc(object, conLin, ...)
```

Arguments

- `object`: an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.
- `conLin`: a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
- `...`: some methods for this generic require additional arguments. None are used in this method.

Value

the condensed linear model with its `logLik` component updated.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`logLik`, `lme`, `recalc`, `reStruct`

Recalculate for varFunc Object

Description

This method function pre-multiples the "Xy" component of `conLin` by a diagonal matrix with diagonal elements given by the weights corresponding to the variance structure represented by `object` and adds the log-likelihood contribution of `object`, given by `logLik(object)`, to the "logLik" component of `conLin`. 
Usage

```r
## S3 method for class 'varFunc'
recalc(object, conLin, ...)
```

Arguments

- `object` an object inheriting from class "varFunc", representing a variance function structure.
- `conLin` a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
- `...` some methods for this generic require additional arguments. None are used in this method.

Value

the recalculated condensed linear model object.

Note

This method function is only used inside model fitting functions, such as `lme` and `gls`, that allow heteroscedastic error terms.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- `recalc`, `varWeights`, `logLik.varFunc`

---

Relaxin

Assay for Relaxin

Description

The Relaxin data frame has 198 rows and 3 columns.

Format

This data frame contains the following columns:

- `Run` an ordered factor with levels `5 < 8 < 9 < 3 < 4 < 2 < 7 < 1 < 6`
- `conc` a numeric vector
- `cAMP` a numeric vector

Source

Description

Intravenous infusion of remifentanil (a strong analgesic) in different rates over varying time periods was applied to a total of 65 patients. Concentration measurements of remifentanil were taken along with several covariates resulting in the Remifentanil data frame with 2107 rows and 12 columns.

Usage

data("Remifentanil", package = "nlme")

Format

This data frame (of class "groupedData", specifically "nfnGroupedData") contains the following columns:

- **ID**: numerical (patient) IDs.
- **Subject**: an *ordered* factor with 65 levels (of the IDs): 30 < 21 < 25 < 23 < 29 < ... < 36 < 6 < 5 < 10 < 9.
- **Time**: time from beginning of infusion in minutes (*numeric*).
- **conc**: remifentanil concentration in [ng / ml] (*numeric*).
- **Rate**: infusion rate in [µg / min].
- **Amt**: amount of remifentanil given in the current time interval in [µg].
- **Age**: age of the patient in years.
- **Sex**: gender of the patient, a *factor* with levels Female and Male.
- **Ht**: height of the patient in cm.
- **Wt**: weight of the patient in kg.
- **BSA**: body surface area (DuBois and DuBois 1916): \( BSA := W^{0.425} \cdot H^{0.725} \cdot 0.007184 \).
- **LBM**: lean body mass (James 1976), with slightly different formula for men \( LBM_m := 1.1Wt - 128(Wt/Ht)^2 \), and women \( LBM_f := 1.07Wt - 148(Wt/Ht)^2 \).

Author(s)

of this help page: Niels Hagenbuch and Martin Maechler, SfS ETH Zurich.

Source

References


Examples

```r
plot(Remifentanil, type = "l", lwd = 2) # shows the 65 patients' remi profiles

## The same on log-log scale (*more* sensible for modeling ?):
plot(Remifentanil, type = "l", lwd = 2, scales = list(log=TRUE))

str(Remifentanil)
summary(Remifentanil)

plot(xtabs(~Subject, Remifentanil))
summary(unclass(table(Remifentanil$Subject)))

## between 20 and 54 measurements per patient (median: 24; mean: 32.42)

## Only first measurement of each patient:
dim(Remi.1 <- Remifentanil[!duplicated(Remifentanil[,"ID"])),]) # 65 x 12

LBMfn <- function(Wt, Ht, Sex) ifelse(Sex == "Female",
1.07 * Wt - 148*(Wt/Ht)^2,
1.1 * Wt - 128*(Wt/Ht)^2)

with(Remi.1, stopifnot(all.equal(BSA, Wt^{0.425} * Ht^{0.725} * 0.007184, tol = 1.5e-5),
all.equal(LBM, LBMfn(Wt, Ht, Sex), tol = 7e-7))

## Rate: typically 3 µg / kg body weight, but:
sunflowerplot(Rate ~ Wt, Remifentanil)
abline(0,3, lty=2, col=adjustcolor("black", 0.5))
```

---

**residuals.gls**

*Extract gls Residuals*

**Description**

The residuals for the linear model represented by `object` are extracted.

**Usage**

```r
## S3 method for class 'gls'
residuals(object, type, ...)
```
Arguments

**object**

an object inheriting from class "gls", representing a generalized least squares fitted linear model, or from class gnls, representing a generalized nonlinear least squares fitted linear model.

**type**

an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "response".

... some methods for this generic function require additional arguments. None are used in this method.

Value

a vector with the residuals for the linear model represented by object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls

gnls

Examples

```r
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary, 
correlation = corAR1(form = ~ 1 | Mare))
residuals(fm1)
```

residuals.glsStruct  Calculate glsStruct Residuals

Description

The residuals for the linear model represented by object are extracted.

Usage

```r
## S3 method for class 'glsStruct'
residuals(object, glsFit, ...)
```
Arguments

object an object inheriting from class "glsStruct", representing a list of linear model components, such as corStruct and "varFunc" objects.

glsFit an optional list with components logLik (log-likelihood), beta (coefficients), sigma (standard deviation for error term), varBeta (coefficients’ covariance matrix), fitted (fitted values), and residuals (residuals). Defaults to attr(object, "glsFit").

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the residuals for the linear model represented by object.

Note

This method function is primarily used inside gls and residuals.gls.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gls, glsStruct, residuals.gls, fitted.glsStruct

residuals.gnlsStruct  Calculate gnlsStruct Residuals

Description

The residuals for the nonlinear model represented by object are extracted.

Usage

## S3 method for class 'gnlsStruct'
residuals(object, ...)

Arguments

object an object inheriting from class "gnlsStruct", representing a list of model components, such as corStruct and varFunc objects, and attributes specifying the underlying nonlinear model and the response variable.

... some methods for this generic require additional arguments. None are used in this method.

Value

a vector with the residuals for the nonlinear model represented by object.
Note

This method function is primarily used inside gnlst and residuals.gnlst.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

gnlst, residuals.gnlst, fitted.gnlstStruct

residuals.lme Extract lme Residuals

Description

The residuals at level $i$ are obtained by subtracting the fitted levels at that level from the response vector (and dividing by the estimated within-group standard error, if type="pearson"). The fitted values at level $i$ are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to $i$.

Usage

```r
## S3 method for class 'lme'
residuals(object, level = Q,
          type = c("response", "pearson", "normalized"), asList = FALSE, ...)
```

Arguments

- `object`: an object inheriting from class "lme", representing a fitted linear mixed-effects model.
- `level`: an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from `object`. Level values increase from outermost to innermost grouping, with level zero corresponding to the population residuals. Defaults to the highest or innermost level of grouping.
- `type`: an optional character string specifying the type of residuals to be used. If "response", as by default, the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided.
- `asList`: an optional logical value. If TRUE and a single value is given in `level`, the returned object is a list with the residuals split by groups; else the returned value is either a vector or a data frame, according to the length of `level`. Defaults to FALSE.
- `...`: some methods for this generic require additional arguments. None are used in this method.
residuals.lmeStruct

Value
_if a single level of grouping is specified in level, the returned value is either a list with the residuals split by groups (asList = TRUE) or a vector with the residuals (asList = FALSE); else, when multiple grouping levels are specified in level, the returned object is a data frame with columns given by the residuals at different levels and the grouping factors. For a vector or data frame result the naresid method is applied._

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
lme, fitted.lme

Examples

```r
fm1 <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
head(residuals(fm1, level = 0:1))
summary(residuals(fm1) / residuals(fm1, type = "p")) # constant scaling factor 1.432
```

Description
_The residuals at level _i_ are obtained by subtracting the fitted values at that level from the response vector. The fitted values at level _i_ are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to _i_.}_

Usage
_## S3 method for class 'lmeStruct'
residuals(object, level, conLin, lmeFit, ...)_

Arguments

- `object` an object inheriting from class "lmeStruct", representing a list of linear mixed-effects model components, such as reStruct, corStruct, and varFunc objects.
- `level` an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from object. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
- `conLin` an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying lme model. Defaults to attr(object, "conLin").
- `lmeFit` an optional list with components beta and b containing respectively the fixed effects estimates and the random effects estimates to be used to calculate the residuals. Defaults to attr(object, "lmeFit").
- `...` some methods for this generic accept optional arguments.
residuals.lmList

Value
if a single level of grouping is specified in level, the returned value is a vector with the residuals at the desired level; else, when multiple grouping levels are specified in level, the returned object is a matrix with columns given by the residuals at different levels.

Note
This method function is primarily used within the lme function.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
lme, residuals.lme, fitted.lmeStruct

residuals.lmList  Extract lmList Residuals

Description
The residuals are extracted from each lm component of object and arranged into a list with as many components as object, or combined into a single vector.

Usage
## S3 method for class 'lmList'
residuals(object, type, subset, asList, ...)

Arguments
object  an object inheriting from class "lmList", representing a list of lm objects with a common model.
subset  an optional character or integer vector naming the lm components of object from which the residuals are to be extracted. Default is NULL, in which case all components are used.
type  an optional character string specifying the type of residuals to be extracted. Options include "response" for the "raw" residuals (observed - fitted), "pearson" for the standardized residuals (raw residuals divided by the estimated residual standard error) using different standard errors for each lm fit, and "pooled.pearson" for the standardized residuals using a pooled estimate of the residual standard error. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "response".
asList  an optional logical value. If TRUE, the returned object is a list with the residuals split by groups; else the returned value is a vector. Defaults to FALSE.
...  some methods for this generic require additional arguments. None are used in this method.
The residuals at level \( i \) are obtained by subtracting the fitted values at that level from the response vector. The fitted values at level \( i \) are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to \( i \) and evaluating the model function at the resulting estimated parameters.

### Examples

```r
fm1 <- lmlist(distance ~ age | Subject, Orthodont)
residuals(fm1)
```

### Description

The residuals at level \( i \) are obtained by subtracting the fitted values at that level from the response vector. The fitted values at level \( i \) are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to \( i \) and evaluating the model function at the resulting estimated parameters.

### Usage

```r
## S3 method for class 'nlmeStruct'
residuals(object, level, conLin, ...)
```

### Arguments

- **object**: an object inheriting from class "nlmeStruct", representing a list of mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.

- **level**: an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from object. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.

- **conLin**: an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (\( X \)) combined with a response vector (\( y \)), and "logLik", corresponding to the log-likelihood of the underlying nlme model. Defaults to `attr(object, "conLin")`.

- **...**: optional arguments to the residuals generic. Not used.

### Value

- if a single level of grouping is specified in `level`, the returned value is a vector with the residuals at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the residuals at different levels.
Note

This method function is primarily used within the \texttt{nlme} function.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

\texttt{nlme}, \texttt{fitted.nlmeStruct}

---

**reStruct**

**Random Effects Structure**

**Description**

This function is a constructor for the \texttt{reStruct} class, representing a random effects structure and consisting of a list of \texttt{pdMat} objects, plus a \texttt{settings} attribute containing information for the optimization algorithm used to fit the associated mixed-effects model.

**Usage**

\begin{verbatim}
reStruct(object, pdClass, REML, data)
## S3 method for class 'reStruct'
print(x, sigma, reEstimates, verbose, ...)
\end{verbatim}

**Arguments**

- \texttt{object} any of the following: (i) a one-sided formula of the form \( x_1+\ldots+x_n \mid g_1/\ldots/g_m \), with \( x_1+\ldots+x_n \) specifying the model for the random effects and \( g_1/\ldots/g_m \) the grouping structure (\( m \) may be equal to 1, in which case no \( / \) is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form \( x_1+\ldots+x_n \mid g \), with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form \( x_1+\ldots+x_n \), or a \texttt{pdMat} object with a formula (i.e. a non-\texttt{NULL} value for \texttt{formula(object)}), or a list of such formulas or \texttt{pdMat} objects. In this case, the grouping structure formula will be derived from the data used to fit the mixed-effects model, which should inherit from class \texttt{groupedData}; (iv) a named list of formulas or \texttt{pdMat} objects as in (iii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the order of the elements in the list; (v) an \texttt{reStruct} object.

- \texttt{pdClass} an optional character string with the name of the \texttt{pdMat} class to be used for the formulas in \texttt{object}. Defaults to \"pdLogChol\" which corresponds to a general positive-definite matrix (Log-Cholesky parametrization).
REML an optional logical value. If TRUE, the associated mixed-effects model will be fitted using restricted maximum likelihood; else, if FALSE, maximum likelihood will be used. Defaults to FALSE.

data an optional data frame in which to evaluate the variables used in the random effects formulas in object. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying pdMat objects. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.

x an object inheriting from class reStruct to be printed.

sigma an optional numeric value used as a multiplier for the square-root factors of the pdMat components (usually the estimated within-group standard deviation from a mixed-effects model). Defaults to 1.

reEstimates an optional list with the random effects estimates for each level of grouping. Only used when verbose = TRUE.

verbose an optional logical value determining if the random effects estimates should be printed. Defaults to FALSE.

... Optional arguments can be given to other methods for this generic. None are used in this method.

Value

an object inheriting from class reStruct, representing a random effects structure.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
groupedData, lme, pdMat, solve.reStruct, summary.reStruct, update.reStruct

Examples

rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
r simulat e.lme (object, nsim = 1, seed = , m2, method = c("REML", "ML"), niterEM = c(40, 200), useGen, ...)

Description

The model object is fit to the data. Using the fitted values of the parameters, nsim new data vectors from this model are simulated. Both object and m2 are fit by maximum likelihood (ML) and/or by restricted maximum likelihood (REML) to each of the simulated data vectors.

Usage

## S3 method for class 'lme'
simulate(object, nsim = 1, seed = , m2, method = c("REML", "ML"), niterEM = c(40, 200), useGen, ...)
simulate.lme

Arguments

object
an object inheriting from class "lme", representing a fitted linear mixed-effects model, or a list containing an lme model specification. If given as a list, it should contain components fixed, data, and random with values suitable for a call to lme. This argument defines the null model.

m2
an "lme" object or a list, like object containing a second lme model specification. This argument defines the alternative model. If given as a list, only those parts of the specification that change between model object and m2 need to be specified.

seed
an optional integer that is passed to set.seed. Defaults to a random integer.

method
an optional character array. If it includes "REML" the models are fit by maximizing the restricted log-likelihood. If it includes "ML" the log-likelihood is maximized. Defaults to c("REML", "ML"), in which case both methods are used.

nsim
an optional positive integer specifying the number of simulations to perform. Defaults to 1. This has changed. Previously the default was 1000.

niterEM
an optional integer vector of length 2 giving the number of iterations of the EM algorithm to apply when fitting the object and m2 to each simulated set of data. Defaults to c(40, 200).

useGen
an optional logical value. If TRUE, the nlminb optimizer is used with numerical derivatives of the log-likelihood. If FALSE, the nlm algorithm is used with an analytic gradient. The default depends on the "pdMat" classes used in object and m2: if both are standard classes (see pdClasses) then defaults to FALSE, otherwise defaults to TRUE.

... optional additional arguments. None are used.

Value

an object of class simulate.lme with components null and alt. Each of these has components ML and/or REML which are matrices. An attribute called seed contains the seed that was used for the random number generator.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

lme, set.seed

Examples

orthSim <-
simulate.lme(list(fixed = distance ~ age, data = Orthodont,
    random = ~ 1 | Subject), nsim = 200,
    m2 = list(random = ~ age | Subject))
solve.pdMat  \hspace{1em} Calculate Inverse of a Positive-Definite Matrix

Description

The positive-definite matrix represented by \code{a} is inverted and assigned to \code{a}.

Usage

\texttt{## S3 method for class \'pdMat\'

solve(\code{a}, \code{b}, ...)\n
Arguments

\code{a} \hspace{1em} an object inheriting from class "\code{pdMat}\", representing a positive definite matrix.
\code{b} \hspace{1em} this argument is only included for consistency with the generic function and is not used in this method function.
\code{...} \hspace{1em} some methods for this generic require additional arguments. None are used in this method.

Value

\code{a} \hspace{1em} \code{pdMat} object similar to \code{a}, but with coefficients corresponding to the inverse of the positive-definite matrix represented by \code{a}.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

\code{pdMat}

Examples

\begin{verbatim}
pd1 <- pdCompSymm(3 * diag(3) + 1)
solve(pd1)
\end{verbatim}

solve.reStruct  \hspace{1em} Apply Solve to an reStruct Object

Description

Solve is applied to each \code{pdMat} component of \code{a}, which results in inverting the positive-definite matrices they represent.

Usage

\texttt{## S3 method for class \'reStruct\'

solve(\code{a}, \code{b}, ...)\n
}}
Soybean

3427

Arguments

a

an object inheriting from class "reStruct", representing a random effects structure and consisting of a list of pdMat objects.

b

this argument is only included for consistency with the generic function and is not used in this method function.

... some methods for this generic require additional arguments. None are used in this method.

Value

an reStruct object similar to a, but with the pdMat components representing the inverses of the matrices represented by the components of a.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

solve.pdMat.reStruct

Examples

rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
B = pdDiag(2 * diag(4), form = ~Educ)))
solve(rs1)

Soybean

Growth of soybean plants

Description

The Soybean data frame has 412 rows and 5 columns.

Format

This data frame contains the following columns:

Plot a factor giving a unique identifier for each plot.
Variety a factor indicating the variety: Forrest (F) or Plant Introduction #416937 (P).
Year a factor indicating the year the plot was planted.
Time a numeric vector giving the time the sample was taken (days after planting).
weight a numeric vector giving the average leaf weight per plant (g).

Details

These data are described in Davidian and Giltinan (1995, 1.1.3, p.7) as “Data from an experiment to compare growth patterns of two genotypes of soybeans: Plant Introduction #416937 (P), an experimental strain, and Forrest (F), a commercial variety.”
Source


Examples

```r
summary(fm1 <- nlsList(SSlogis, data = Soybean))
```

---

**splitFormula**  
*Split a Formula*

**Description**

Splits the right hand side of `form` into a list of subformulas according to the presence of `sep`. The left hand side of `form`, if present, will be ignored. The length of the returned list will be equal to the number of occurrences of `sep` in `form` plus one.

**Usage**

```r
splitFormula(form, sep)
```

**Arguments**

- `form`  
a formula object.
- `sep`  
an optional character string specifying the separator to be used for splitting the formula. Defaults to `/`.

**Value**

a list of formulas, corresponding to the split of `form` according to `sep`.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`formula`

**Examples**

```r
splitFormula(~ g1/g2/g3)
```
Spruce Growth of Spruce Trees

Description

The Spruce data frame has 1027 rows and 4 columns.

Format

This data frame contains the following columns:

- **Tree**  a factor giving a unique identifier for each tree.
- **days**  a numeric vector giving the number of days since the beginning of the experiment.
- **logSize**  a numeric vector giving the logarithm of an estimate of the volume of the tree trunk.
- **plot**  a factor identifying the plot in which the tree was grown.

Details

Diggle, Liang, and Zeger (1994, Example 1.3, page 5) describe data on the growth of spruce trees that have been exposed to an ozone-rich atmosphere or to a normal atmosphere.

Source


summary.corStruct Summarize a corStruct Object

Description

This method function prepares object to be printed using the print.summary method, by changing its class and adding a structName attribute to it.

Usage

```r
## S3 method for class 'corStruct'
summary(object, structName, ...)
```

Arguments

- **object**  an object inheriting from class "corStruct", representing a correlation structure.
- **structName**  an optional character string defining the type of correlation structure associated with object, to be used in the print.summary method. Defaults to class(object)[1].
- **...**  some methods for this generic require additional arguments. None are used in this method.
**Value**

an object identical to `object`, but with its class changed to `summary.corStruct` and an additional attribute `structName`. The returned value inherits from the same classes as `object`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

corClasses, corNatural, Initialize.corStruct, summary

**Examples**

cs1 <- corAR1(0.2)
summary(cs1)

---

**summary.gls**

*Summarize a Generalized Least Squares gls Object*

**Description**

Additional information about the linear model fit represented by `object` is extracted and included as components of `object`.

**Usage**

```r
## S3 method for class 'gls'
summary(object, verbose, ...)
```

**Arguments**

- `object`:
an object inheriting from class "gls", representing a generalized least squares fitted linear model.
- `verbose`:
an optional logical value used to control the amount of output when the object is printed. Defaults to FALSE.
- `...`:
some methods for this generic require additional arguments. None are used in this method.

**Value**

an object inheriting from class `summary.gls` with all components included in `object` (see `glsObject` for a full description of the components) plus the following components:

- `corBeta`:
  approximate correlation matrix for the coefficients estimates
- `tTable`:
  a matrix with columns `Value`, `Std. Error`, `t-value`, and `p-value` representing respectively the coefficients estimates, their approximate standard errors, the ratios between the estimates and their standard errors, and the associated p-value under a $t$ approximation. Rows correspond to the different coefficients.
residuals
if more than five observations are used in the gls fit, a vector with the minimum,
first quartile, median, third quartile, and maximum of the residuals distribution;
else the residuals.

AIC
the Akaike Information Criterion corresponding to object.

BIC
the Bayesian Information Criterion corresponding to object.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
AIC, BIC, gls, summary

Examples
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
correlation = corAR1(form = ~ 1 | Mare))
summary(fm1)
coef(summary(fm1)) # "the matrix"

summary.lme

Summarize an lme Object

Description
Additional information about the linear mixed-effects fit represented by object is extracted and
included as components of object. The returned object has a print and a coef method, the latter
returning the coefficient’s tTtable.

Usage
## S3 method for class 'lme'
summary(object, adjustSigma, verbose, ...)
## S3 method for class 'summary.lme'
print(x, verbose = FALSE, ...)

Arguments

object
an object inheriting from class "lme", representing a fitted linear mixed-effects
model.

adjustSigma
an optional logical value. If TRUE and the estimation method used to obtain
object was maximum likelihood, the residual standard error is multiplied by
\sqrt{\frac{n_{\text{obs}}}{n_{\text{obs}} - n_{\text{par}}}}, converting it to a REML-like estimate. This argument is
only used when a single fitted object is passed to the function. Default is TRUE.

verbose
an optional logical value used to control the amount of output in the
print.summary.lme method. Defaults to FALSE.

...
additional optional arguments passed to methods, mainly for the print method.

x
a "summary.lme" object.
Value

an object inheriting from class summary.lme with all components included in object (see \link{lmeObject} for a full description of the components) plus the following components:

corFixed approximate correlation matrix for the fixed effects estimates.
tTable a matrix with columns named Value, Std. Error, DF, t-value, and p-value representing respectively the fixed effects estimates, their approximate standard errors, the denominator degrees of freedom, the ratios between the estimates and their standard errors, and the associated p-value from a t distribution. Rows correspond to the different fixed effects.

residuals if more than five observations are used in the lme fit, a vector with the minimum, first quartile, median, third quartile, and maximum of the innermost grouping level residuals distribution; else the innermost grouping level residuals.

AIC the Akaike Information Criterion corresponding to object.
BIC the Bayesian Information Criterion corresponding to object.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

AIC, BIC, lme.

Examples

fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
(s1 <- summary(fm1))
coef(s1) # the (coef | Std.E | t | P-v ) matrix
Value

A list with summary statistics obtained by applying `summary.lm` to the elements of `object`, inheriting from class `summary.lmList`. The components of `value` are:

- **call**: A list containing an image of the `lmList` call that produced `object`.
- **coefficients**: A three-dimensional array with summary information on the `lm` coefficients. The first dimension corresponds to the names of the object components, the second dimension is given by "Value", "Std. Error", "t value", and "Pr(>|t|)", corresponding, respectively, to the coefficient estimates and their associated standard errors, t-values, and p-values. The third dimension is given by the coefficients names.
- **correlation**: A three-dimensional array with the correlations between the individual `lm` coefficient estimates. The first dimension corresponds to the names of the object components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the correlations between that coefficient and the remaining coefficients, by `lm` component.
- **cov.unscaled**: A three-dimensional array with the unscaled variances/covariances for the individual `lm` coefficient estimates (giving the estimated variance/covariance for the coefficients, when multiplied by the estimated residual errors). The first dimension corresponds to the names of the object components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the unscaled covariances between that coefficient and the remaining coefficients, by `lm` component.
- **df**: An array with the number of degrees of freedom for the model and for residuals, for each `lm` component.
- **df.residual**: The total number of degrees of freedom for residuals, corresponding to the sum of residuals `df` of all `lm` components.
- **fstatistics**: An array with the F test statistics and corresponding degrees of freedom, for each `lm` component.
- **pool**: The value of the `pool` argument to the function.
- **r.squared**: A vector with the multiple R-squared statistics for each `lm` component.
- **residuals**: A list with components given by the residuals from individual `lm` fits.
- **RSE**: The pooled estimate of the residual standard error.
- **sigma**: A vector with the residual standard error estimates for the individual `lm` fits.
- **terms**: The terms object used in fitting the individual `lm` components.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`lmList`, `summary`

Examples

```r
fm1 <- lmList(distance ~ age | Subject, Orthodont)
summary(fm1)
```
summary.nlsList

### Description

The summary function is applied to each nls component of object to produce summary information on the individual fits, which is organized into a list of summary statistics. The returned object is suitable for printing with the `print.summary.nlsList` method.

### Usage

```r
## S3 method for class 'nlsList'
summary(object, ...)
```

### Arguments

- `object`: an object inheriting from class "nls", representing a list of model components, such as `reStruct`, `corStruct`, and `varFunc` objects.
- `...`: some methods for this generic require additional arguments. None are used in this method.

### Value

A list with elements given by the summarized components of object. The returned value is of class `summary.nlsList`, also inheriting from the same classes as `object`.

### Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

### See Also

`reStruct`, `summary`

### Examples

```r
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),
                  corStruct = corAR1(0.3))
summary(lms1)
```
**Arguments**

- **object**: an object inheriting from class "nlsList", representing a list of nls fitted objects.
- **...**: optional arguments to the summary.lmList method. One such optional argument is pool, a logical value indicating whether a pooled estimate of the residual standard error should be used. Default is attr(object, "pool").

**Value**

A list with summary statistics obtained by applying summary to the elements of object, inheriting from class summary.nlsList. The components of value are:

- **call**: a list containing an image of the nlsList call that produced object.
- **parameters**: a three dimensional array with summary information on the nls coefficients. The first dimension corresponds to the names of the object components, the second dimension is given by "Value", "Std. Error", "t value", and "Pr(>|t|)", corresponding, respectively, to the coefficient estimates and their associated standard errors, t-values, and p-values. The third dimension is given by the coefficients names.
- **correlation**: a three dimensional array with the correlations between the individual nls coefficient estimates. The first dimension corresponds to the names of the object components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the correlations between that coefficient and the remaining coefficients, by nls component.
- **cov.unscaled**: a three dimensional array with the unscaled variances/covariances for the individual lm coefficient estimates (giving the estimated variance/covariance for the coefficients, when multiplied by the estimated residual errors). The first dimension corresponds to the names of the object components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the unscaled covariances between that coefficient and the remaining coefficients, by nls component.
- **df**: an array with the number of degrees of freedom for the model and for residuals, for each nls component.
- **df.residual**: the total number of degrees of freedom for residuals, corresponding to the sum of residuals df of all nls components.
- **pool**: the value of the pool argument to the function.
- **RSE**: the pooled estimate of the residual standard error.
- **sigma**: a vector with the residual standard error estimates for the individual lm fits.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

nlsList, summary

**Examples**

```r
fm1 <- nlsList(SSasymp, Loblolly)
summary(fm1)
```
summary.pdMat  Summarize a pdMat Object

Description

Attributes structName and noCorrelation, with the values of the corresponding arguments to the method function, are appended to object and its class is changed to summary.pdMat.

Usage

```r
## S3 method for class 'pdMat'
summary(object, structName, noCorrelation, ...)
```

Arguments

- `object` an object inheriting from class "pdMat", representing a positive definite matrix.
- `structName` an optional character string with a description of the pdMat class. Default depends on the method function: "Blocked" for pdBlocked, "Compound Symmetry" for pdCompSymm, "Diagonal" for pdDiag, "Multiple of an Identity" for pdIdent, "General Positive-Definite, Natural Parametrization" for pdNatural, "General Positive-Definite" for pdSymm, and data.class(object) for pdMat.
- `noCorrelation` an optional logical value indicating whether correlations are to be printed in print.summary.pdMat. Default depends on the method function: FALSE for pdDiag and pdIdent, and TRUE for all other classes.
- `...` some methods for this generic require additional arguments. None are used in this method.

Value

an object similar to object, with additional attributes structName and noCorrelation, inheriting from class summary.pdMat.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

print.summary.pdMat, pdMat

Examples

```r
summary(pdSymm(diag(4)))
```
summary.varFunc

Summarize "varFunc" Object

Description
A structName attribute, with the value of corresponding argument, is appended to object and its class is changed to summary.varFunc.

Usage
## S3 method for class 'varFunc'
summary(object, structName, ...)

Arguments
- object: an object inheriting from class "varFunc", representing a variance function structure.
- structName: an optional character string with a description of the varFunc class. Default depends on the method function:
  - for varComb: "Combination of variance functions",
  - for varConstPower: "Constant plus power of variance covariate",
  - for varConstProp: "Constant plus proportion of variance covariate",
  - for varExp: "Exponential of variance covariate",
  - for varIdent: "Different standard deviations per stratum",
  - for varPower: "Power of variance covariate",
  - for varFunc: data.class(object).
- ...: some methods for this generic require additional arguments. None are used in this method.

Value
an object similar to object, with an additional attribute structName, inheriting from class summary.varFunc.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also
varClasses, varFunc

Examples
vf1 <- varPower(0.3, form = -age)
vf1 <- Initialize(vf1, Orthodont)
summary(vf1)
Description

The Tetracycline1 data frame has 40 rows and 4 columns.

Format

This data frame contains the following columns:

- **conc**: a numeric vector
- **Time**: a numeric vector
- **Subject**: an ordered factor with levels 5 < 3 < 2 < 4 < 1
- **Formulation**: a factor with levels tetrachel tetracycl

Source


Description

The Tetracycline2 data frame has 40 rows and 4 columns.

Format

This data frame contains the following columns:

- **conc**: a numeric vector
- **Time**: a numeric vector
- **Subject**: an ordered factor with levels 4 < 5 < 2 < 1 < 3
- **Formulation**: a factor with levels Berkmycin tetramycin

Source

update.modelStruct  
Update a modelStruct Object

Description

This method function updates each element of object, allowing the access to data.

Usage

```r
## S3 method for class 'modelStruct'
update(object, data, ...)
```

Arguments

- **object**: an object inheriting from class "modelStruct", representing a list of model components, such as corStruct and varFunc objects.
- **data**: a data frame in which to evaluate the variables needed for updating the elements of object.
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value

an object similar to object (same class, length, and names), but with updated elements.

Note

This method function is primarily used within model fitting functions, such as lme and gls, that allow model components such as variance functions.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

- `reStruct`

update.varFunc  
Update varFunc Object

Description

If the formula(object) includes a "." term, representing a fitted object, the variance covariate needs to be updated upon completion of an optimization cycle (in which the variance function weights are kept fixed). This method function allows a reevaluation of the variance covariate using the current fitted object and, optionally, other variables in the original data.
Usage

## S3 method for class 'varFunc'
update(object, data, ...)

Arguments

- **object**: an object inheriting from class "varFunc", representing a variance function structure.
- **data**: a list with a component named "." with the current version of the fitted object (from which fitted values, coefficients, and residuals can be extracted) and, if necessary, other variables used to evaluate the variance covariate(s).
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value

if formula(object) includes a "." term, an varFunc object similar to object, but with the variance covariate reevaluated at the current fitted object value; else object is returned unchanged.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

needUpdate, covariate<-.varFunc

---

**varClasses**

<table>
<thead>
<tr>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Available standard classes:</td>
</tr>
<tr>
<td>- varExp: exponential of a variance covariate.</td>
</tr>
<tr>
<td>- varPower: power of a variance covariate.</td>
</tr>
<tr>
<td>- varConstPower: constant plus power of a variance covariate.</td>
</tr>
<tr>
<td>- varConstProp: constant plus proportion of a variance covariate.</td>
</tr>
<tr>
<td>- varIdent: constant variance(s), generally used to allow different variances according to the levels of a classification factor.</td>
</tr>
<tr>
<td>- varFixed: fixed weights, determined by a variance covariate.</td>
</tr>
<tr>
<td>- varComb: combination of variance functions.</td>
</tr>
</tbody>
</table>

**Description**

Standard classes of variance function structures (varFunc) available in the nlme package. Covariates included in the variance function, denoted by variance covariates, may involve functions of the fitted model object, such as the fitted values and the residuals. Different coefficients may be assigned to the levels of a classification factor.
**Note**

Users may define their own `varFunc` classes by specifying a constructor function and, at a minimum, methods for the functions `coef`, `coef<-`, and `initialize`. For examples of these functions, see the methods for class `varPower`.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**


**See Also**

`varComb`, `varConstPower`, `varConstProp`, `varExp`, `varFixed`, `varIdent`, `varPower`, `summary.varFunc`

---

**Description**

This function is a constructor for the `varComb` class, representing a combination of variance functions. The corresponding variance function is equal to the product of the variance functions of the `varFunc` objects listed in ... .

**Usage**

`varComb(...)`

**Arguments**

... objects inheriting from class `varFunc` representing variance function structures.

**Value**

a `varComb` object representing a combination of variance functions, also inheriting from class `varFunc`.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**


**See Also**

`varClasses`, `varWeights.varComb`, `coef.varComb`
Examples

vf1 <- varComb(varIdent(form = ~1|Sex), varPower())

---

**varConstPower**  
*Constant Plus Power Variance Function*

**Description**

This function is a constructor for the varConstPower class, representing a constant plus power variance function structure. Letting $v$ denote the variance covariate and $\sigma^2(v)$ denote the variance function evaluated at $v$, the constant plus power variance function is defined as $\sigma^2(v) = (\theta_1 + |v|^{\theta_2})^2$, where $\theta_1, \theta_2$ are the variance function coefficients. When a grouping factor is present, different $\theta_1, \theta_2$ are used for each factor level.

**Usage**

`varConstPower(const, power, form, fixed)`

**Arguments**

- `const, power`  
  optional numeric vectors, or lists of numeric values, with, respectively, the coefficients for the constant and the power terms. Both arguments must have length one, unless a grouping factor is specified in `form`. If either argument has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in `form`. If a grouping factor is present in `form` and the argument has length one, its value will be assigned to all grouping levels. Only positive values are allowed for `const`. Default is `numeric(0)`, which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).

- `form`  
  an optional one-sided formula of the form $\sim v$, or $\sim v \mid g$, specifying a variance covariate $v$ and, optionally, a grouping factor $g$ for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using `\``, representing a fitted model object from which fitted values (`fitted(.)`) and residuals (`resid(.)`) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in `form`, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the `*` operator, as in $\sim v \mid g1 * g2 * g3$. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to `$\sim$ fitted(.)` representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.

- `fixed`  
  an optional list with components `const` and/or `power`, consisting of numeric vectors, or lists of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in `form`, the components of `fixed` must have names identifying which coefficients are to be fixed. Coefficients included in `fixed` are not allowed to vary during the optimization of an objective function. Defaults to `NULL`, corresponding to no fixed coefficients.
Value

A varConstPower object representing a constant plus power variance function structure, also inher-
iting from class varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

varClasses, varWeights.varFunc, coef.varConstPower

Examples

t <- varConstPower(1.2, 0.2, form = ~age|Sex)

Description

This function is a constructor for the varConstProp class, representing a variance function structure
corresponding to a two-component error model (additive and proportional error). Letting \( v \) denote
the variance covariate and \( \sigma^2(v) \) denote the variance function evaluated at \( v \), the two-component
variance function is defined as \( \sigma^2(v) = a^2 + b^2 \times v^2 \), where \( a \) is the additive component and \( b \) is
the relative error component. In order to avoid overparameterisation of the model, it is recommended
to use the possibility to fix sigma, preferably to a value of 1 (see examples).

Usage

varConstProp(const, prop, form, fixed)

Arguments

const, prop  optional numeric vectors, or lists of numeric values, with, respectively, the coef-
cicients for the constant and the proportional error terms. Both arguments must
have length one, unless a grouping factor is specified in form. If either argument
has length greater than one, it must have names which identify its elements to
the levels of the grouping factor defined in form. If a grouping factor is present
in form and the argument has length one, its value will be assigned to all group-
ing levels. Only positive values are allowed for const. Default is 0.1 for both
const and prop.

form  an optional one-sided formula of the form \( \sim v \), or \( \sim v | g \), specifying a variance
covariate \( v \) and, optionally, a grouping factor \( g \) for the coefficients. The variance
covariate must evaluate to a numeric vector and may involve expressions using
\( \cdot \), representing a fitted model object from which fitted values (fitted(.))
and residuals (resid(.)) can be extracted (this allows the variance covariate
to be updated during the optimization of an object function). When a grouping factor is present in \texttt{form}, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the \texttt{*} operator, as in \texttt{~ v | g1 * g2 * g3}. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to \texttt{~ fitted(.)} representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.

\textbf{fixed} an optional list with components \texttt{const} and/or \texttt{power}, consisting of numeric vectors, or lists of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in \texttt{form}, the components of \texttt{fixed} must have names identifying which coefficients are to be fixed. Coefficients included in \texttt{fixed} are not allowed to vary during the optimization of an objective function. Defaults to \texttt{NULL}, corresponding to no fixed coefficients.

\textbf{Value}

a \texttt{varConstProp} object representing a constant plus proportion variance function structure, also inheriting from class \texttt{varFunc}.

\textbf{Note}

The error model underlying this variance function structure can be understood to result from two uncorrelated sequences of standardized random variables (Lavielle(2015), p. 55) and has been proposed for use in analytical chemistry (Werner et al. (1978), Wilson et al. (2004)) and chemical degradation kinetics (Ranke and Meinecke (2019)). Note that the two-component error model proposed by Rocke and Lorenzato (1995) assumed a log-normal distribution of residuals at high absolute values, which is not compatible with the \texttt{varFunc} structures in package \texttt{nlme}.

\textbf{Author(s)}

José Pinheiro and Douglas Bates (for \texttt{varConstPower}) and Johannes Ranke (adaptation to \texttt{varConstProp}).

\textbf{References}


See Also

varClasses, varWeights, varFunc, coef.varFunc

Examples

# Generate some synthetic data using the two-component error model and use
# different variance functions, also with fixed sigma in order to avoid
# overparameterisation in the case of a constant term in the variance function
times <- c(0, 1, 3, 7, 14, 28, 56, 120)
pred <- 100 * exp(- 0.03 * times)
sd_pred <- sqrt(3^2 + 0.07^2 * pred^2)
n_replicates <- 2

set.seed(123456)
syn_data <- data.frame(
  time = rep(times, each = n_replicates),
  value = rnorm(length(times) * n_replicates, rep(pred, each = n_replicates),
                 rep(sd_pred, each = n_replicates)))
syn_data$value <- ifelse(syn_data$value < 0, NA, syn_data$value)

f_const <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
                 data = syn_data, na.action = na.omit,
                 start = list(parent_0 = 100, lrc = -3))
f_varPower <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
                    data = syn_data, na.action = na.omit,
                    start = list(parent_0 = 100, lrc = -3),
                    weights = varPower())
f_varConstPower <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
                          data = syn_data, na.action = na.omit,
                          start = list(parent_0 = 100, lrc = -3),
                          weights = varConstPower())
f_varConstPower_sf <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
                           data = syn_data, na.action = na.omit,
                           control = list(sigma = 1),
                           start = list(parent_0 = 100, lrc = -3),
                           weights = varConstPower())
f_varConstProp <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
                        data = syn_data, na.action = na.omit,
                        start = list(parent_0 = 100, lrc = -3),
                        weights = varConstProp())
f_varConstProp_sf <- gnls(value ~ SSasymp(time, 0, parent_0, lrc),
                         data = syn_data, na.action = na.omit,
                         start = list(parent_0 = 100, lrc = -3),
                         control = list(sigma = 1),
                         weights = varConstProp())

AIC(f_const, f_varPower, f_varConstPower, f_varConstPower_sf,
    f_varConstProp, f_varConstProp_sf)

# The error model parameters 3 and 0.07 are approximately recovered
intervals(f_varConstProp_sf)
VarCorr

Extract variance and correlation components

Description

This function calculates the estimated variances, standard deviations, and correlations between the random-effects terms in a linear mixed-effects model, of class "lme", or a nonlinear mixed-effects model, of class "nlme". The within-group error variance and standard deviation are also calculated.

Usage

VarCorr(x, sigma = 1, ...)
## S3 method for class 'lme'
VarCorr(x, sigma = x$sigma, rdig = 3, ...)
## S3 method for class 'pdMat'
VarCorr(x, sigma = 1, rdig = 3, ...)
## S3 method for class 'pdBlocked'
VarCorr(x, sigma = 1, rdig = 3, ...)

Arguments

x a fitted model object, usually an object inheriting from class "lme".
sigma an optional numeric value used as a multiplier for the standard deviations. The default is x$sigma or 1 depending on class(x).
rdig an optional integer value specifying the number of digits used to represent correlation estimates. Default is 3.
... further optional arguments passed to other methods (none for the methods documented here).

Value

a matrix with the estimated variances, standard deviations, and correlations for the random effects. The first two columns, named Variance and StdDev, give, respectively, the variance and the standard deviations. If there are correlation components in the random effects model, the third column, named Corr, and the remaining unnamed columns give the estimated correlations among random effects within the same level of grouping. The within-group error variance and standard deviation are included as the last row in the matrix.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

lme, nlme
Examples

```r
fm1 <- lme(distance ~ age, data = Orthodont, random = ~age)
VarCorr(fm1)
```

Description

This function is a constructor for the `varExp` class, representing an exponential variance function structure. Letting $v$ denote the variance covariate and $\sigma^2(v)$ denote the variance function evaluated at $v$, the exponential variance function is defined as $\sigma^2(v) = \exp(2\theta v)$, where $\theta$ is the variance function coefficient. When a grouping factor is present, a different $\theta$ is used for each factor level.

Usage

```
varExp(value, form, fixed)
```

Arguments

- **value**: an optional numeric vector, or list of numeric values, with the variance function coefficients. Value must have length one, unless a grouping factor is specified in `form`. If `value` has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in `form`. If a grouping factor is present in `form` and `value` has length one, its value will be assigned to all grouping levels. Default is `numeric(0)`, which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).

- **form**: an optional one-sided formula of the form `~ v`, or `~ v | g`, specifying a variance covariate $v$ and, optionally, a grouping factor $g$ for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using `"."`, representing a fitted model object from which fitted values (fitted(.)) and residuals (resid(.)) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in `form`, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the `*` operator, like in `~ v | g1 * g2 * g3`. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to `~ fitted(.)` representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.

- **fixed**: an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in `form`, `fixed` must have names identifying which coefficients are to be fixed. Coefficients included in `fixed` are not allowed to vary during the optimization of an objective function. Defaults to `NULL`, corresponding to no fixed coefficients.

Value

A `varExp` object representing an exponential variance function structure, also inheriting from class `varFunc`. 
**varFixed**

**Author(s)**
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**

**See Also**
varClasses, varWeights.varFunc, coef.varExp

**Examples**

```r
vf1 <- varExp(0.2, form = ~age|Sex)
```

---

**Description**
This function is a constructor for the `varFixed` class, representing a variance function with fixed variances. Letting \( v \) denote the variance covariate defined in `value`, the variance function \( \sigma^2(v) \) for this class is \( \sigma^2(v) = |v| \). The variance covariate \( v \) is evaluated once at initialization and remains fixed thereafter. No coefficients are required to represent this variance function.

**Usage**

```r
varFixed(value)
```

**Arguments**

- `value` a one-sided formula of the form \(~ v\) specifying a variance covariate \( v \). Grouping factors are ignored.

**Value**
a `varFixed` object representing a fixed variance function structure, also inheriting from class `varFunc`.

**Author(s)**
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**

**See Also**
varClasses, varWeights.varFunc, varFunc

**Examples**

```r
vf1 <- varFixed(~age)
```
**Description**

If `object` is a one-sided formula, it is used as the argument to `varFixed` and the resulting object is returned. Else, if `object` inherits from class `varFunc`, it is returned unchanged.

**Usage**

`varFunc(object)`

**Arguments**

- `object`: either an one-sided formula specifying a variance covariate, or an object inheriting from class `varFunc`, representing a variance function structure.

**Value**

an object from class `varFunc`, representing a variance function structure.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**See Also**

- `summary.varFunc`, `varFixed`, `varWeights.varFunc`, `coef.varFunc`

**Examples**

```
vf1 <- varFunc(~age)
```

---

**Description**

This function is a constructor for the `varIdent` class, representing a constant variance function structure. If no grouping factor is present in `form`, the variance function is constant and equal to one, and no coefficients required to represent it. When `form` includes a grouping factor with \( M > 1 \) levels, the variance function allows \( M \) different variances, one for each level of the factor. For identifiability reasons, the coefficients of the variance function represent the ratios between the variances and a reference variance (corresponding to a reference group level). Therefore, only \( M - 1 \) coefficients are needed to represent the variance function. By default, if the elements in `value` are unnamed, the first group level is taken as the reference level.

**Usage**

`varIdent(value, form, fixed)`
Arguments

value

an optional numeric vector, or list of numeric values, with the variance function coefficients. If no grouping factor is present in form, this argument is ignored, as the resulting variance function contains no coefficients. If value has length one, its value is repeated for all coefficients in the variance function. If value has length greater than one, it must have length equal to the number of grouping levels minus one and names which identify its elements to the levels of the grouping factor. Only positive values are allowed for this argument. Default is numeric(0), which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).

form

an optional one-sided formula of the form \( \sim v \), or \( \sim v \mid g \), specifying a variance covariate \( v \) and, optionally, a grouping factor \( g \) for the coefficients. The variance covariate is ignored in this variance function. When a grouping factor is present in form, a different coefficient value is used for each of its levels less one reference level (see description section below). Several grouping variables may be simultaneously specified, separated by the * operator, like in \( \sim v \mid g1 * g2 * g3 \). In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to \( \sim 1 \).

fixed

an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. It must have names identifying which coefficients are to be fixed. Coefficients included in fixed are not allowed to vary during the optimization of an objective function. Defaults to NULL, corresponding to no fixed coefficients.

Value

a varIdent object representing a constant variance function structure, also inheriting from class varFunc.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

varClasses, varWeights.varFunc, coef.varIdent

Examples

vf1 <- varIdent(c(Female = 0.5), form = ~ 1 | Sex)
Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include default, gls and lme. See the appropriate method documentation for a description of the arguments.

Usage

Variogram(object, distance, ...)

Arguments

object a numeric vector with the values to be used for calculating the semi-variogram, usually a residual vector from a fitted model.
distance a numeric vector with the pairwise distances corresponding to the elements of object. The order of the elements in distance must correspond to the pairs (1,2), (1,3), ..., (n-1,n), with n representing the length of object, and must have length n(n-1)/2.
...
some methods for this generic function require additional arguments.

Value

will depend on the method function used; see the appropriate documentation.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also


Examples

```r
## see the method function documentation
```
Description
This method function calculates the semi-variogram values corresponding to the Exponential correlation model, using the estimated coefficients corresponding to object, at the distances defined by distance.

Usage

```r
## S3 method for class 'corExp'
Variogram(object, distance, sig2, length.out, ...)
```

Arguments

- **object**: an object inheriting from class "corExp", representing an exponential spatial correlation structure.
- **distance**: an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to NULL, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
- **sig2**: an optional numeric value representing the process variance. Defaults to 1.
- **length.out**: an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance = NULL`. Defaults to 50.
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

corExp, plot.Variogram, Variogram

Examples

```r
stopifnot(require("stats", quietly = TRUE))
cs1 <- corExp(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```
Variogram.corGaus

Calculate Semi-variogram for a corGaus Object

Description
This method function calculates the semi-variogram values corresponding to the Gaussian correlation model, using the estimated coefficients corresponding to object, at the distances defined by distance.

Usage
## S3 method for class 'corGaus'
Variogram(object, distance, sig2, length.out, ...)

Arguments
- **object**: an object inheriting from class "corGaus", representing a Gaussian spatial correlation structure.
- **distance**: an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to NULL, in which case a sequence of length length.out between the minimum and maximum values of getCovariate(object) is used.
- **sig2**: an optional numeric value representing the process variance. Defaults to 1.
- **length.out**: an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when distance = NULL. Defaults to 50.
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value
a data frame with columns variog and dist representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class Variogram.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also
corGaus, plot.Variogram, Variogram

Examples
cs1 <- corGaus(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
**Variogram.corLin**

**Calculate Semi-variogram for a corLin Object**

**Description**

This method function calculates the semi-variogram values corresponding to the Linear correlation model, using the estimated coefficients corresponding to object, at the distances defined by distance.

**Usage**

```r
## S3 method for class 'corLin'
Variogram(object, distance, sig2, length.out, ...)
```

**Arguments**

- `object` an object inheriting from class "corLin", representing an Linear spatial correlation structure.
- `distance` an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to NULL, in which case a sequence of length length.out between the minimum and maximum values of get Covariate(object) is used.
- `sig2` an optional numeric value representing the process variance. Defaults to 1.
- `length.out` an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when distance = NULL. Defaults to 50.
- `...` some methods for this generic require additional arguments. None are used in this method.

**Value**

A data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class Variogram.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**


**See Also**

corLin, plot.Variogram, Variogram

**Examples**

```r
cs1 <- corLin(15, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```
### Variogram.corRatio

**Calculate Semi-variogram for a corRatio Object**

#### Description

This method function calculates the semi-variogram values corresponding to the Rational Quadratic correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

#### Usage

```r
## S3 method for class 'corRatio'
Variogram(object, distance, sig2, length.out, ...)
```

#### Arguments

- `object`: an object inheriting from class "corRatio", representing an Rational Quadratic spatial correlation structure.
- `distance`: an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to NULL, in which case a sequence of length `length.out` between the minimum and maximum values of `getCovariate(object)` is used.
- `sig2`: an optional numeric value representing the process variance. Defaults to 1.
- `length.out`: an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when `distance = NULL`. Defaults to 50.
- `...`: some methods for this generic require additional arguments. None are used in this method.

#### Value

A data frame with columns `vario` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

#### Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

#### References


#### See Also

corRatio, plot.Variogram, Variogram

#### Examples

```r
cs1 <- corRatio(7, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```
Variogram.corSpatial  Calculate Semi-variogram for a corSpatial Object

Description
This method function calculates the semi-variogram values corresponding to the model defined in FUN, using the estimated coefficients corresponding to object, at the distances defined by distance.

Usage
## S3 method for class 'corSpatial'
Variogram(object, distance, sig2, length.out, FUN, ...)

Arguments
- **object**: an object inheriting from class "corSpatial", representing spatial correlation structure.
- **distance**: an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to NULL, in which case a sequence of length length.out between the minimum and maximum values of getCovariate(object) is used.
- **sig2**: an optional numeric value representing the process variance. Defaults to 1.
- **length.out**: an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when distance = NULL. Defaults to 50.
- **FUN**: a function of two arguments, the distance and the range corresponding to object, specifying the semi-variogram model.
- **...**: some methods for this generic require additional arguments. None are used in this method.

Value
a data frame with columns variog and dist representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class Variogram.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also

Examples
cs1 <- corExp(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1, FUN = function(x, y) (1 - exp(-x/y)))[1:10,]
**Variogram.corSpher**

**Calculate Semi-variogram for a corSpher Object**

**Description**

This method function calculates the semi-variogram values corresponding to the Spherical correlation model, using the estimated coefficients corresponding to object, at the distances defined by distance.

**Usage**

```r
## S3 method for class 'corSpher'
Variogram(object, distance, sig2, length.out, ...)
```

**Arguments**

- `object` an object inheriting from class "corSpher", representing an Spherical spatial correlation structure.
- `distance` an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to NULL, in which case a sequence of length length.out between the minimum and maximum values of get Covariate(object) is used.
- `sig2` an optional numeric value representing the process variance. Defaults to 1.
- `length.out` an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when distance = NULL. Defaults to 50.
- `...` some methods for this generic require additional arguments. None are used in this method.

**Value**

A data frame with columns variog and dist representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class Variogram.

**Author(s)**

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

**References**


**See Also**

corSpher, plot.Variogram, Variogram

**Examples**

```r
cs1 <- corSpher(15, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```
Variogram.default  Calculate Semi-variogram

Description

This method function calculates the semi-variogram for an arbitrary vector object, according to the distances in distance. For each pair of elements \(x, y\) in object, the corresponding semi-variogram is \((x - y)^2/2\). The semi-variogram is useful for identifying and modeling spatial correlation structures in observations with constant expectation and constant variance.

Usage

## Default S3 method:
Variogram(object, distance, ...)

Arguments

object    a numeric vector with the values to be used for calculating the semi-variogram, usually a residual vector from a fitted model.
distance  a numeric vector with the pairwise distances corresponding to the elements of object. The order of the elements in distance must correspond to the pairs \((1,2), (1,3), \ldots, (n-1,n)\), with \(n\) representing the length of object, and must have length \(n(n-1)/2\).

...      some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns \(\text{vario}\) and \(\text{dist}\) representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class \text{Variogram}.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

Variogram, Variogram.gls, Variogram.lme, plot.Variogram

Examples

```r
fm1 <- lm(follicles ~ sin(2 * pi * Time) + cos(2 * pi * Time), Ovary,
          subset = Mare == 1)
Variogram(resid(fm1), dist(1:29))[1:10,]
```
Variogram.gls

Calculate Semi-variogram for Residuals from a gls Object

Description

This method function calculates the semi-variogram for the residuals from a gls fit. The semi-variogram values are calculated for pairs of residuals within the same group level, if a grouping factor is present. If collapse is different from "none", the individual semi-variogram values are collapsed using either a robust estimator (robust = TRUE) defined in Cressie (1993), or the average of the values within the same distance interval. The semi-variogram is useful for modeling the error term correlation structure.

Usage

## S3 method for class 'gls'
Variogram(object, distance, form, resType, data, na.action, maxDist, length.out, collapse, nint, breaks, robust, metric, ...)

Arguments

object an object inheriting from class "gls", representing a generalized least squares fitted model.
distance an optional numeric vector with the distances between residual pairs. If a grouping variable is present, only the distances between residual pairs within the same group should be given. If missing, the distances are calculated based on the values of the arguments form, data, and metric, unless object includes a corSpatial element, in which case the associated covariate (obtained with the getCovariate method) is used.
form an optional one-sided formula specifying the covariate(s) to be used for calculating the distances between residual pairs and, optionally, a grouping factor for partitioning the residuals (which must appear to the right of a | operator in form). Default is ~1, implying that the observation order within the groups is used to obtain the distances.
resType an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
data an optional data frame in which to interpret the variables in form. By default, the same data used to fit object is used.
na.action a function that indicates what should happen when the data contain NAs. The default action (na.fail) causes an error message to be printed and the function to terminate, if there are any incomplete observations.
maxDist an optional numeric value for the maximum distance used for calculating the semi-variogram between two residuals. By default all residual pairs are included.
length.out: an optional integer value. When object includes a corSpatial element, its semi-variogram values are calculated and this argument is used as the length.out argument to the corresponding Variogram method. Defaults to 50.

collapse: an optional character string specifying the type of collapsing to be applied to the individual semi-variogram values. If equal to "quantiles", the semi-variogram values are split according to quantiles of the distance distribution, with equal number of observations per group, with possibly varying distance interval lengths. Else, if "fixed", the semi-variogram values are divided according to distance intervals of equal lengths, with possibly different number of observations per interval. Else, if "none", no collapsing is used and the individual semi-variogram values are returned. Defaults to "quantiles".

nint: an optional integer with the number of intervals to be used when collapsing the semi-variogram values. Defaults to 20.

robust: an optional logical value specifying if a robust semi-variogram estimator should be used when collapsing the individual values. If TRUE the robust estimator is used. Defaults to FALSE.

breaks: an optional numeric vector with the breakpoints for the distance intervals to be used in collapsing the semi-variogram values. If not missing, the option specified in collapse is ignored.

metric: an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

...: some methods for this generic require additional arguments. None are used in this method.

Value

A data frame with columns variog and dist representing, respectively, the semi-variogram values and the corresponding distances. If the semi-variogram values are collapsed, an extra column, n.pairs, with the number of residual pairs used in each semi-variogram calculation, is included in the returned data frame. If object includes a corSpatial element, a data frame with its corresponding semi-variogram is included in the returned value, as an attribute "modelVariog". The returned value inherits from class Variogram.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

gls, Variogram, Variogram.default, Variogram.lme, plot.Variogram
Examples

```r
fm1 <- gls(weight ~ Time * Diet, BodyWeight)
Vm1 <- Variogram(fm1, form = ~ Time | Rat)
print(head(Vm1), digits = 3)
```

Description

This method function calculates the semi-variogram for the within-group residuals from an \texttt{lme} fit. The semi-variogram values are calculated for pairs of residuals within the same group. If \texttt{collapse} is different from "none", the individual semi-variogram values are collapsed using either a robust estimator (\texttt{robust = TRUE}) defined in Cressie (1993), or the average of the values within the same distance interval. The semi-variogram is useful for modeling the error term correlation structure.

Usage

```r
## S3 method for class 'lme'
Variogram(object, distance, form, resType, data, na.action, maxDist, length.out, collapse, nint, breaks, robust, metric, ...)
```

Arguments

- \texttt{object}: an object inheriting from class \texttt{"lme"}, representing a fitted linear mixed-effects model.
- \texttt{distance}: an optional numeric vector with the distances between residual pairs. If a grouping variable is present, only the distances between residual pairs within the same group should be given. If missing, the distances are calculated based on the values of the arguments \texttt{form}, \texttt{data}, and \texttt{metric}, unless \texttt{object} includes a \texttt{corSpatial} element, in which case the associated covariate (obtained with the \texttt{getCovariate} method) is used.
- \texttt{form}: an optional one-sided formula specifying the covariate(s) to be used for calculating the distances between residual pairs and, optionally, a grouping factor for partitioning the residuals (which must appear to the right of a | operator in \texttt{form}). Default is \texttt{~1}, implying that the observation order within the groups is used to obtain the distances.
- \texttt{resType}: an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
- \texttt{data}: an optional data frame in which to interpret the variables in \texttt{form}. By default, the same data used to fit \texttt{object} is used.
- \texttt{na.action}: a function that indicates what should happen when the data contain NAs. The default action (\texttt{na.fail}) causes an error message to be printed and the function to terminate, if there are any incomplete observations.
maxDist  an optional numeric value for the maximum distance used for calculating the semi-variogram between two residuals. By default all residual pairs are included.

length.out  an optional integer value. When object includes a corSpatial element, its semi-variogram values are calculated and this argument is used as the length.out argument to the corresponding Variogram method. Defaults to 50.

collapse  an optional character string specifying the type of collapsing to be applied to the individual semi-variogram values. If equal to "quantiles", the semi-variogram values are split according to quantiles of the distance distribution, with equal number of observations per group, with possibly varying distance interval lengths. Else, if "fixed", the semi-variogram values are divided according to distance intervals of equal lengths, with possibly different number of observations per interval. Else, if "none", no collapsing is used and the individual semi-variogram values are returned. Defaults to "quantiles".

nint  an optional integer with the number of intervals to be used when collapsing the semi-variogram values. Defaults to 20.

robust  an optional logical value specifying if a robust semi-variogram estimator should be used when collapsing the individual values. If TRUE the robust estimator is used. Defaults to FALSE.

breaks  an optional numeric vector with the breakpoints for the distance intervals to be used in collapsing the semi-variogram values. If not missing, the option specified in collapse is ignored.

metric  an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".

...  some methods for this generic require additional arguments. None are used in this method.

Value

a data frame with columns variog and dist representing, respectively, the semi-variogram values and the corresponding distances. If the semi-variogram values are collapsed, an extra column, n.pairs, with the number of residual pairs used in each semi-variogram calculation, is included in the returned data frame. If object includes a corSpatial element, a data frame with its corresponding semi-variogram is included in the returned value, as an attribute "modelVariog". The returned value inherits from class Variogram.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

lme, Variogram, Variogram.default, Variogram.gls, plot.Variogram
**Examples**

```r
fm1 <- lme(weight ~ Time * Diet, data=BodyWeight, ~ Time | Rat)
Variogram(fm1, form = ~ Time | Rat, nint = 10, robust = TRUE)
```

**Description**

This function is a constructor for the `varPower` class, representing a power variance function structure. Letting $v$ denote the variance covariate and $\sigma^2(v)$ denote the variance function evaluated at $v$, the power variance function is defined as $\sigma^2(v) = |v|^{2\theta}$, where $\theta$ is the variance function coefficient. When a grouping factor is present, a different $\theta$ is used for each factor level.

**Usage**

```r
varPower(value, form, fixed)
```

**Arguments**

- `value`: an optional numeric vector, or list of numeric values, with the variance function coefficients. Value must have length one, unless a grouping factor is specified in `form`. If `value` has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in `form`. If a grouping factor is present in `form` and `value` has length one, its value will be assigned to all grouping levels. Default is `numeric(0)`, which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).

- `form`: an optional one-sided formula of the form `~ v`, or `~ v | g`, specifying a variance covariate $v$ and, optionally, a grouping factor $g$ for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using ".", representing a fitted model object from which fitted values (fitted(.)) and residuals (resid(.)) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in `form`, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the `*` operator, like in `~ v | g1 * g2 * g3`. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to `~ fitted(.)` representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.

- `fixed`: an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in `form`, `fixed` must have names identifying which coefficients are to be fixed. Coefficients included in `fixed` are not allowed to vary during the optimization of an objective function. Defaults to `NULL`, corresponding to no fixed coefficients.

**Value**

A `varPower` object representing a power variance function structure, also inheriting from class `varFunc`. 
Description

The inverse of the standard deviations corresponding to the variance function structure represented by object are returned.

Usage

varWeights(object)

Arguments

object

an object inheriting from class varFunc, representing a variance function structure.

Value

if object has a weights attribute, its value is returned; else NULL is returned.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

logLik.varFunc, varWeights

Examples

vf1 <- varPower(0.2, form = ~age|Sex)

varWeights(vf1)[1:10]
Variance Weights for glsStruct Object

Description
If object includes a varStruct component, the inverse of the standard deviations of the variance function structure represented by the corresponding varFunc object are returned; else, a vector of ones of length equal to the number of observations in the data frame used to fit the associated linear model is returned.

Usage
## S3 method for class 'glsStruct'
varWeights(object)

Arguments
object
an object inheriting from class "glsStruct", representing a list of linear model components, such as corStruct and "varFunc" objects.

Value
if object includes a varStruct component, a vector with the corresponding variance weights; else, or a vector of ones.

Author(s)
José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References

See Also
varWeights

Variance Weights for lmeStruct Object

Description
If object includes a varStruct component, the inverse of the standard deviations of the variance function structure represented by the corresponding varFunc object are returned; else, a vector of ones of length equal to the number of observations in the data frame used to fit the associated linear mixed-effects model is returned.

Usage
## S3 method for class 'lmeStruct'
varWeights(object)
Arguments

object an object inheriting from class "lmeStruct", representing a list of linear mixed-effects model components, such as reStruct, corStruct, and varFunc objects.

Value

if object includes a varStruct component, a vector with the corresponding variance weights; else, or a vector of ones.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

References


See Also

varWeights

---

Wafer Modeling of Analog MOS Circuits

---

Description

The Wafer data frame has 400 rows and 4 columns.

Format

This data frame contains the following columns:

- Wafer a factor with levels 1 2 3 4 5 6 7 8 9 10
- Site a factor with levels 1 2 3 4 5 6 7 8
- voltage a numeric vector
- current a numeric vector

Source

Wheat Yields by growing conditions

Description
The Wheat data frame has 48 rows and 4 columns.

Format
This data frame contains the following columns:
- **Tray** an ordered factor with levels 3 < 1 < 2 < 4 < 5 < 6 < 8 < 9 < 7 < 12 < 11 < 10
- **Moisture** a numeric vector
- **fertilizer** a numeric vector
- **DryMatter** a numeric vector

Source

Wheat2 Wheat Yield Trials

Description
The Wheat2 data frame has 224 rows and 5 columns.

Format
This data frame contains the following columns:
- **Block** an ordered factor with levels 4 < 2 < 3 < 1
- **variety** a factor with levels ARAPAHOE BRULE BUCKSKIN CENTURA CENTURK78 CHEYENNE CODY COLT GAGE HOMESTEAD KS831374 LANCER LANCOTA NE83404 NE83406 NE83407 NE83432 NE83498 NE83T12 NE84557 NE85556 NE85623 NE86482 NE86501 NE86503 NE86507 NE86509 NE86527 NE86582 NE86606 NE86607 NE86T666 NE87403 NE87408 NE87409 NE87446 NE87451 NE87457 NE87463 NE87499 NE87512 NE87513 NE87522 NE87612 NE87613 NE87615 NE87619 NE87627 NORKAN REDLAND ROUGHRIDER SCOUT66 SIOUXLAND TAM107 TAM200 VONA
- **yield** a numeric vector
- **latitude** a numeric vector
- **longitude** a numeric vector

Source
Description

This method function extracts sub-matrices from the positive-definite matrix represented by x.

Usage

```r
## S3 method for class 'pdMat'
x[i, j, drop = TRUE]
## S3 replacement method for class 'pdMat'
x[i, j] <- value
```

Arguments

- `x`: an object inheriting from class “pdMat” representing a positive-definite matrix.
- `i, j`: optional subscripts applying respectively to the rows and columns of the positive-definite matrix represented by object. When i (j) is omitted, all rows (columns) are extracted.
- `drop`: a logical value. If TRUE, single rows or columns are converted to vectors. If FALSE the returned value retains its matrix representation.
- `value`: a vector, or matrix, with the replacement values for the relevant piece of the matrix represented by x.

Value

if i and j are identical, the returned value will be pdMat object with the same class as x. Otherwise, the returned value will be a matrix. In the case a single row (or column) is selected, the returned value may be converted to a vector, according to the rules above.

Author(s)

José Pinheiro and Douglas Bates <bates@stat.wisc.edu>

See Also

`.pdMat`

Examples

```r
pd1 <- pdSymm(diag(3))
pd1[1, , drop = FALSE]
pd1[1:2, 1:2] <- 3 * diag(2)
```
Chapter 26

The nnet package

class.ind  Generates Class Indicator Matrix from a Factor

Description

Generates a class indicator function from a given factor.

Usage

class.ind(cl)

Arguments

cl factor or vector of classes for cases.

Value

a matrix which is zero except for the column corresponding to the class.

References


Examples

# The function is currently defined as
class.ind <- function(cl)
{
  n <- length(cl)
  cl <- as.factor(cl)
  x <- matrix(0, n, length(levels(cl)) )
  x[1:n] + n*(unclass(cl)-1)] <- 1
  dimnames(x) <- list(names(cl), levels(cl))
  x
}

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**Description**

Fits multinomial log-linear models via neural networks.

**Usage**

```r
multinom(formula, data, weights, subset, na.action,
         contrasts = NULL, Hess = FALSE, summ = 0, censored = FALSE,
         model = FALSE, ...)
```

**Arguments**

- **formula**: a formula expression as for regression models, of the form `response ~ predictors`. The response should be a factor or a matrix with `K` columns, which will be interpreted as counts for each of `K` classes. A log-linear model is fitted, with coefficients zero for the first class. An offset can be included: it should be a numeric matrix with `K` columns if the response is either a matrix with `K` columns or a factor with `K` >= 2 classes, or a numeric vector for a response factor with 2 levels. See the documentation of `formula()` for other details.
- **data**: an optional data frame in which to interpret the variables occurring in `formula`.
- **weights**: optional case weights in fitting.
- **subset**: expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
- **na.action**: a function to filter missing data.
- **contrasts**: a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
- **Hess**: logical for whether the Hessian (the observed/expected information matrix) should be returned.
- **summ**: integer; if non-zero summarize by deleting duplicate rows and adjust weights. Methods 1 and 2 differ in speed (2 uses C); method 3 also combines rows with the same `X` and different `Y`, which changes the baseline for the deviance.
- **censored**: if `Y` is a matrix with `K` columns, interpret the entries as one for possible classes, zero for impossible classes, rather than as counts.
- **model**: logical. If true, the model frame is saved as component `model` of the returned object.
- **...**: additional arguments for `nnet`.

**Details**

`multinom` calls `nnet`. The variables on the rhs of the formula should be roughly scaled to [0,1] or the fit will be slow or may not converge at all.
Value

A nnet object with additional components:

deviance the residual deviance, compared to the full saturated model (that explains individual observations exactly). Also, minus twice log-likelihood.
edf the (effective) number of degrees of freedom used by the model
AIC the AIC for this fit.
Hessian (if Hess is true).
model (if model is true).

References


See Also

nnet

Examples

oc <- options(contrasts = c("contr.treatment", "contr.poly"))
library(MASS)
example(birthwt)
(bwt.mu <- multinom(low ~ ., bwt))
options(oc)

nnet

Fit Neural Networks

Description

Fit single-hidden-layer neural network, possibly with skip-layer connections.

Usage

nnet(x, ...)

## S3 method for class 'formula'
nnet(formula, data, weights, ..., 
    subset, na.action, contrasts = NULL)

## Default S3 method:
nnet(x, y, weights, size, Wts, mask, 
    linout = FALSE, entropy = FALSE, softmax = FALSE, 
    censored = FALSE, skip = FALSE, rang = 0.7, decay = 0, 
    maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000, 
    abstol = 1.0e-4, reltol = 1.0e-8, ...)
Arguments

- **formula**: A formula of the form `class ~ x1 + x2 + ...`
- **x**: matrix or data frame of x values for examples.
- **y**: matrix or data frame of target values for examples.
- **weights**: (case) weights for each example – if missing defaults to 1.
- **size**: number of units in the hidden layer. Can be zero if there are skip-layer units.
- **data**: Data frame from which variables specified in `formula` are preferentially to be taken.
- **subset**: An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
- **na.action**: A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is `na.omit`, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
- **contrasts**: a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
- **Wts**: initial parameter vector. If missing chosen at random.
- **mask**: logical vector indicating which parameters should be optimized (default all).
- **linout**: switch for linear output units. Default logistic output units.
- **entropy**: switch for entropy (= maximum conditional likelihood) fitting. Default by least-squares.
- **softmax**: switch for softmax (log-linear model) and maximum conditional likelihood fitting. `linout`, `entropy`, `softmax` and `censored` are mutually exclusive.
- **censored**: A variant on `softmax`, in which non-zero targets mean possible classes. Thus for `softmax` a row of `(0, 1, 1)` means one example each of classes 2 and 3, but for `censored` it means one example whose class is only known to be 2 or 3.
- **skip**: switch to add skip-layer connections from input to output.
- **rang**: Initial random weights on `[-rang, rang]`. Value about 0.5 unless the inputs are large, in which case it should be chosen so that `rang * max(|x|)` is about 1.
- **decay**: parameter for weight decay. Default 0.
- **maxit**: maximum number of iterations. Default 100.
- **Hess**: If true, the Hessian of the measure of fit at the best set of weights found is returned as component `Hessian`.
- **trace**: switch for tracing optimization. Default `TRUE`.
- **MaxNWts**: The maximum allowable number of weights. There is no intrinsic limit in the code, but increasing `MaxNWts` will probably allow fits that are very slow and time-consuming.
- **abstol**: Stop if the fit criterion falls below `abstol`, indicating an essentially perfect fit.
- **reltol**: Stop if the optimizer is unable to reduce the fit criterion by a factor of at least `1 - reltol`.
- **...**: arguments passed to or from other methods.
Details

If the response in formula is a factor, an appropriate classification network is constructed; this has one output and entropy fit if the number of levels is two, and a number of outputs equal to the number of classes and a softmax output stage for more levels. If the response is not a factor, it is passed on unchanged to nnet.default.

Optimization is done via the BFGS method of optim.

Value

object of class "nnet" or "nnet.formula". Mostly internal structure, but has components

- wts: the best set of weights found
- value: value of fitting criterion plus weight decay term.
- fitted.values: the fitted values for the training data.
- residuals: the residuals for the training data.
- convergence: 1 if the maximum number of iterations was reached, otherwise 0.

References


See Also

predict.nnet, nnetHess

Examples

# use half the iris data
ir <- rbind(iris3[,1], iris3[,2], iris3[,3])
targets <- class.ind( c(rep("s", 50), rep("c", 50), rep("v", 50)) )
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
ir1 <- nnet(ir[samp,], targets[samp,], size = 2, rang = 0.1,
    decay = 5e-4, maxit = 200)
test.cl <- function(true, pred) {
    true <- max.col(true)
    cres <- max.col(pred)
    table(true, cres)
}
test.cl(targets[-samp,], predict(ir1, ir[-samp,]))

# or
ird <- data.frame(rbind(iris3[,1], iris3[,2], iris3[,3]),
    species = factor(c(rep("s",50), rep("c", 50), rep("v", 50)))))
ir.nn2 <- nnet(species ~ ., data = ird, subset = samp, size = 2, rang = 0.1,
    decay = 5e-4, maxit = 200)
table(ird$species[-samp], predict(ir.nn2, ird[-samp,], type = "class"))
Evaluates Hessian for a Neural Network

Description

Evaluates the Hessian (matrix of second derivatives) of the specified neural network. Normally called via argument Hess=TRUE to nnet or via vcov.multinom.

Usage

nnetHess(net, x, y, weights)

Arguments

- net: object of class nnet as returned by nnet.
- x: training data.
- y: classes for training data.
- weights: the (case) weights used in the nnet fit.

Value

square symmetric matrix of the Hessian evaluated at the weights stored in the net.

References


See Also

nnet, predict.nnet

Examples

# use half the iris data
ir <- rbind(iris3[,1], iris3[,2], iris3[,3])
targets <- matrix(c(rep(c(1,0,0),50), rep(c(0,1,0),50), rep(c(0,0,1),50)),
150, 3, byrow=TRUE)
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
ir1 <- nnet(ir[samp,], targets[samp,], size=2, rang=0.1, decay=5e-4, maxit=200)
eigen(nnetHess(ir1, ir[samp,], targets[samp,], TRUE)$values
predict.nnet

Predict New Examples by a Trained Neural Net

Description

Predict new examples by a trained neural net.

Usage

## S3 method for class 'nnet'
predict(object, newdata, type = c("raw","class"), ...)

Arguments

object an object of class nnet as returned by nnet.
newdata matrix or data frame of test examples. A vector is considered to be a row vector comprising a single case.
type Type of output
... arguments passed to or from other methods.

Details

This function is a method for the generic function predict() for class "nnet". It can be invoked by calling predict(x) for an object x of the appropriate class, or directly by calling predict.nnet(x) regardless of the class of the object.

Value

If type = "raw", the matrix of values returned by the trained network; if type = "class", the corresponding class (which is probably only useful if the net was generated by nnet.formula).

References


See Also

nnet, which.is.max

Examples

# use half the iris data
ir <- rbind(iris3[,1], iris3[,2], iris3[,3])
targets <- class.ind( c(rep("s", 50), rep("c", 50), rep("v", 50)) )
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
ir1 <- nnet(ir[samp,], targets[samp,,], size = 2, rang = 0.1,
decay = 5e-4, maxit = 200)
test.cl <- function(true, pred){
  true <- max.col(true)
  cres <- max.col(pred)
  table(true, cres)
```r
which.is.max

Find Maximum Position in Vector

Description
Find the maximum position in a vector, breaking ties at random.

Usage
which.is.max(x)

Arguments
x a vector

Details
Ties are broken at random.

Value
index of a maximal value.

References

See Also
max.col, which.max which takes the first of ties.

Examples
## Not run: ## this is incomplete
pred <- predict(nnet, test)
table(true, apply(pred, 1, which.is.max))
## End(Not run)
```
Chapter 27

The rpart package

---

car.test.frame  Automobile Data from 'Consumer Reports' 1990

Description

The car.test.frame data frame has 60 rows and 8 columns, giving data on makes of cars taken from the April, 1990 issue of Consumer Reports. This is part of a larger dataset, some columns of which are given in cu.summary.

Usage

car.test.frame

Format

This data frame contains the following columns:

Price  a numeric vector giving the list price in US dollars of a standard model
Country of origin, a factor with levels 'France', 'Germany', 'Japan', 'Japan/USA', 'Korea', 'Mexico', 'Sweden' and 'USA'
Reliability  a numeric vector coded 1 to 5.
Mileage  fuel consumption miles per US gallon, as tested.
Type  a factor with levels Compact Large Medium Small Sporty Van
Weight  kerb weight in pounds.
Disp.  the engine capacity (displacement) in litres.
HP  the net horsepower of the vehicle.

Source

Consumer Reports, April, 1990, pp. 235–288 quoted in
See Also

car90, cu.summary

Examples

```r
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
summary(z.auto)
```

---

**car90**  
*Automobile Data from 'Consumer Reports' 1990*

**Description**


**Usage**

```r
data(car90)
```

**Format**

The data frame contains the following columns

- **Country**  
a factor giving the country in which the car was manufactured
- **Disp**  
engine displacement in cubic inches
- **Disp2**  
engine displacement in liters
- **Eng.Rev**  
engine revolutions per mile, or engine speed at 60 mph
- **Front.Hd**  
distance between the car’s head-liner and the head of a 5 ft. 9 in. front seat passenger, in inches, as measured by CU
- **Frt.Leg.Room**  
maximum front leg room, in inches, as measured by CU
- **Frt.Shld**  
front shoulder room, in inches, as measured by CU
- **Gear.Ratio**  
the overall gear ratio, high gear, for manual transmission
- **Gear2**  
the overall gear ratio, high gear, for automatic transmission
- **HP**  
net horsepower
- **HP.revs**  
the red line—the maximum safe engine speed in rpm
- **Height**  
height of car, in inches, as supplied by manufacturer
- **Length**  
overall length, in inches, as supplied by manufacturer
- **Luggage**  
luggage space
- **Mileage**  
a numeric vector of gas mileage in miles/gallon as tested by CU; contains NAs.
- **Model2**  
alternate name, if the car was sold under two labels
- **Price**  
list price with standard equipment, in dollars
- **Rear.Hd**  
distance between the car’s head-liner and the head of a 5 ft 9 in. rear seat passenger, in inches, as measured by CU
- **Rear.Seating**  
rear fore-and-aft seating room, in inches, as measured by CU
RearShld  rear shoulder room, in inches, as measured by CU

Reliability  an ordered factor with levels 'Much worse' < 'worse' < 'average' < 'better' < 'Much better': contains NAs.

Rim  factor giving the rim size

Sratio.m Number of turns of the steering wheel required for a turn of 30 foot radius, manual steering

Sratio.p Number of turns of the steering wheel required for a turn of 30 foot radius, power steering

Steering  steering type offered: manual, power, or both

Tank  fuel refill capacity in gallons

Tires  factor giving tire size

Trans1  manual transmission, a factor with levels '', 'man.4', 'man.5' and 'man.6'

Trans2  automatic transmission, a factor with levels '', 'auto.3', 'auto.4', and 'auto.CVT'. No car is missing both the manual and automatic transmission variables, but several had both as options

Turning  the radius of the turning circle in feet

Type  a factor giving the general type of car. The levels are: ‘Small’, ‘Sporty’, ‘Compact’, ‘Medium’, ‘Large’, ‘Van’

Weight  an order statistic giving the relative weights of the cars; 1 is the lightest and 111 is the heaviest

Wheel.base  length of wheelbase, in inches, as supplied by manufacturer

Width  width of car, in inches, as supplied by manufacturer

Source

This is derived (with permission) from the data set car.all in S-PLUS, but with some further clean up of variable names and definitions.

See Also

car.test.frame, cu.summary for extracts from other versions of the dataset.

Examples

data(car90)
plot(car90$Price/1000, car90$Weight,
    xlab = "Price (thousands)", ylab = "Weight (lbs)"
    mlowess <- function(x, y, ...) {
        keep <- !(is.na(x) | is.na(y))
        lowess(x[keep], y[keep], ...)
    }}
with(car90, lines(mlowess(Price/1000, Weight, f = 0.5)))
Automobile Data from 'Consumer Reports' 1990

Description

The cu.summary data frame has 117 rows and 5 columns, giving data on makes of cars taken from the April, 1990 issue of Consumer Reports.

Usage

cu.summary

Format

This data frame contains the following columns:

Price a numeric vector giving the list price in US dollars of a standard model
Country of origin, a factor with levels 'Brazil', 'England', 'France', 'Germany', 'Japan', 'Japan/USA', 'Korea', 'Mexico', 'Sweden' and 'USA'
Reliability an ordered factor with levels 'Much worse' < 'worse' < 'average' < 'better' < 'Much better'
Mileage fuel consumption miles per US gallon, as tested.
Type a factor with levels Compact Large Medium Small Sporty Van

Source

Consumer Reports, April, 1990, pp. 235–288 quoted in

See Also

car.test.frame, car90

Examples

fit <- rpart(Price ~ Mileage + Type + Country, cu.summary)
par(xpd = TRUE)
plot(fit, compress = TRUE)
text(fit, use.n = TRUE)
**kyphosis**

*Data on Children who have had Corrective Spinal Surgery*

**Description**

The *kyphosis* data frame has 81 rows and 4 columns. representing data on children who have had corrective spinal surgery.

**Usage**

`kyphosis`

**Format**

This data frame contains the following columns:

- **Kyphosis** a factor with levels `absent` `present` indicating if a kyphosis (a type of deformation) was present after the operation.
- **Age** in months
- **Number** the number of vertebrae involved
- **Start** the number of the first (topmost) vertebra operated on.

**Source**


**Examples**

```r
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
fit2 <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis, 
              parms = list(prior = c(0.65, 0.35), split = "information"))
fit3 <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis, 
              control = rpart.control(cp = 0.05))
par(mfrow = c(1,2), xpd = TRUE)
plot(fit)
text(fit, use.n = TRUE)
plot(fit2)
text(fit2, use.n = TRUE)
```

**labels.rpart**

*Create Split Labels For an Rpart Object*

**Description**

This function provides labels for the branches of an `rpart` tree.

**Usage**

```r
## S3 method for class 'rpart'
labels(object, digits = 4, minlength = 1L, pretty, collapse = TRUE, ...)
```
Arguments

object fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
digits the number of digits to be used for numeric values. All of the rpart functions that call labels explicitly set this value, with options("digits") as the default.
minlength the minimum length for abbreviation of character or factor variables. If 0 no abbreviation is done; if 1 single English letters are used, first lower case than upper case (with a maximum of 52 levels). If the value is greater than , the abbreviate function is used, passed the minlength argument.
pretty an argument included for compatibility with the original Splus tree package: pretty = 0 implies minlength = 0L, pretty = NULL implies minlength = 1L, and pretty = TRUE implies minlength = 4L.
collapse logical. The returned set of labels is always of the same length as the number of nodes in the tree.

If collapse = TRUE (default), the returned value is a vector of labels for the branch leading into each node, with "root" as the label for the top node.

If FALSE, the returned value is a two column matrix of labels for the left and right branches leading out from each node, with "leaf" as the branch labels for terminal nodes.

... optional arguments to abbreviate.

Value

Vector of split labels (collapse = TRUE) or matrix of left and right splits (collapse = FALSE) for the supplied rpart object. This function is called by printing methods for rpart and is not intended to be called directly by the users.

See Also

abbreviate

meanvar.rpart         Mean-Variance Plot for an Rpart Object

Description

Creates a plot on the current graphics device of the deviance of the node divided by the number of observations at the node. Also returns the node number.

Usage

meanvar(tree, ...)  

## S3 method for class 'rpart'
meanvar(tree, xlab = "ave(y)", ylab = "ave(deviance)", ...)
Arguments

- **tree**: fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.
- **xlab**: x-axis label for the plot.
- **ylab**: y-axis label for the plot.
- **...**: additional graphical parameters may be supplied as arguments to this function.

Value

An invisible list containing the following vectors is returned.

- **x**: fitted value at terminal nodes (yval).
- **y**: deviance of node divided by number of observations at node.
- **label**: node number.

Side Effects

A plot is put on the current graphics device.

See Also

- `plot.rpart`

Examples

```r
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
meanvar(z.auto, log = 'xy')
```

---

**na.rpart**  
*Handles Missing Values in an Rpart Object*

Description

Handles missing values in an "rpart" object.

Usage

```r
na.rpart(x)
```

Arguments

- **x**: a model frame.

Details

Default function that handles missing values when calling the function `rpart`. It omits cases where part of the response is missing or all the explanatory variables are missing.
path.rpart

Follow Paths to Selected Nodes of an Rpart Object

Description

Returns a names list where each element contains the splits on the path from the root to the selected nodes.

Usage

path.rpart(tree, nodes, pretty = 0, print.it = TRUE)

Arguments

tree  fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.

nodes an integer vector containing indices (node numbers) of all nodes for which paths are desired. If missing, user selects nodes as described below.

pretty an integer denoting the extent to which factor levels in split labels will be abbreviated. A value of (0) signifies no abbreviation. A NULL, the default, signifies using elements of letters to represent the different factor levels.

print.it Logical. Denotes whether paths will be printed out as nodes are interactively selected. Irrelevant if nodes argument is supplied.

Details

The function has a required argument as an rpart object and a list of nodes as optional arguments. Omitting a list of nodes will cause the function to wait for the user to select nodes from the dendrogram. It will return a list, with one component for each node specified or selected. The component contains the sequence of splits leading to that node. In the graphical interaction, the individual paths are printed out as nodes are selected.

Value

A named (by node) list, each element of which contains all the splits on the path from the root to the specified or selected nodes.

Graphical Interaction

A dendrogram of the rpart object is expected to be visible on the graphics device, and a graphics input device (e.g. a mouse) is required. Clicking (the selection button) on a node selects that node. This process may be repeated any number of times. Clicking the exit button will stop the selection process and return the list of paths.

References

This function was modified from path.tree in S.

See Also

rpart
Examples

```r
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
print(fit)
path.rpart(fit, nodes = c(11, 22))
```

---

### plot.rpart

#### Plot an Rpart Object

Plots an `rpart` object on the current graphics device.

**Usage**

```r
## S3 method for class 'rpart'
plot(x, uniform = FALSE, branch = 1, compress = FALSE, nspace,
     margin = 0, minbranch = 0.3, branch.col = 1, branch.lty = 1,
     branch.lwd = 1, ...)
```

**Arguments**

- `x` a fitted object of class "rpart", containing a classification, regression, or rate tree.
- `uniform` if `TRUE`, uniform vertical spacing of the nodes is used; this may be less cluttered when fitting a large plot onto a page. The default is to use a non-uniform spacing proportional to the error in the fit.
- `branch` controls the shape of the branches from parent to child node. Any number from 0 to 1 is allowed. A value of 1 gives square shouldered branches, a value of 0 give V shaped branches, with other values being intermediate.
- `compress` if `FALSE`, the leaf nodes will be at the horizontal plot coordinates of 1:nleaves. If `TRUE`, the routine attempts a more compact arrangement of the tree. The compaction algorithm assumes `uniform=TRUE`; surprisingly, the result is usually an improvement even when that is not the case.
- `nspace` the amount of extra space between a node with children and a leaf, as compared to the minimal space between leaves. Applies to compressed trees only. The default is the value of `branch`.
- `margin` an extra fraction of white space to leave around the borders of the tree. (Long labels sometimes get cut off by the default computation).
- `minbranch` set the minimum length for a branch to `minbranch` times the average branch length. This parameter is ignored if `uniform=TRUE`. Sometimes a split will give very little improvement, or even (in the classification case) no improvement at all. A tree with branch lengths strictly proportional to improvement leaves no room to squeeze in node labels.
- `branch.col` set the color of the branches.
- `branch.lty` set the line type of the branches.
- `branch.lwd` set the line width of the branches.
- `...` arguments to be passed to or from other methods.
plotcp

Plot a Complexity Parameter Table for an Rpart Fit

Description

Gives a visual representation of the cross-validation results in an rpart object.

Usage

plotcp(x, minline = TRUE, lty = 3, col = 1,
upper = c("size", "splits", "none"), ...)

Arguments

x an object of class "rpart"
minline whether a horizontal line is drawn 1SE above the minimum of the curve.
lty line type for this line
col colour for this line
upper what is plotted on the top axis: the size of the tree (the number of leaves), the number of splits or nothing.
... additional plotting parameters
**Details**

The set of possible cost-complexity prunings of a tree from a nested set. For the geometric means of the intervals of values of \( cp \) for which a pruning is optimal, a cross-validation has (usually) been done in the initial construction by `rpart`. The ctp table in the fit contains the mean and standard deviation of the errors in the cross-validated prediction against each of the geometric means, and these are plotted by this function. A good choice of \( cp \) for pruning is often the leftmost value for which the mean lies below the horizontal line.

**Value**

None.

**Side Effects**

A plot is produced on the current graphical device.

**See Also**

`rpart`, `printcp`, `rpart.object`

---

**Description**

Generates a PostScript presentation plot of an `rpart` object.

**Usage**

```r
def post(tree, ...)  # S3 method for class 'rpart'
post(tree, title.,
      filename = paste(deparse(substitute(tree)), ".ps", sep = ""),
      digits = getOption("digits") - 2, pretty = TRUE,
      use.n = TRUE, horizontal = TRUE, ...)
```

**Arguments**

- `tree`: fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.
- `title`: a title which appears at the top of the plot. By default, the name of the `rpart` endpoint is printed out.
- `filename`: ASCII file to contain the output. By default, the name of the file is the name of the object given by `rpart` (with the suffix `.ps` added). If `filename = ""`, the plot appears on the current graphical device.
- `digits`: number of significant digits to include in numerical data.
pretty

an integer denoting the extent to which factor levels will be abbreviated in the character strings defining the splits; (0) signifies no abbreviation of levels. A NULL signifies using elements of letters to represent the different factor levels. The default (TRUE) indicates the maximum possible abbreviation.

use.n

Logical. If TRUE (default), adds to the label #events level1/ #events level2/ etc. for method class, n for method anova, and #events/n for methods poisson and exp).

horizontal

Logical. If TRUE (default), plot is horizontal. If FALSE, plot appears as landscape.

... other arguments to the postscript function.

Details

The plot created uses the functions plot.rpart and text.rpart (with the fancy option). The settings were chosen because they looked good to us, but other options may be better, depending on the rpart object. Users are encouraged to write their own function containing favorite options.

Side Effects

a plot of rpart is created using the postscript driver, or the current device if filename = "".

See Also

plot.rpart, rpart, text.rpart, abbreviate

Examples

## Not run:
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
post(z.auto, file = "") # display tree on active device
# now construct postscript version on file "pretty.ps"
# with no title
post(z.auto, file = "pretty.ps", title = "")
z.hp <- rpart(Mileage ~ Weight + HP, car.test.frame)
post(z.hp)
## End(Not run)

predict.rpart

Predictions from a Fitted Rpart Object

Description

Returns a vector of predicted responses from a fitted rpart object.

Usage

## S3 method for class 'rpart'
predict(object, newdata,
        type = c("vector", "prob", "class", "matrix"),
        na.action = na.pass, ...)
predict.rpart

Arguments

object  fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.

newdata  data frame containing the values at which predictions are required. The predictors referred to in the right side of formula(object) must be present by name in newdata. If missing, the fitted values are returned.

type  character string denoting the type of predicted value returned. If the rpart object is a classification tree, then the default is to return prob predictions, a matrix whose columns are the probability of the first, second, etc. class. (This agrees with the default behavior of tree). Otherwise, a vector result is returned.

na.action  a function to determine what should be done with missing values in newdata. The default is to pass them down the tree using surrogates in the way selected when the model was built. Other possibilities are na.omit and na.fail.

...  further arguments passed to or from other methods.

Details

This function is a method for the generic function predict for class "rpart". It can be invoked by calling predict for an object of the appropriate class, or directly by calling predict.rpart regardless of the class of the object.

Value

A new object is obtained by dropping newdata down the object. For factor predictors, if an observation contains a level not used to grow the tree, it is left at the deepest possible node and frame$yval at the node is the prediction.

If type = "vector":
vector of predicted responses. For regression trees this is the mean response at the node, for Poisson trees it is the estimated response rate, and for classification trees it is the predicted class (as a number).

If type = "prob":
(for a classification tree) a matrix of class probabilities.

If type = "matrix":
a matrix of the full responses (frame$yval if this exists, otherwise frame$yval). For regression trees, this is the mean response, for Poisson trees it is the response rate and the number of events at that node in the fitted tree, and for classification trees it is the concatenation of at least the predicted class, the class counts at that node in the fitted tree, and the class probabilities (some versions of rpart may contain further columns).

If type = "class":
(for a classification tree) a factor of classifications based on the responses.

See Also

predict, rpart.object

Examples

z.auto <- rpart(Mileage ~ Weight, car.test.frame)
predict(z.auto)
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
predict(fit, type = "prob") # class probabilities (default)
predict(fit, type = "vector") # level numbers
predict(fit, type = "class") # factor
predict(fit, type = "matrix") # level number, class frequencies, probabilities

sub <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
fit <- rpart(Species ~ ., data = iris, subset = sub)
fit
table(predict(fit, iris[-sub,], type = "class"), iris[-sub, "Species"])

print.rpart

Print an Rpart Object

Description
This function prints an rpart object. It is a method for the generic function print of class "rpart".

Usage
## S3 method for class 'rpart'
print(x, minlength = 0, spaces = 2, digits =getOption("digits"),
     nsmall = min(20, digits), ...) 

Arguments
x fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
minlength Controls the abbreviation of labels: see labels.rpart.
spaces the number of spaces to indent nodes of increasing depth.
digits the number of digits of numbers to print.
nsmall the number of digits to the right of the decimal. See format.
cp prune all nodes with a complexity less than cp from the printout. Ignored if unspecified.
... arguments to be passed to or from other methods.

Details
This function is a method for the generic function print for class "rpart". It can be invoked by calling print for an object of the appropriate class, or directly by calling print.rpart regardless of the class of the object.

Side Effects
A semi-graphical layout of the contents of x$frame is printed. Indentation is used to convey the tree topology. Information for each node includes the node number, split, size, deviance, and fitted value. For the "class" method, the class probabilities are also printed.
printcp

See Also

print, rpart.object, summary.rpart, printcp

Examples

z.auto <- rpart(Mileage ~ Weight, car.test.frame)
z.auto
## Not run: node, split, n, deviance, yval
 * denotes terminal node

1) root 60 1354.58300 24.58333
  2) Weight>=2567.5 45 361.20000 22.46667
     4) Weight>=3087.5 22 61.31818 20.40909 *
     5) Weight<3087.5 23 117.65220 24.43478
        10) Weight>=2747.5 15 60.40000 23.80000 *
        11) Weight<2747.5 8 39.87500 25.62500 *
  3) Weight<2567.5 15 186.93330 30.93333 *

## End(Not run)

printcp

Displays CP table for Fitted Rpart Object

Description

Displays the cp table for fitted rpart object.

Usage

printcp(x, digits = getOption("digits") - 2)

Arguments

x
fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.

digits
the number of digits of numbers to print.

Details

Prints a table of optimal prunings based on a complexity parameter.

See Also

summary.rpart, rpart.object
Examples

```r
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
printcp(z.auto)
## Not run:
Regression tree:
rpart(formula = Mileage ~ Weight, data = car.test.frame)

Variables actually used in tree construction:
[1] Weight

Root node error: 1354.6/60 = 22.576

<table>
<thead>
<tr>
<th>CP</th>
<th>nsplit</th>
<th>rel error</th>
<th>xerror</th>
<th>xstd</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.595349</td>
<td>0</td>
<td>1.00000</td>
<td>1.03436</td>
</tr>
<tr>
<td>2</td>
<td>0.134528</td>
<td>1</td>
<td>0.40465</td>
<td>0.60508</td>
</tr>
<tr>
<td>3</td>
<td>0.012828</td>
<td>2</td>
<td>0.27012</td>
<td>0.45153</td>
</tr>
<tr>
<td>4</td>
<td>0.010000</td>
<td>3</td>
<td>0.25729</td>
<td>0.44826</td>
</tr>
</tbody>
</table>

## End(Not run)
```

prune.rpart

Cost-complexity Pruning of an Rpart Object

Description

Determines a nested sequence of subtrees of the supplied `rpart` object by recursively snipping off the least important splits, based on the complexity parameter (`cp`).

Usage

```r
prune(tree, ...)
```

## S3 method for class 'rpart'
```r
prune(tree, cp, ...)
```

Arguments

- `tree` : fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.
- `cp` : Complexity parameter to which the `rpart` object will be trimmed.
- `...` : further arguments passed to or from other methods.

Value

A new `rpart` object that is trimmed to the value `cp`.

See Also

`rpart`
Examples

z.auto <- rpart(Mileage ~ Weight, car.test.frame)
zp <- prune(z.auto, cp = 0.1)
plot(zp) # plot smaller rpart object

residuals.rpart Residuals From a Fitted rpart Object

Description

Method for residuals for an rpart object.

Usage

## S3 method for class 'rpart'
residuals(object, type = c("usual", "pearson", "deviance"), ...)

Arguments

  object fitted model object of class "rpart".
  type Indicates the type of residual desired.
           For regression or anova trees all three residual definitions reduce to y - fitted. This is the residual returned for user method trees as well.
           For classification trees the usual residuals are the misclassification losses L(actual, predicted) where L is the loss matrix. With default losses this residual is 0/1 for correct/incorrect classification. The pearson residual is (1-fitted)/sqrt(fitted(1-fitted)) and the deviance residual is sqrt(minus twice logarithm of fitted).
           For poisson and exp (or survival) trees, the usual residual is the observed - expected number of events. The pearson and deviance residuals are as defined in McCullagh and Nelder.
           ... further arguments passed to or from other methods.

Value

Vector of residuals of type type from a fitted rpart object.

References


Examples

fit <- rpart(skips ~ Opening + Solder + Mask + PadType + Panel,
data = solder.balance, method = "anova")
summary(residuals(fit))
plot(predict(fit), residuals(fit))
rpart

Recursive Partitioning and Regression Trees

Description
Fit a rpart model

Usage
rpart(formula, data, weights, subset, na.action = na.rpart, method,
model = FALSE, x = FALSE, y = TRUE, parms, control, cost, ...)

Arguments
formula a formula, with a response but no interaction terms. If this is a data frame, it is
taken as the model frame (see model.frame).
data an optional data frame in which to interpret the variables named in the formula.
weights optional case weights.
subset optional expression saying that only a subset of the rows of the data should be
used in the fit.
na.action the default action deletes all observations for which y is missing, but keeps those
in which one or more predictors are missing.
method one of "anova", "poisson", "class" or "exp". If method is missing then the
routine tries to make an intelligent guess. If y is a survival object, then method = 
"exp" is assumed, if y has 2 columns then method = "poisson" is assumed, if
y is a factor then method = "class" is assumed, otherwise method = "anova" is
assumed. It is wisest to specify the method directly, especially as more criteria
may added to the function in future.
Alternatively, method can be a list of functions named init, split and eval.
Examples are given in the file 'tests/usersplits.R' in the sources, and in the
vignettes 'User Written Split Functions'.
model if logical: keep a copy of the model frame in the result? If the input value for
model is a model frame (likely from an earlier call to the rpart function), then
this frame is used rather than constructing new data.
x keep a copy of the x matrix in the result.
y keep a copy of the dependent variable in the result. If missing and model is
supplied this defaults to FALSE.
parms optional parameters for the splitting function.
Anova splitting has no parameters.
Poisson splitting has a single parameter, the coefficient of variation of the prior
distribution on the rates. The default value is 1.
Exponential splitting has the same parameter as Poisson.
For classification splitting, the list can contain any of: the vector of prior prob-
babilities (component prior), the loss matrix (component loss) or the splitting
index (component split). The priors must be positive and sum to 1. The loss
matrix must have zeros on the diagonal and positive off-diagonal elements. The
splitting index can be gini or information. The default priors are proportional
to the data counts, the losses default to 1, and the split defaults to gini.
control: a list of options that control details of the rpart algorithm. See \rpart.control. 
cost: a vector of non-negative costs, one for each variable in the model. Defaults to 
one for all variables. These are scalings to be applied when considering splits, 
so the improvement on splitting on a variable is divided by its cost in deciding 
which split to choose.

Arguments to \rpart.control may also be specified in the call to \rpart. They 
are checked against the list of valid arguments.

Details

This differs from the tree function in S mainly in its handling of surrogate variables. In most 
details it follows Breiman et. al (1984) quite closely. R package \texttt{tree} provides a re-implementation 
of tree.

Value

An object of class \texttt{rpart}. See \texttt{rpart.object}.

References

Trees}. Wadsworth.

See Also

\texttt{rpart.control}, \texttt{rpart.object}, \texttt{summary.rpart}, \texttt{print.rpart}

Examples

```r
fit <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis)
fit2 <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis, 
parms = list(prior = c(.65,.35), split = "information"))
fit3 <- rpart(Kyphosis ~ Age + Number + Start, data = kyphosis, 
control = rpart.control(cp = 0.05))
par(mfrow = c(1,2), xpd = NA) # otherwise on some devices the text is clipped
plot(fit)
text(fit, use.n = TRUE)
plot(fit2)
text(fit2, use.n = TRUE)
```
Arguments

**minsplit**
the minimum number of observations that must exist in a node in order for a split to be attempted.

**minbucket**
the minimum number of observations in any terminal <leaf> node. If only one of minbucket or minsplit is specified, the code either sets minsplit to minbucket*3 or minbucket to minsplit/3, as appropriate.

**cp**
complexity parameter. Any split that does not decrease the overall lack of fit by a factor of cp is not attempted. For instance, with anova splitting, this means that the overall R-squared must increase by cp at each step. The main role of this parameter is to save computing time by pruning off splits that are obviously not worthwhile. Essentially, the user informs the program that any split which does not improve the fit by cp will likely be pruned off by cross-validation, and that hence the program need not pursue it.

**maxcompete**
the number of competitor splits retained in the output. It is useful to know not just which split was chosen, but which variable came in second, third, etc.

**maxsurrogate**
the number of surrogate splits retained in the output. If this is set to zero the compute time will be reduced, since approximately half of the computational time (other than setup) is used in the search for surrogate splits.

**usesurrogate**
how to use surrogates in the splitting process. 0 means display only; an observation with a missing value for the primary split rule is not sent further down the tree. 1 means use surrogates, in order, to split subjects missing the primary variable; if all surrogates are missing the observation is not split. For value 2, if all surrogates are missing, then send the observation in the majority direction. A value of 0 corresponds to the action of tree, and 2 to the recommendations of Breiman et.al (1984).

**xval**
number of cross-validations.

**surrogatestyle**
controls the selection of a best surrogate. If set to 0 (default) the program uses the total number of correct classification for a potential surrogate variable, if set to 1 it uses the percent correct, calculated over the non-missing values of the surrogate. The first option more severely penalizes covariates with a large number of missing values.

**maxdepth**
Set the maximum depth of any node of the final tree, with the root node counted as depth 0. Values greater than 30 rpart will give nonsense results on 32-bit machines.

... mop up other arguments.

Value

A list containing the options.

See Also

rpart
rpart.exp

Initialization function for exponential fitting

Description

This function does the initialization step for rpart, when the response is a survival object. It rescales the data so as to have an exponential baseline hazard and then uses Poisson methods. This function would rarely if ever be called directly by a user.

Usage

rpart.exp(y, offset, parms, wt)

Arguments

- **y**: the response, which will be of class Surv
- **offset**: optional offset
- **parms**: parameters controlling the fit. This is a list with components shrink and method. The first is the prior for the coefficient of variation of the predictions. The second is either "deviance" or "sqrt" and is the measure used for cross-validation. If values are missing the defaults are used, which are "deviance" for the method, and a shrinkage of 1.0 for the deviance method and 0 for the square root.
- **wt**: case weights, if present

Value

a list with the necessary initialization components

Author(s)

Terry Therneau

See Also

rpart

rpart.object

Recursive Partitioning and Regression Trees Object

Description

These are objects representing fitted rpart trees.
Value

frame

data frame with one row for each node in the tree. The row.names of frame contain the (unique) node numbers that follow a binary ordering indexed by node depth. Columns of frame include var, a factor giving the names of the variables used in the split at each node (leaf nodes are denoted by the level "<leaf>"); n, the number of observations reaching the node, wt, the sum of case weights for observations reaching the node, dev, the deviance of the node; yval, the fitted value of the response at the node; and splits, a two column matrix of left and right split labels for each node. Also included in the frame are complexity, the complexity parameter at which this split will collapse, ncompete, the number of competitor splits recorded, and nsurrogate, the number of surrogate splits recorded.

Extra response information which may be present is in yval2, which contains the number of events at the node (poisson tree), or a matrix containing the fitted class, the class counts for each node, the class probabilities and the 'node probability' (classification trees).

where

an integer vector of the same length as the number of observations in the root node, containing the row number of frame corresponding to the leaf node that each observation falls into.

call

an image of the call that produced the object, but with the arguments all named and with the actual formula included as the formula argument. To re-evaluate the call, say update(tree).

terms

an object of class c("terms", "formula") (see terms.object) summarizing the formula. Used by various methods, but typically not of direct relevance to users.

splits

a numeric matrix describing the splits: only present if there are any. The row label is the name of the split variable, and columns are count, the number of observations (which are not missing and are of positive weight) sent left or right by the split (for competitor splits this is the number that would have been sent left or right had this split been used, for surrogate splits it is the number missing the primary split variable which were decided using this surrogate), ncat, the number of categories or levels for the variable (+/-1 for a continuous variable), improve, which is the improvement in deviance given by this split, or, for surrogates, the concordance of the surrogate with the primary, and index, the numeric split point. The last column adj gives the adjusted concordance for surrogate splits. For a factor, the index column contains the row number of the csplit matrix. For a continuous variable, the sign of ncat determines whether the subset x < cutpoint or x > cutpoint is sent to the left.

csplit

an integer matrix. (Only present only if at least one of the split variables is a factor or ordered factor.) There is a row for each such split, and the number of columns is the largest number of levels in the factors. Which row is given by the index column of the splits matrix. The columns record 1 if that level of the factor goes to the left, 3 if it goes to the right, and 2 if that level is not present at this node of the tree (or not defined for the factor).

method

character string: the method used to grow the tree. One of "class", "exp", "poisson", "anova" or "user" (if splitting functions were supplied).

cptable

a matrix of information on the optimal prunings based on a complexity parameter.
variable.importance
  a named numeric vector giving the importance of each variable. (Only present if there are any splits.) When printed by summary.rpart these are rescaled to add to 100.

numresp
  integer number of responses; the number of levels for a factor response.

parms, control
  a record of the arguments supplied, which defaults filled in.

functions
  the summary, print and text functions for method used.

ordered
  a named logical vector recording for each variable if it was an ordered factor.

na.action
  (where relevant) information returned by model.frame on the special handling of NAs derived from the na.action argument.

There may be attributes "xlevels" and "levels" recording the levels of any factor splitting variables and of a factor response respectively.

Optional components include the model frame (model), the matrix of predictors (x) and the response variable (y) used to construct the rpart object.

Structure
The following components must be included in a legitimate rpart object.

See Also
rpart.

---

rsq.rpart

Plots the Approximate R-Square for the Different Splits

Description
Produces 2 plots. The first plots the r-square (apparent and apparent - from cross-validation) versus the number of splits. The second plots the Relative Error(cross-validation) +/- 1-SE from cross-validation versus the number of splits.

Usage
rsq.rpart(x)

Arguments
  x  fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.

Side Effects
Two plots are produced.

Note
The labels are only appropriate for the "anova" method.
**Examples**

```r
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
rsq.rpart(z.auto)
```

---

**Description**

Creates a "snipped" rpart object, containing the nodes that remain after selected subtrees have been snipped off. The user can snip nodes using the toss argument, or interactively by clicking the mouse button on specified nodes within the graphics window.

**Usage**

```r
snip.rpart(x, toss)
```

**Arguments**

- `x` fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.
- `toss` an integer vector containing indices (node numbers) of all subtrees to be snipped off. If missing, user selects branches to snip off as described below.

**Details**

A dendrogram of `rpart` is expected to be visible on the graphics device, and a graphics input device (e.g., a mouse) is required. Clicking (the selection button) on a node displays the node number, sample size, response y-value, and Error (dev). Clicking a second time on the same node snips that subtree off and visually erases the subtree. This process may be repeated an number of times. Warnings result from selecting the root or leaf nodes. Clicking the exit button will stop the snipping process and return the resulting `rpart` object.

See the documentation for the specific graphics device for details on graphical input techniques.

**Value**

A `rpart` object containing the nodes that remain after specified or selected subtrees have been snipped off.

**Warning**

Visually erasing the plot is done by over-plotting with the background colour. This will do nothing if the background is transparent (often true for screen devices).

**See Also**

- `plot.rpart`
solder.balance

Examples

```r
## dataset not in R
## Not run:
z.survey <- rpart(market.survey) # grow the rpart object
plot(z.survey) # plot the tree
z.survey2 <- snip.rpart(z.survey, toss = 2) # trim subtree at node 2
plot(z.survey2) # plot new tree

# can also interactively select the node using the mouse in the
# graphics window

## End(Not run)
```

## solder.balance

### Soldering of Components on Printed-Circuit Boards

#### Description

The `solder.balance` data frame has 720 rows and 6 columns, representing a balanced subset of a designed experiment varying 5 factors on the soldering of components on printed-circuit boards.

The `solder` data frame is the full version of the data with 900 rows. It is located in both the `rpart` and the `survival` packages.

#### Usage

```r
solder
```

#### Format

This data frame contains the following columns:

- **Opening**: a factor with levels ‘L’, ‘M’ and ‘S’ indicating the amount of clearance around the mounting pad.
- **Solder**: a factor with levels ‘Thick’ and ‘Thin’ giving the thickness of the solder used.
- **Mask**: a factor with levels ‘A1.5’, ‘A3’, ‘B3’ and ‘B6’ indicating the type and thickness of mask used.
- **Panel**: 1:3 indicating the panel on a board being tested.
- **skips**: a numeric vector giving the number of visible solder skips.

#### Source


#### Examples

```r
fit <- rpart(skips ~ Opening + Solder + Mask + PadType + Panel,
             data = solder.balance, method = "anova")
summary(residuals(fit))
plot(predict(fit), residuals(fit))
```
**stagec**  
*Stage C Prostate Cancer*

**Description**
A set of 146 patients with stage C prostate cancer, from a study exploring the prognostic value of flow cytometry.

**Usage**
data(stagec)

**Format**
A data frame with 146 observations on the following 8 variables.

- **pgtime**  Time to progression or last follow-up (years)
- **pgstat**  1 = progression observed, 0 = censored
- **age**  age in years
- **eet**  early endocrine therapy, 1 = no, 2 = yes
- **g2**  percent of cells in G2 phase, as found by flow cytometry
- **grade**  grade of the tumor, Farrow system
- **gleason**  grade of the tumor, Gleason system
- **ploidy**  the ploidy status of the tumor, from flow cytometry. Values are ‘diploid’, ‘tetraploid’, and ‘aneuploid’

**Details**
A tumor is called diploid (normal complement of dividing cells) if the fraction of cells in G2 phase was determined to be 13% or less. Aneuploid cells have a measurable fraction with a chromosome count that is neither 24 nor 48, for these the G2 percent is difficult or impossible to measure.

**Examples**
```r
require(survival)
rpart(Surv(pgtime, pgstat) ~ ., stagec)
```

---

**summary.rpart**  
*Summarize a Fitted Rpart Object*

**Description**
Returns a detailed listing of a fitted rpart object.

**Usage**
```r
## S3 method for class 'rpart'
summary(object, cp = 0, digits = getOption("digits"), file, ...)
```
text.rpart

Arguments

object  fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.
digits  Number of significant digits to be used in the result.
cp  trim nodes with a complexity of less than cp from the listing.
file  write the output to a given file name. (Full listings of a tree are often quite long).
...  arguments to be passed to or from other methods.

Details

This function is a method for the generic function summary for class "rpart". It can be invoked by calling summary for an object of the appropriate class, or directly by calling summary.rpart regardless of the class of the object.

It prints the call, the table shown by printcp, the variable importance (summing to 100) and details for each node (the details depending on the type of tree).

See Also

summary.rpart.object.printcp.

Examples

## a regression tree
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
summary(z.auto)

## a classification tree with multiple variables and surrogate splits.
summary(rpart(Kyphosis ~ Age + Number + Start, data = kyphosis))

---

text.rpart  Place Text on a Dendrogram Plot

Description

Labels the current plot of the tree dendrogram with text.

Usage

## S3 method for class 'rpart'
text(x, splits = TRUE, label, FUN = text, all = FALSE,
      pretty = NULL, digits =getOption("digits") - 3, use.n = FALSE,
      fancy = FALSE, fwidth = 0.8, fheight = 0.8, bg = par("bg"),
      minlength = 1L, ...)
Arguments

x fitted model object of class "rpart". This is assumed to be the result of some function that produces an object with the same named components as that returned by the rpart function.

splits logical flag. If TRUE (default), then the splits in the tree are labeled with the criterion for the split.

label For compatibility with rpart2, ignored in this version (with a warning).

FUN the name of a labeling function, e.g. text.

all Logical. If TRUE, all nodes are labeled, otherwise just terminal nodes.

minlength the length to use for factor labels. A value of 1 causes them to be printed as 'a', 'b', .... Larger values use abbreviations of the label names. See the labels.rpart function for details.

pretty an alternative to the minlength argument, see labels.rpart.

digits number of significant digits to include in numerical labels.

use.n Logical. If TRUE, adds to label (#events level1/ #events level2/ etc. for class, n for anova, and #events/n for poisson and exp).

fancy Logical. If TRUE, nodes are represented by ellipses (interior nodes) and rectangles (leaves) and labeled by yval. The edges connecting the nodes are labeled by left and right splits.

fwidth Relates to option fancy and the width of the ellipses and rectangles. If fwidth < 1 then it is a scaling factor (default = 0.8). If fwidth > 1 then it represents the number of character widths (for current graphical device) to use.

fheight Relates to option fancy and the height of the ellipses and rectangles. If fheight < 1 then it is a scaling factor (default = 0.8). If fheight > 1 then it represents the number of character heights (for current graphical device) to use.

bg The color used to paint the background to annotations if fancy = TRUE.

... Graphical parameters may also be supplied as arguments to this function (see par). As labels often extend outside the plot region it can be helpful to specify xpd = TRUE.

Side Effects

the current plot of a tree dendrogram is labeled.

See Also
text.plot.rpart, rpart, labels.rpart, abbreviate

Examples

defree.tr <- rpart(y ~ ., freeny)
par(xpd = TRUE)
plot(free.tr)
text(free.tr, use.n = TRUE, all = TRUE)
xpred.rpart

Return Cross-Validated Predictions

Description

Gives the predicted values for an \texttt{rpart} fit, under cross validation, for a set of complexity parameter values.

Usage

\texttt{xpred.rpart(fit, xval = 10, cp, return.all = FALSE)}

Arguments

- \texttt{fit}: a object of class \texttt{"rpart"}.
- \texttt{xval}: number of cross-validation groups. This may also be an explicit list of integers that define the cross-validation groups.
- \texttt{cp}: the desired list of complexity values. By default it is taken from the \texttt{cptable} component of the fit.
- \texttt{return.all}: if FALSE return only the first element of the prediction

Details

Complexity penalties are actually ranges, not values. If the \texttt{cp} values found in the table were \(0.36, 0.28, \text{and} 0.13\), for instance, this means that the first row of the table holds for all complexity penalties in the range \([0.36, 1]\), the second row for \texttt{cp} in the range \([0.28, 0.36]\) and the third row for \([0.13, 0.28]\). By default, the geometric mean of each interval is used for cross validation.

Value

A matrix with one row for each observation and one column for each complexity value. If \texttt{return.all} is TRUE and the prediction for each node is a vector, then the result will be an array containing all of the predictions. When the response is categorical, for instance, the result contains the predicted class followed by the class probabilities of the selected terminal node; \texttt{result[1,,]} will be the matrix of predicted classes, \texttt{result[2,,]} the matrix of class 1 probabilities, etc.

See Also

\texttt{rpart}

Examples

\begin{verbatim}
fit <- rpart(Mileage ~ Weight, car.test.frame)
xmat <- xpred.rpart(fit)
xerr <- (xmat - car.test.frame$Mileage)^2
apply(xerr, 2, sum)  # cross-validated error estimate

# approx same result as rel. error from printcp(fit)
apply(xerr, 2, sum)/var(car.test.frame$Mileage)
printcp(fit)
\end{verbatim}
Chapter 28

The spatial package

### anova.trls

Anova tables for fitted trend surface objects

**Description**

Compute analysis of variance tables for one or more fitted trend surface model objects; where `anova.trls` is called with multiple objects, it passes on the arguments to `anovalist.trls`.

**Usage**

```r
## S3 method for class 'trls'
anova(object, ...)
anovalist.trls(object, ...)
```

**Arguments**

- `object` A fitted trend surface model object from `surf.ls`
- `...` Further objects of the same kind

**Value**

`anova.trls` and `anovalist.trls` return objects corresponding to their printed tabular output.

**References**


**See Also**

`surf.ls`
correlogram

Examples

library(stats)
data(topo, package="MASS")
topo0 <- surf.ls(0, topo)
topo1 <- surf.ls(1, topo)
topo2 <- surf.ls(2, topo)
topo3 <- surf.ls(3, topo)
topo4 <- surf.ls(4, topo)
anova(topo0, topo1, topo2, topo3, topo4)
summary(topo4)

correlogram

Compute Spatial Correlograms

Description

Compute spatial correlograms of spatial data or residuals.

Usage

correlogram(krig, nint, plotit = TRUE, ...)

Arguments

krig  trend-surface or kriging object with columns x, y, and z
nint  number of bins used
plotit logical for plotting
...   parameters for the plot

Details

Divides range of data into nint bins, and computes the covariance for pairs with separation in each bin, then divides by the variance. Returns results for bins with 6 or more pairs.

Value

x and y coordinates of the correlogram, and cnt, the number of pairs averaged per bin.

Side Effects

Plots the correlogram if plotit = TRUE.

References


See Also

variogram
Examples

```r
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
correlogram(topo.kr, 25)
d <- seq(0, 7, 0.1)
lines(d, expcov(d, 0.7))
```

### Description
Spatial covariance functions for use with `surf.gls`.

### Usage

```r
expcov(r, d, alpha = 0, se = 1)
gaucov(r, d, alpha = 0, se = 1)
sphercov(r, d, alpha = 0, se = 1, D = 2)
```

### Arguments

- `r`: vector of distances at which to evaluate the covariance
- `d`: range parameter
- `alpha`: proportion of nugget effect
- `se`: standard deviation at distance zero
- `D`: dimension of spheres.

### Value
vector of covariance values.

### References


### See Also

- `surf.gls`

### Examples

```r
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
correlogram(topo.kr, 25)
d <- seq(0, 7, 0.1)
lines(d, expcov(d, 0.7))
```
Kaver

**Average K-functions from Simulations**

**Description**

Forms the average of a series of (usually simulated) K-functions.

**Usage**

```r
Kaver(fs, nsim, ...)
```

**Arguments**

- `fs`: full scale for K-fn
- `nsim`: number of simulations
- `...`: arguments to simulate one point process object

**Value**

list with components `x` and `y` of the average K-fn on L-scale.

**References**


**See Also**

`Kfn`, `Kenvl`

**Examples**

```r
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 40), type="b")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
lims <- Kenvl(10,100,Psim(69))
lines(lims$x,lims$lower, lty=2, col="green")
lines(lims$x,lims$upper, lty=2, col="green")
lines(Kaver(10,25,Strauss(69,0.5,3.5)), col="red")
```
**Kenvl**

*Compute Envelope and Average of Simulations of K-fns*

**Description**

Computes envelope (upper and lower limits) and average of simulations of K-fns.

**Usage**

```r
Kenvl(fs, nsim, ...)
```

**Arguments**

- `fs`: full scale for K-fn
- `nsim`: number of simulations
- `...`: arguments to produce one simulation

**Value**

List with components:

- `x`: distances
- `lower`: min of K-fns
- `upper`: max of K-fns
- `aver`: average of K-fns

**References**


**See Also**

- `Kfn`, `Kaver`

**Examples**

```r
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 40), type="b")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
lims <- Kenvl(10,100,Psim(69))
lines(lims$x,lims$lower, lty=2, col="green")
lines(lims$x,lims$upper, lty=2, col="green")
lines(Kaver(10,25,Strauss(69,0.5,3.5)), col="red")
```
Kfn

Compute K-fn of a Point Pattern

Description

Actually computes \( L = \sqrt{K/\pi} \).

Usage

Kfn(pp, fs, k=100)

Arguments

pp a list such as a pp object, including components x and y
fs full scale of the plot
k number of regularly spaced distances in (0, fs)

Details

relies on the domain D having been set by ppinit or ppregion.

Value

A list with components

x vector of distances
y vector of L-fn values
k number of distances returned – may be less than k if fs is too large
dmin minimum distance between pair of points
lm maximum deviation from \( L(t) = t \)

References


See Also

ppinit, ppregion, Kaver, Kenvl

Examples

towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="s", xlab="distance", ylab="L(t)")
ppgetregion

\textit{Get Domain for Spatial Point Pattern Analyses}

\begin{description}
\item[Description] Retrieves the rectangular domain \((x_l, x_u) \times (y_l, y_u)\) from the underlying \(C\) code.
\item[Usage] \texttt{ppgetregion()}
\item[Value] A vector of length four with names \(c("x_l", "x_u", "y_l", "y_u")\).
\item[See Also] \texttt{ppregion}
\end{description}

\begin{description}
\item[ppinit] \textit{Read a Point Process Object from a File}

\item[Description] Read a file in standard format and create a point process object.
\item[Usage] \texttt{ppinit(file)}
\item[Arguments]
\begin{description}
\item[file] string giving file name
\end{description}
\item[Details] The file should contain
the number of points
a header (ignored)
\(x_l\) \(x_u\) \(y_l\) \(y_u\) scale
\(x\) \(y\) (repeated \(n\) times)
\item[Value] class "pp" object with components \(x, y, x_l, x_u, y_l, y_u\)
Side Effects

Calls `ppregion` to set the domain.

References


See Also

`ppregion`

Examples

towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")

---

pplik function

Pseudo-likelihood Estimation of a Strauss Spatial Point Process

Description

Pseudo-likelihood estimation of a Strauss spatial point process.

Usage

```r
pplik(pp, R, ng=50, trace=FALSE)
```

Arguments

- `pp`: a pp object
- `R`: the fixed parameter R
- `ng`: use a `ng x ng` grid with border R in the domain for numerical integration.
- `trace`: logical? Should function evaluations be printed?

Value

estimate for \( c \) in the interval \([0, 1]\).

References


See Also

`Strauss`

Examples

```r
pines <- ppinit("pines.dat")
pplik(pines, 0.7)
```
**ppregion**  
*Set Domain for Spatial Point Pattern Analyses*

### Description

Sets the rectangular domain \((xl, xu) \times (yl, yu)\).

### Usage

```r
ppregion(xl = 0, xu = 1, yl = 0, yu = 1)
```

### Arguments

- `xl`  
  Either `xl` or a list containing components `xl`, `xu`, `yl`, `yu` (such as a point-process object)

- `xu`, `yl`, `yu`  
  Other limits of the rectangle if given separately.

### Value

None

### Side Effects

Initializes variables in the C subroutines.

### References


### See Also

ppinit, ppgetregion

---

**predict.trls**  
*Predict method for trend surface fits*

### Description

Predicted values based on trend surface model object

### Usage

```r
## S3 method for class 'trls'
predict(object, x, y, ...)
```

### Arguments

- `object`  
  Fitted trend surface model object returned by `surf.ls`

- `x`  
  Vector of prediction location eastings (x coordinates)

- `y`  
  Vector of prediction location northings (y coordinates)

- `...`  
  Further arguments passed to or from other methods.
Value

predict.trls produces a vector of predictions corresponding to the prediction locations. To display the output with image or contour, use trmat or convert the returned vector to matrix form.

References


See Also

surf.ls, trmat

Examples

data(topo, package="MASS")
topo2 <- surf.ls(2, topo)
topo4 <- surf.ls(4, topo)
x <- c(1.78, 2.21)
y <- c(6.15, 6.15)
z2 <- predict(topo2, x, y)
z4 <- predict(topo4, x, y)
cat("2nd order predictions:", z2, "\n4th order predictions:", z4, "\n")
Psim

Simulate Binomial Spatial Point Process

Description

Simulate Binomial spatial point process.

Usage

Psim(n)

Arguments

n  number of points

Details

relies on the region being set by ppinit or ppregion.

Value

list of vectors of x and y coordinates.

Side Effects

uses the random number generator.

References


See Also

SSI, Strauss

Examples

towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="s", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
semat

Evaluate Kriging Standard Error of Prediction over a Grid

Description

Evaluate Kriging standard error of prediction over a grid.

Usage

semat(obj, xl, xu, yl, yu, n, se)

Arguments

obj object returned by surf.gls
xl limits of the rectangle for grid
xu ditto
yl ditto
yu ditto
n use n x n grid within the rectangle
se standard error at distance zero as a multiple of the supplied covariance. Otherwise estimated, and it assumed that a correlation function was supplied.

Value

list with components x, y and z suitable for contour and image.

References


See Also

surf.gls, trmat, prmat

Examples

data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
contour(prsurf, levels=seq(700, 925, 25))

sesurf <- semat(topo.kr, 0, 6.5, 0, 6.5, 30)
contour(sesurf, levels=c(22,25))
Simulates Sequential Spatial Inhibition Point Process

Description

Simulates SSI (sequential spatial inhibition) point process.

Usage

SSI(n, r)

Arguments

n  number of points
r  inhibition distance

Details

uses the region set by ppinit or ppregion.

Value

list of vectors of x and y coordinates

Side Effects

uses the random number generator.

Warnings

will never return if r is too large and it cannot place n points.

References


See Also

Psim, Strauss

Examples

towns <- ppinit("towns.dat")
par(pty = "s")
plot(Kfn(towns, 10), type = "b", xlab = "distance", ylab = "L(t)")
lines(Kaver(10, 25, SSI(69, 1.2)))
Simulates Strauss spatial point process.

Usage

```
Strauss(n, c=0, r)
```

Arguments

- `n`: number of points
- `c`: parameter in \([0, 1]\). \(c = 0\) corresponds to complete inhibition at distances up to \(r\).
- `r`: inhibition distance

Details

Uses spatial birth-and-death process for \(4n\) steps, or for \(40n\) steps starting from a binomial pattern on the first call from another function. Uses the region set by `ppinit` or `ppregion`.

Value

List of vectors of \(x\) and \(y\) coordinates

Side Effects

Uses the random number generator

References


See Also

`Psim`, `SSI`

Examples

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
lines(Kaver(10, 25, Strauss(69,0.5,3.5)))
```
Fits a Trend Surface by Generalized Least-squares

Description
Fits a trend surface by generalized least-squares.

Usage
surf.gls(np, covmod, x, y, z, nx = 1000, ...)

Arguments
np
degree of polynomial surface
covmod
function to evaluate covariance or correlation function
x
x coordinates or a data frame with columns x, y, z
y
y coordinates
z
z coordinates. Will supersede x$z
nx
Number of bins for table of the covariance. Increasing adds accuracy, and increases size of the object.
...
parameters for covmod

Value
list with components
beta
the coefficients
x
y
z
and others for internal use only.

References

See Also
trmat, surf.ls, prmat, semat, expcov, gauccov, sphercov

Examples
library(MASS) # for eqscplot
data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)
prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
surf.ls

fits a trend surface by least-squares.

Usage

surf.ls(np, x, y, z)

Arguments

np degree of polynomial surface
x x coordinates or a data frame with columns x, y, z
y y coordinates
z z coordinates. Will supersede x$z

Value

list with components

beta the coefficients
x
y
z and others for internal use only.

References


See Also

trmat, surf.gls
Examples

library(MASS) # for eqscplot
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)
points(topo)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)
plot(topo.kr, add = TRUE)
title(xlab= "Circle radius proportional to Cook's influence statistic")

trls.influence

Regression diagnostics for trend surfaces

description
This function provides the basic quantities which are used in forming a variety of diagnostics for checking the quality of regression fits for trend surfaces calculated by surf.ls.

Usage

trls.influence(object)

## S3 method for class 'trls'
plot(x, border = "red", col = NA, pch = 4, cex = 0.6,
     add = FALSE, div = 8, ...)

Arguments

object, x Fitted trend surface model from surf.ls
div scaling factor for influence circle radii in plot.trls
add add influence plot to existing graphics if TRUE
border, col, pch, cex, ...
        additional graphical parameters

Value

trls.influence returns a list with components:

r raw residuals as given by residuals.trls
hii diagonal elements of the Hat matrix
stresid standardised residuals
Di Cook’s statistic

References

See Also

surf.ls, influence.measures, plot.lm

Examples

library(MASS)  # for eqscplot
data(topo, package = "MASS")
topo2 <- surf.ls(2, topo)
infl.topo2 <- trls.influence(topo2)
(cand <- as.data.frame(infl.topo2)[abs(infl.topo2$sstresid) > 1.5, ])
cand.xy <- topo[as.integer(rownames(cand)), c("x", "y")]
trsurf <- trmat(topo2, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE, col = "grey")
plot(topo2, add = TRUE, div = 3)
points(cand.xy, pch = 16, col = "orange")
text(cand.xy, labels = rownames(cand.xy), pos = 4, offset = 0.5)

---

trmat

Evaluate Trend Surface over a Grid

Description

Evaluate trend surface over a grid.

Usage

trmat(obj, xl, xu, yl, yu, n)

Arguments

obj  object returned by surf.ls or surf.gls
xl   limits of the rectangle for grid
xu   ditto
yl   ditto
yu   ditto
n    use n x n grid within the rectangle

Value

list with components x, y and z suitable for contour and image.

References


See Also

surf.ls, surf.gls
variogram

Examples

```r
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
```
Chapter 29

The survival package

\[ aareg \]

Aalen’s additive regression model for censored data

Description

Returns an object of class "aareg" that represents an Aalen model.

Usage

\[ aareg(formula, data, weights, subset, na.action, 
qrtol=1e-07, nmin, dfbeta=FALSE, taper=1, 
test = c('aalen', 'variance', 'nrisk'), cluster, 
model=FALSE, x=FALSE, y=FALSE) \]

Arguments

- **formula**: a formula object, with the response on the left of a ‘~’ operator and the terms, separated by + operators, on the right. The response must be a Surv object. Due to a particular computational approach that is used, the model MUST include an intercept term. If "-1" is used in the model formula the program will ignore it.

- **data**: data frame in which to interpret the variables named in the formula, subset, and weights arguments. This may also be a single number to handle some special cases – see below for details. If data is missing, the variables in the model formula should be in the search path.

- **weights**: vector of observation weights. If supplied, the fitting algorithm minimizes the sum of the weights multiplied by the squared residuals (see below for additional technical details). The length of weights must be the same as the number of observations. The weights must be nonnegative and it is recommended that they be strictly positive, since zero weights are ambiguous. To exclude particular observations from the model, use the subset argument instead of zero weights.

- **subset**: expression specifying which subset of observations should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating the observation numbers to be included, or a character vector of the observation names that should be included. All observations are included by default.
na.action  a function to filter missing data. This is applied to the model frame after any subset argument has been applied. The default is na.fail, which returns an error if any missing values are found. An alternative is na.exclude, which deletes observations that contain one or more missing values.

qr_tol  tolerance for detection of singularity in the QR decomposition

nmin  minimum number of observations for an estimate; defaults to 3 times the number of covariates. This essentially truncates the computations near the tail of the data set, when n is small and the calculations can become numerically unstable.

dfbeta  should the array of dfbeta residuals be computed. This implies computation of the sandwich variance estimate. The residuals will always be computed if there is a cluster term in the model formula.

taper  allows for a smoothed variance estimate. Var(x), where x is the set of covariates, is an important component of the calculations for the Aalen regression model. At any given time point t, it is computed over all subjects who are still at risk at time t. The taper argument allows smoothing these estimates, for example taper=(1:4)/4 would cause the variance estimate used at any event time to be a weighted average of the estimated variance matrices at the last 4 death times, with a weight of 1 for the current death time and decreasing to 1/4 for prior event times. The default value gives the standard Aalen model.

test  selects the weighting to be used, for computing an overall “average” coefficient vector over time and the subsequent test for equality to zero.

cluster  the clustering group, optional. The variable will be searched for in the data argument.

model, x, y  should copies of the model frame, the x matrix of predictors, or the response vector y be included in the saved result.

Details

The Aalen model assumes that the cumulative hazard $H(t)$ for a subject can be expressed as $a(t) + X B(t)$, where $a(t)$ is a time-dependent intercept term, $X$ is the vector of covariates for the subject (possibly time-dependent), and $B(t)$ is a time-dependent matrix of coefficients. The estimates are inherently non-parametric; a fit of the model will normally be followed by one or more plots of the estimates.

The estimates may become unstable near the tail of a data set, since the increment to $B$ at time $t$ is based on the subjects still at risk at time $t$. The tolerance and/or nmin parameters may act to truncate the estimate before the last death. The taper argument can also be used to smooth out the tail of the curve. In practice, the addition of a taper such as 1:10 appears to have little effect on death times when n is still reasonably large, but can considerably dampen wild oscillations in the tail of the plot.

Value

an object of class "aareg" representing the fit, with the following components:

n  vector containing the number of observations in the data set, the number of event times, and the number of event times used in the computation

times  vector of sorted event times, which may contain duplicates

nrisk  vector containing the number of subjects at risk, of the same length as times

coefficient  matrix of coefficients, with one row per event and one column per covariate

test.statistic  the value of the test statistic, a vector with one element per covariate
aareg

test.var variance-covariance matrix for the test
test the type of test; a copy of the test argument above
tweight matrix of weights used in the computation, one row per event
call a copy of the call that produced this result

References

See Also
print.aareg, summary.aareg, plot.aareg

Examples
# Fit a model to the lung cancer data set
lfit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung, nmin=1)
## Not run:
lfit
Call:
aareg(formula = Surv(time, status) ~ age + sex + ph.ecog, data = lung, nmin = 1 )

n=227 (1 observations deleted due to missing values)
138 out of 138 unique event times used

slope coef se(coef) z p
Intercept 5.26e-03 5.99e-03 4.74e-03 1.26 0.207000
age 4.26e-05 7.02e-05 7.23e-05 0.97 0.332000
sex -3.29e-03 -4.02e-03 1.22e-03 -3.30 0.000976
ph.ecog 3.14e-03 3.80e-03 1.03e-03 3.70 0.000214

Chisq=26.73 on 3 df, p=6.7e-06; test weights=aalen

plot(lfit[4], ylim=c(-4,4)) # Draw a plot of the function for ph.ecog
## End(Not run)

# A fit to the multiple-infection data set of children with
# Chronic Granulomatous Disease. See section 8.5 of Therneau and Grambsch.
fita2 <- aareg(Surv(tstart, tstop, status) ~ treat + age + inherit +
 steroids + cluster(id), data=cgd)
## Not run:

n= 203
69 out of 70 unique event times used

slope coef se(coef) robust se z p
Intercept 0.004670 0.017800 0.002780 4.55 5.30e-06
aeqSurv

Adjudicate near ties in a Surv object

Description

The check for tied survival times can fail due to floating point imprecision, which can make actual ties appear to be distinct values. Routines that depend on correct identification of ties pairs will then give incorrect results, e.g., a Cox model. This function rectifies these.

Usage

```
aeqSurv(x, tolerance = sqrt(.Machine$double.eps))
```

Arguments

- `x` a Surv object
- `tolerance` the tolerance used to detect values that will be considered equal

Details

This routine is called by both `survfit` and `coxph` to deal with the issue of ties that get incorrectly broken due to floating point imprecision. See the short vignette on tied times for a simple example. Use the `timefix` argument of `survfit` or `coxph.control` to control the option if desired.

The rule for ‘equality’ is identical to that used by the `all.equal` routine. Pairs of values that are within round off error of each other are replaced by the smaller value. An error message is generated if this process causes a 0 length time interval to be created.

Value

a Surv object identical to the original, but with ties restored.

Author(s)

Terry Therneau

See Also

`survfit`, `coxph.control`
aggregate.survfit

Average survival curves

Description

For a survfit object containing multiple curves, create average curves over a grouping.

Usage

## S3 method for class 'survfit'
aggregate(x, by = NULL, FUN = mean, ...)

Arguments

x
a survfit object which has a data dimension.

by
an optional list or vector of grouping elements, each as long as
dim(x)["data"].

FUN
a function to compute the summary statistic of interest.

... optional further arguments to FUN.

Details

The primary use of this is to take an average over multiple survival curves that were created from a
modeling function. That is, a marginal estimate of the survival. It is primarily used to average over
multiple predicted curves from a Cox model.

Value

a survfit object of lower dimension.

See Also

survfit

Examples

cfit <- coxph(Surv(futime, death) ~ sex + age*hgb, data=mgus2)
# marginal effect of sex, after adjusting for the others
dummy <- rbind(mgus2, mgus2)
dummy$sex <- rep(c("F", "M"), each=nrow(mgus2)) # population data set
dummy <- na.omit(dummy) # don't count missing hgb in our "population
csurv <- survfit(cfit, newdata=dummy) # don't count missing hgb in our "population
csurv2 <- aggregate(csurv, dummy$sex)
agreg.fit

Cox model fitting functions

Description
These are the functions called by coxph that do the actual computation. In certain situations, e.g. a simulation, it may be advantageous to call these directly rather than the usual coxph call using a model formula.

Usage
agreg.fit(x, y, strata, offset, init, control, weights, method, rownames, resid=TRUE, nocenter=NULL)
coxph.fit(x, y, strata, offset, init, control, weights, method, rownames, resid=TRUE, nocenter=NULL)

Arguments
x Matix of predictors. This should not include an intercept.
y a Surv object containing either 2 columns (coxph.fit) or 3 columns (agreg.fit).
strata a vector containing the stratification, or NULL
offset optional offset vector
init initial values for the coefficients
control the result of a call to coxph.control
weights optional vector of weights
method method for handling ties, one of "breslow" or "efron"
rownames this is only needed for a NULL model, in which case it contains the rownames (if any) of the original data.
resid compute and return residuals.
nocenter an optional list of values. Any column of the X matrix whose values lie strictly within that set will not be recentered. Note that the coxph function has (-1, 0, 1) as the default.

Details
This routine does no checking that arguments are the proper length or type. Only use it if you know what you are doing!
The resid and concordance arguments will save some compute time for calling routines that only need the likelihood, the generation of a permutation distribution for instance.

Value
a list containing results of the fit

Author(s)
Terry Therneau
See Also

coxph

aml

Acute Myelogenous Leukemia survival data

Description

Survival in patients with Acute Myelogenous Leukemia. The question at the time was whether the standard course of chemotherapy should be extended ('maintainance') for additional cycles.

Usage

aml
leukemia
data(cancer, package="survival")

Format

time: survival or censoring time
status: censoring status
x: maintenance chemotherapy given? (factor)

Source


anova.coxph

Analysis of Deviance for a Cox model.

Description

Compute an analysis of deviance table for one or more Cox model fits, based on the log partial likelihood.

Usage

## S3 method for class 'coxph'
anova(object, ..., test = 'Chisq')

Arguments

object An object of class coxph
... Further coxph objects
test a character string. The appropriate test is a chisquare, all other choices result in no test being done.
Details

Specifying a single object gives a sequential analysis of deviance table for that fit. That is, the reductions in the model Cox log-partial-likelihood as each term of the formula is added in turn are given in as the rows of a table, plus the log-likelihoods themselves. A robust variance estimate is normally used in situations where the model may be mis-specified, e.g., multiple events per subject. In this case a comparison of likelihood values does not make sense (differences no longer have a chi-square distribution), and anova will refuse to print results.

If more than one object is specified, the table has a row for the degrees of freedom and loglikelihood for each model. For all but the first model, the change in degrees of freedom and loglik is also given. (This only make statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain test statistics (and P values) comparing the reduction in loglik for each row.

Value

An object of class "anova" inheriting from class "data.frame".

Warning

The comparison between two or more models by anova will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values.

See Also

coxph, anova.

Examples

fit <- coxph(Surv(futime, fustat) ~ resid.ds * rx + ecog.ps, data = ovarian)
anova(fit)
fit2 <- coxph(Surv(futime, fustat) ~ resid.ds + rx + ecog.ps, data=ovarian)
anova(fit2,fit)

attrassign

Create new-style "assign" attribute

Description

The “assign” attribute on model matrices describes which columns come from which terms in the model formula. It has two versions. R uses the original version, but the alternate version found in S-plus is sometimes useful.

Usage

attrassign(object, ...)

## Default S3 method:
attrassign(object, tt,...)

## S3 method for class 'lm'
attrassign(object,...)
Arguments

- `object`: model matrix or linear model object
- `tt`: terms object
- `...`: further arguments for other methods

Details

For instance consider the following

\[
\text{survreg(Surv(time, status) ~ age + sex + factor(ph.ecog), lung)}
\]

R gives the compact for for `assign`, a vector (0, 1, 2, 3, 3, 3); which can be read as “the first column of the X matrix (intercept) goes with none of the terms, the second column of X goes with term 1 of the model equation, the third column of X with term 2, and columns 4-6 with term 3”.

The alternate (S-Plus default) form is a list

\[
\begin{align*}
$(\text{Intercept}) & \ 1 \\
$\text{age} & \ 2 \\
$\text{sex} & \ 3 \\
$\text{factor(ph.ecog)} & \ 4 \ 5 \ 6
\end{align*}
\]

Value

A list with names corresponding to the term names and elements that are vectors indicating which columns come from which terms

See Also

- `terms`
- `model.matrix`

Examples

```r
formula <- Surv(time, status)~factor(ph.ecog)
tt <- terms(formula)
mf <- model.frame(tt, data=lung)
mm <- model.matrix(tt, mf)
## a few rows of data
mm[1:3,]
## old-style assign attribute
attr(mm, "assign")
## alternate style assign attribute
attrassign(mm, tt)
```
Description

Compute the predicted survival curve for a Cox model.

Usage

basehaz(fit, newdata, centered=TRUE)

Arguments

fit  a coxph fit
newdata  a data frame containing one row for each predicted survival curve, said row contains the covariate values for that curve
centered  ignored if the newdata argument is present. Otherwise, if TRUE return data from a predicted survival curve for the covariate values fit$mean, if FALSE return a prediction for all covariates equal to zero.

Details

This function is simply an alias for survfit, which does the actual work and has a richer set of options. The alias exists only because some users look for predicted survival estimates under this name.

The function returns a data frame containing the time, cumhaz and optionally the strata (if the fitted Cox model used a strata statement), which are copied the survfit result. Results for all covariates =0 are a standard form found in textbooks, however, due to possible overflow in the exp() function this can be a very bad idea in practice.

Value

a data frame with variable names of hazard, time and optionally strata. The first is actually the cumulative hazard.

See Also

survfit.coxph
**Bladder Cancer Recurrences**

**Description**

Data on recurrences of bladder cancer, used by many people to demonstrate methodology for recurrent event modelling.

Bladder1 is the full data set from the study. It contains all three treatment arms and all recurrences for 118 subjects; the maximum observed number of recurrences is 9.

Bladder is the data set that appears most commonly in the literature. It uses only the 85 subjects with nonzero follow-up who were assigned to either thiotepa or placebo, and only the first four recurrences for any patient. The status variable is 1 for recurrence and 0 for everything else (including death for any reason). The data set is laid out in the competing risks format of the paper by Wei, Lin, and Weissfeld.

Bladder2 uses the same subset of subjects as bladder, but formatted in the (start, stop] or Anderson-Gill style. Note that in transforming from the WLW to the AG style data set there is a quite common programming mistake that leads to extra follow-up time for 12 subjects: all those with follow-up beyond their 4th recurrence. This "follow-up" is a side effect of throwing away all events after the fourth while retaining the last follow-up time variable from the original data. The bladder2 data set found here does not make this mistake, but some analyses in the literature have done so; it results in the addition of a small amount of immortal time bias and shrinks the fitted coefficients towards zero.

**Usage**

```r
bladder1
bladder
bladder2
data(cancer, package="survival")
```

**Format**

**bladder1**

- **id**: Patient id
- **treatment**: Placebo, pyridoxine (vitamin B6), or thiotepa
- **number**: Initial number of tumours (8=8 or more)
- **size**: Size (cm) of largest initial tumour
- **recur**: Number of recurrences
- **start,stop**: The start and end time of each time interval
- **status**: End of interval code, 0=censored, 1=recurrence, 2=death from bladder disease, 3=death other/unknown cause
- **rtumor**: Number of tumors found at the time of a recurrence
- **rsize**: Size of largest tumor at a recurrence
- **enum**: Event number (observation number within patient)

**bladder**
id: Patient id
rx: Treatment 1=placebo 2=thiotepa
number: Initial number of tumours (8=8 or more)
size: size (cm) of largest initial tumour
stop: recurrence or censoring time
enum: which recurrence (up to 4)

bladder2

id: Patient id
rx: Treatment 1=placebo 2=thiotepa
number: Initial number of tumours (8=8 or more)
size: size (cm) of largest initial tumour
start: start of interval (0 or previous recurrence time)
stop: recurrence or censoring time
enum: which recurrence (up to 4)

Source

---

**blogit**

*Bounded link functions*

**Description**
Alternate link functions that impose bounds on the input of their link function

**Usage**

```r
blogit(edge = 0.05)
bprobit(edge= 0.05)
bcloglog(edge=.05)
blog(edge=.05)
```

**Arguments**

`edge` input values less than the cutpoint are replaced with the cutpoint. For all be blog input values greater than (1-edge) are replaced with (1-edge)
**brier**

**Details**

When using survival psuedovalues for binomial regression, the raw data can be outside the range (0,1), yet we want to restrict the predicted values to lie within that range. A natural way to deal with this is to use glm with family = gaussian(link= "logit"). But this will fail. The reason is that the family object has a component linkfun that does not accept values outside of (0,1).

This function is only used to create initial values for the iteration step, however. Mapping the offending input argument into the range of (edge, 1-edge) before computing the link results in starting estimates that are good enough. The final result of the fit will be no different than if explicit starting estimates were given using the etastart or mustart arguments. These functions create copies of the logit, probit, and complimentary log-log families that differ from the standard ones only in this use of a bounded input argument, and are called a "bounded logit" = blogit, etc.

The same argument hold when using RMST (area under the curve) pseudovalues along with a log link to ensure positive predictions, though in this case only the lower boundary needs to be mapped.

**Value**

a family object of the same form as make.family.

**See Also**

stats{make.family}

**Examples**

```r
py <- pseudo(survfit(Surv(time, status) ~1, lung), time=730) #2 year survival
range(py)
pfit <- glm(py ~ ph.ecog, data=lung, family=gaussian(link=blogit()))
# For each +1 change in performance score, the odds of 2 year survival
# are multiplied by 1/2 = exp of the coefficient.
```

---

**brier**  
*Compute the Brier score for a Cox model*

**Description**

Compute the Brier score, for a coxph model

**Usage**

```r
brier(fit, times, newdata, ties = TRUE, detail = FALSE, timefix = TRUE, efron = FALSE)
```

**Arguments**

- `fit` result of a coxph fit
- `times` time points at which to create the score
- `newdata` optional, used to validate a prior fit with new data
- `ties` if TRUE, treat tied event/censoring times properly
- `detail` if TRUE, the returned object has more detail. This can be useful for debugging or for instruction.
timefix deal with near ties in the data. See the tied times vignette.
efron use the same survival estimate for the NULL model as was used in the coxph call

Details

Far more details are found in the vignette. At any time point tau, the scaled Brier score is essentially the R-squared statistic where \( y = \) the 0/1 variable “event at or before tau”, \( \hat{y} \) that is the probability of an event by tau, as predicted by the model, and the \( ybar \) is the predicted probability without covariate, normally from a Kaplan-Meier. If \( R^2 = 1 - \sum(y - \hat{y})^2 / \sum(y - \mu)^2 \), the Brier score is formally only the numerator of the second term. The rescaled value is much more useful, however.

Many, perhaps even most algorithms do not properly deal with a tied censoring time/event time pair. The tied option is present mostly verify that we get the same answer, when we make the same mistake. The numerical size of the inaccuracy is very small; just large enough to generate concern that this function is incorrect.

A sensible argument can be made that the NULL model should be a coxph call with no covariates, rather than the Kaplan-Meier; but it turns out that the effect is very slight. This is allowed by the efron argument.

Value

a list with components

rsquared the \( R^2 \) value, a scaled Brier score. This will be a vector with one entry for each time point.
brier the brier score, a vector with one entry per time point	
times the time points at which the score was computed

Author(s)

Terry Therneau

See Also

ttright

Examples

cfit <- coxph(Surv(rtime, recur) ~ age + meno + size + pmin(nodes,11),
data= rotterdam)
round(cfit$concordance["concordance"], 3) # some predictive power
brier(cfit, times=c(4,6)*365.25) # values at 4 and 6 years
cch

Fits proportional hazards regression model to case-cohort data

Description

Returns estimates and standard errors from relative risk regression fit to data from case-cohort studies. A choice is available among the Prentice, Self-Prentice and Lin-Ying methods for unstratified data. For stratified data the choice is between Borgan I, a generalization of the Self-Prentice estimator for unstratified case-cohort data, and Borgan II, a generalization of the Lin-Ying estimator.

Usage

cch(formula, data, subcoh, id, stratum=NULL, cohort.size,
method =c("Prentice","SelfPrentice","LinYing","I.Borgan","II.Borgan"),
robust=FALSE)

Arguments

formula A formula object that must have a Surv object as the response. The Surv object must be of type "right", or of type "counting".
subcoh Vector of indicators for subjects sampled as part of the sub-cohort. Code 1 or TRUE for members of the sub-cohort, 0 or FALSE for others. If data is a data frame then subcoh may be a one-sided formula.
id Vector of unique identifiers, or formula specifying such a vector.
stratum A vector of stratum indicators or a formula specifying such a vector
cohort.size Vector with size of each stratum original cohort from which subcohort was sampled
data An optional data frame in which to interpret the variables occurring in the formula.
method Three procedures are available. The default method is "Prentice", with options for "SelfPrentice" or "LinYing".
robust For "LinYing" only, if robust=TRUE, use design-based standard errors even for phase I

Details

Implements methods for case-cohort data analysis described by Therneau and Li (1999). The three methods differ in the choice of "risk sets" used to compare the covariate values of the failure with those of others at risk at the time of failure. "Prentice" uses the sub-cohort members "at risk" plus the failure if that occurs outside the sub-cohort and is score unbiased. "SelfPren" (Self-Prentice) uses just the sub-cohort members "at risk". These two have the same asymptotic variance-covariance matrix. "LinYing" (Lin-Ying) uses the all members of the sub-cohort and all failures outside the sub-cohort who are "at risk". The methods also differ in the weights given to different score contributions.

The data argument must not have missing values for any variables in the model. There must not be any censored observations outside the subcohort.
Value

An object of class "cch" incorporating a list of estimated regression coefficients and two estimates of their asymptotic variance-covariance matrix.

- `coef`: regression coefficients.
- `naive.var`: Self-Prentice model based variance-covariance matrix.
- `var`: Lin-Ying empirical variance-covariance matrix.

Author(s)

Norman Breslow, modified by Thomas Lumley

References


See Also
twophase and svycoxph in the "survey" package for more general two-phase designs. http://faculty.washington.edu/tlumley/survey/

Examples

```r
## The complete Wilms Tumor Data
## (Breslow and Chatterjee, Applied Statistics, 1999)
## subcohort selected by simple random sampling.
##
## subcoh <- nwtco$in.subcohort
## selcoh <- with(nwtco, rel==1|subcoh==1)
## ccoh.data <- nwtco[selcoh,]
## ccoh.data$subcohort <- subcoh[selcoh]
##
## ccoh.data$histol <- factor(ccoh.data$histol,labels=c("FH","UH"))
## ccoh.data$stage <- factor(ccoh.data$stage,labels=c("I","II","III","IV"))
## ccoh.data$age <- ccoh.data$age/12 # Age in years
##
## ## Standard case-cohort analysis: simple random subcohort
##
```
fit.ccP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data, subcoh = ~subcohort, id=~seqno, cohort.size=4028)

fit.ccSP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data, subcoh = ~subcohort, id=~seqno, cohort.size=4028, method="SelfPren")

summary(fit.ccSP)
##
## (post-)stratified on instit
##
stratsizes<-table(nwtco$instit)
fit.BI<- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data, subcoh = ~subcohort, id=~seqno, stratum=~instit, cohort.size=stratsizes, method="I.Borgan")

summary(fit.BI)

cgd

**Chronic Granulotamous Disease data**

**Description**

Data are from a placebo controlled trial of gamma interferon in chronic granulotomous disease (CGD). Contains the data on time to serious infections observed through end of study for each patient.

**Usage**

cgd
data(cgd)

**Format**

- **id**  subject identification number
- **center**  enrolling center
- **random**  date of randomization
- **treatment**  placebo or gamma interferon
- **sex**  sex
- **age**  age in years, at study entry
- **height**  height in cm at study entry
- **weight**  weight in kg at study entry
- **inherit**  pattern of inheritance
- **steroids**  use of steroids at study entry, 1=yes
- **propylac**  use of prophylactic antibiotics at study entry
hos.cat  a categorization of the centers into 4 groups  
tstart, tstop  start and end of each time interval  
status 1=the interval ends with an infection  
enum  observation number within subject  

details  
The cgd0 data set is in the form found in the references, with one line per patient and no recoding of the variables. The cgd data set (this one) has been cast into (start, stop] format with one line per event, and covariates such as center recoded as factors to include meaningful labels.  

Source  
Fleming and Harrington, Counting Processes and Survival Analysis, appendix D.2.  

See Also  
link{cgd0}  

cgd0  

Chronic Granulotomous Disease data  

Description  
Data are from a placebo controlled trial of gamma interferon in chronic granulotomous disease (CGD). Contains the data on time to serious infections observed through end of study for each patient.  

Usage  
cgd0  

Format  

id  subject identification number  
center  enrolling center  
random  date of randomization  
treatment  placebo or gamma interferon  
sex  sex  
age  age in years, at study entry  
height  height in cm at study entry  
weight  weight in kg at study entry  
inherit  pattern of inheritance  
steroids  use of steroids at study entry, 1=yes  
propylac  use of prophylactic antibiotics at study entry  
hos.cat  a categorization of the centers into 4 groups  
futime  days to last follow-up  
etime1-etime7  up to 7 infection times for the subject
Details

The cgdraw data set (this one) is in the form found in the references, with one line per patient and no recoding of the variables.

The cgd data set has been further processed so as to have one line per event, with covariates such as center recoded as factors to include meaningful labels.

Source

Fleming and Harrington, Counting Processes and Survival Analysis, appendix D.2.

See Also

cgd

cipoisson  Confidence limits for the Poisson

Description

Confidence interval calculation for Poisson rates.

Usage

cipoisson(k, time = 1, p = 0.95, method = c("exact", "anscombe"))

Arguments

- k: Number of successes
- time: Total time on trial
- p: Probability level for the (two-sided) interval
- method: The method for computing the interval.

Details

The likelihood method is based on equation 10.10 of Feller, which relates poisson probabilities to tail area of the gamma distribution. The Anscombe approximation is based on the fact that sqrt(k + 3/8) has a nearly constant variance of 1/4, along with a continuity correction.

There are many other proposed intervals: Patil and Kulkarni list and evaluate 19 different suggestions from the literature!. The exact intervals can be overly broad for very small values of k, many of the other approaches try to shrink the lengths, with varying success.

Value

A vector, matrix, or array. If both k and time are single values the result is a vector of length 2 containing the lower and upper limits. If either or both are vectors the result is a matrix with two columns. If k is a matrix or array, the result will be an array with one more dimension; in this case the dimensions and dimnames (if any) of k are preserved.
References


See Also

ppois, qpois

Examples

cipoisson(4) # 95\% confidence limit
# lower  upper
# 1.089865 10.24153
ppois(4, 10.24153) # chance of seeing 4 or fewer events with large rate
# [1] 0.02500096
1-ppois(3, 1.08986) # chance of seeing 4 or more, with a small rate
# [1] 0.02499961

clogit

Conditional logistic regression

Description

Estimates a logistic regression model by maximising the conditional likelihood. Uses a model formula of the form case.status~exposure+strata(matched.set). The default is to use the exact conditional likelihood, a commonly used approximate conditional likelihood is provided for compatibility with older software.

Usage

clogit(formula, data, weights, subset, na.action, method=c("exact", "approximate", "efron", "breslow"), ...

Arguments

formula Model formula
data data frame
weights optional, names the variable containing case weights
subset optional, subset the data
na.action optional na.action argument. By default the global option na.action is used.
method use the correct (exact) calculation in the conditional likelihood or one of the approximations
... optional arguments, which will be passed to coxph.control
Details

It turns out that the loglikelihood for a conditional logistic regression model = loglik from a Cox model with a particular data structure. Proving this is a nice homework exercise for a PhD statistics class; not too hard, but the fact that it is true is surprising.

When a well tested Cox model routine is available many packages use this ‘trick’ rather than writing a new software routine from scratch, and this is what the clogit routine does. In detail, a stratified Cox model with each case/control group assigned to its own stratum, time set to a constant, status of 1=case 0=control, and using the exact partial likelihood has the same likelihood formula as a conditional logistic regression. The clogit routine creates the necessary dummy variable of times (all 1) and the strata, then calls coxph.

The computation of the exact partial likelihood can be very slow, however. If a particular strata had say 10 events out of 20 subjects we have to add up a denominator that involves all possible ways of choosing 10 out of 20, which is \( \frac{20!}{10! \cdot 10!} \) = 184756 terms. Gail et al describe a fast recursion method which partly ameliorates this; it was incorporated into version 2.36-11 of the survival package. The computation remains infeasible for very large groups of ties, say 100 ties out of 500 subjects, and may even lead to integer overflow for the subscripts – in this latter case the routine will refuse to undertake the task. The Efron approximation is normally a sufficiently accurate substitute.

Most of the time conditional logistic modeling is applied data with 1 case + k controls per set, in which case all of the approximations for ties lead to exactly the same result. The ’approximate’ option maps to the Breslow approximation for the Cox model, for historical reasons.

Case weights are not allowed when the exact option is used, as the likelihood is not defined for fractional weights. Even with integer case weights it is not clear how they should be handled. For instance if there are two deaths in a strata, one with weight=1 and one with weight=2, should the likelihood calculation consider all subsets of size 2 or all subsets of size 3? Consequently, case weights are ignored by the routine in this case.

Value

An object of class "clogit", which is a wrapper for a "coxph" object.

References


Author(s)

Thomas Lumley

See Also

strata, coxph, glm

Examples

```r
## Not run: clogit(case ~ spontaneous + induced + strata(stratum), data=infert)

# A multinomial response recoded to use clogit
# The revised data set has one copy per possible outcome level, with new
# variable tocc = target occupation for this copy, and case = whether
```
# that is the actual outcome for each subject.
# See the reference below for the data.
resp <- levels(logan$occupation)
n <- nrow(logan)
indx <- rep(1:n, length(resp))
logan2 <- data.frame(logan[indx,],
       id = indx,
       tocc = factor(rep(resp, each=n)))
logan2$case <- (logan2$occupation == logan2$tocc)
clogit(case ~ tocc + tocc:education + strata(id), logan2)

cluster

Description

This is a special function used in the context of survival models. It identifies correlated groups of observations, and is used on the right hand side of a formula. This style is now discouraged, use the cluster option instead.

Usage

cluster(x)

Arguments

x

A character, factor, or numeric variable.

Details

The function’s only action is semantic, to mark a variable as the cluster indicator. The resulting variance is what is known as the “working independence” variance in a GEE model. Note that one cannot use both a frailty term and a cluster term in the same model, the first is a mixed-effects approach to correlation and the second a GEE approach, and these don’t mix.

Value

x

See Also

coxph, survreg

Examples

marginal.model <- coxph(Surv(time, status) ~ rx, data= rats, cluster=litter, subset=(sex=='f'))
frailty.model <- coxph(Surv(time, status) ~ rx + frailty(litter), rats, subset=(sex=='f'))
Description

These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are two records per person, one for recurrence and one for death.

Usage

colon
data(cancer, package="survival")

Format

<table>
<thead>
<tr>
<th>id</th>
<th>id</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
<td>1 for all patients</td>
</tr>
<tr>
<td>rx</td>
<td>Treatment - Observation, Lev(amisole), Lev(amisole)+5-FU</td>
</tr>
<tr>
<td>sex</td>
<td>1=male</td>
</tr>
<tr>
<td>age</td>
<td>in years</td>
</tr>
<tr>
<td>obstruct</td>
<td>obstruction of colon by tumour</td>
</tr>
<tr>
<td>perfor</td>
<td>perforation of colon</td>
</tr>
<tr>
<td>adhere</td>
<td>adherence to nearby organs</td>
</tr>
<tr>
<td>nodes</td>
<td>number of lymph nodes with detectable cancer</td>
</tr>
<tr>
<td>time</td>
<td>days until event or censoring</td>
</tr>
<tr>
<td>status</td>
<td>censoring status</td>
</tr>
<tr>
<td>differ</td>
<td>differentiation of tumour (1=well, 2=moderate, 3=poor)</td>
</tr>
<tr>
<td>extent</td>
<td>Extent of local spread (1=submucosa, 2=muscle, 3=serosa, 4=contiguous structures)</td>
</tr>
<tr>
<td>surg</td>
<td>time from surgery to registration (0=short, 1=long)</td>
</tr>
<tr>
<td>node4</td>
<td>more than 4 positive lymph nodes</td>
</tr>
<tr>
<td>etype</td>
<td>event type: 1=recurrence, 2=death</td>
</tr>
</tbody>
</table>

Note

The study is originally described in Laurie (1989). The main report is found in Moertel (1990). This data set is closest to that of the final report in Moertel (1991). A version of the data with less follow-up time was used in the paper by Lin (1994).

Peter Higgins has pointed out a data inconsistency, revealed by `table(colon$nodes, colon$node4)`. We don’t know which of the two variables is actually correct so have elected not to ‘fix’ it. (Real data has warts, why not have some in the example data too?)
concordance

References


concordance

Compute the concordance statistic for data or a model

Description

The concordance statistic compute the agreement between an observed response and a predictor. It is closely related to Kendall’s tau-a and tau-b, Goodman’s gamma, and Somers’ d, all of which can also be calculated from the results of this function.

Usage

concordance(object, ...)  
## S3 method for class 'formula'  
concordance(object, data, weights, subset, na.action,  
cluster, ymin, ymax, timewt= c("n", "S", "S/G", "n/G2", "I"),  
influence=0, ranks = FALSE, reverse=FALSE, timefix=TRUE, keepstrata=10, ...)  
## S3 method for class 'lm'  
concordance(object, ..., newdata, cluster, ymin, ymax,  
influence=0, ranks=FALSE, timefix=TRUE, keepstrata=10)  
## S3 method for class 'coxph'  
concordance(object, ..., newdata, cluster, ymin, ymax,  
timewt= c("n", "S", "S/G", "n/G2", "I"), influence=0,  
ranks=FALSE, timefix=TRUE, keepstrata=10)  
## S3 method for class 'survreg'  
concordance(object, ..., newdata, cluster, ymin, ymax,  
timewt= c("n", "S", "S/G", "n/G2", "I"), influence=0,  
ranks=FALSE, timefix=TRUE, keepstrata=10)

Arguments

object

A fitted model or a formula. The formula should be of the form y ~ x or y ~ x + strata(z) with a single numeric or survival response and a single predictor. Counts of concordant, discordant and tied pairs are computed separately per stratum, and then added.
data

weights

subset

na.action

... multiple fitted models are allowed. Only applicable if object is a model object.

newdata

cluster

ymin, ymax

timewt

influence

ranks

reverse

timefix

keepstrata

Details

The concordance is an estimate of $P r(x_i < x_j | y_i < y_j)$, for a model fit replace $x$ with $\hat{y}$, the predicted response from the model. For a survival outcome some pairs of values are not comparable, e.g., censored at time 5 and a death at time 6, as we do not know if the first observation will or will not outlive the second. In this case the total number of evaluable pairs is smaller.

Relations to other statistics: For continuous x and y, 2C - 1 is equal to Somers’ d. If the response is binary, C is equal to the area under the receiver operating curve or AUC. For a survival response and binary predictor C is the numerator of the Gehan-Wilcoxon test.

A naive computation requires adding up over all $n(n-1)/2$ comparisons, which can be quite slow for large data sets. This routine uses an $O(n \log(n))$ algorithm. At each uncensored event time $y$, compute the rank of $x$ for the subject who had the event as compared to the $x$ values for all others with a longer survival, where the rank has value between 0 and 1. The concordance is a weighted mean of these ranks, determined by the timewt option. The rank vector can be efficiently updated as subjects are added to the risk set. For further details see the vignette.

The variance is based on an infinitesimal jackknife. One advantage of this approach is that it also gives a valid covariance for the covariance based on multiple different predicted values, even if those predictions come from quite different models. See for instance the example below which has a poisson and two non-nested Cox models. This has been useful to compare a machine learning model to a Cox model fit, say. It is absolutely critical, however, that the predicted values line up
exactly, with the same observation in each row; otherwise the result will be nonsense. (Be alert to 
the impact of missing values.)

The \texttt{timewt} option is only applicable to censored data. In this case the default corresponds to 
Harrell’s C statistic, which is closely related to the Gehan-Wilcoxon test; \texttt{timewt=“S”} corresponds 
to the Peto-Wilcoxon, \texttt{timewt=“S/G”} is suggested by Schemper, and \texttt{timewt=“n/G2”} corresponds 
to Uno’s C. It turns out that the Schemper and Uno weights are computationally identical, we have 
retained both option labels as a user convenience. The \texttt{timewt= “I”} option is related to the log-rank 
statistic.

When the number of strata is very large, such as in a conditional logistic regression for instance 
(\texttt{clogit} function), a much faster computation is available when the individual strata results are not 
retained; use \texttt{keepstrata=}FALSE or \texttt{keepstrata=}0 to do so. In the general case the \texttt{keepstrata=10} 
default simply keeps the printout managable: it retains and prints per-strata counts if the number 
of strata is $<=10$.

\textbf{Value}

An object of class \texttt{concordance} containing the following components:

- \texttt{concordance}: the estimated concordance value or values
- \texttt{count}: a vector containing the number of concordant pairs, discordant, tied on x but not y, tied on y but not x, and tied on both x and y
- \texttt{n}: the number of observations
- \texttt{var}: a vector containing the estimated variance of the concordance based on the infinitesimal jackknife (IJ) method. If there are multiple models it contains the estimated variance/covariance matrix.
- \texttt{cvar}: a vector containing the estimated variance(s) of the concordance values, based on the variance formula for the associated score test from a proportional hazards model. (This was the primary variance used in the \texttt{survConcordance} function.)
- \texttt{dfbeta}: optional, the vector of leverage estimates for the concordance
- \texttt{influence}: optional, the matrix of leverage values for each of the counts, one row per observation
- \texttt{ranks}: optional, a data frame containing the Somers’ d rank at each event time, along with the time weight, and the case weight of the observation. The time weighted sum of the ranks will equal concordant pairs - discordant pairs.

\textbf{Note}

A coxph model that has a numeric failure may have undefined predicted values, in which case the 
concordance will be NULL.

Computation for an existing coxph model along with \texttt{newdata} has some subtleties with respect to 
extra arguments in the original call. These include

- \texttt{tt()} terms in the model. This is not supported with \texttt{newdata}.
- \texttt{subset}. Any subset clause in the original call is ignored, i.e., not applied to the new data.
- \texttt{strata()} terms in the model. The new data is expected to have the strata variable(s) found in the 
  original data set, with concordance computed within strata. The levels of the strata variable 
  need not be the same as in the original data.
- \texttt{id} or \texttt{cluster} directives. This has not yet been sorted out.
concordance

Author(s)

Terry Therneau

References


H Uno, T Cai, M Pencina, R D’Agostino and Lj Wei, On the C-statistics for evaluating overall adequacy of risk prediction procedures with censored survival data, Statistics in Medicine, 2011.

See Also

coxph

Examples

```r
fit1 <- coxph(Surv(ptime, pstat) ~ age + sex + mspike, mgus2)
concordance(fit1, timewt="n/G2") # Uno’s weighting

# logistic regression
fit2 <- glm(I(sex=='M') ~ age + log(creatinine), binomial, data= flchain)
concordance(fit2) # equal to the AUC

# compare multiple models
options(na.action = na.exclude) # predict all 1384 obs, including missing
fit3 <- glm(pstat ~ age + sex + mspike + offset(log(ptime)),
            poisson, data= mgus2)
fit4 <- coxph(Surv(ptime, pstat) ~ age + sex + mspike, mgus2)
fit5 <- coxph(Surv(ptime, pstat) ~ age + sex + hgb + creat, mgus2)

tdata <- mgus2; tdata$ptime <- 60 # prediction at 60 months
p3 <- predict(fit3, newdata=tdata)
p4 <- predict(fit4) # high risk scores predict shorter survival
p5 <- predict(fit5)
options(na.action = na.omit) # return to the R default

cfit <- concordance(Surv(ptime, pstat) ~ p3 + p4 + p5, mgus2)
cfit
round(coef(cfit), 3)
round(cov2cor(vcov(cfit)), 3) # high correlation

test <- c(1, -1, 0) # contrast vector for model 1 - model 2
round(c(difference = test %*% coef(cfit),
        sd= sqrt(test %*% vcov(cfit) %*% test)), 3)
```
Description

This is the working routine behind the concordance function. It is not meant to be called by users, but is available for other packages to use. Input arguments, for instance, are assumed to all be the correct length and type, and missing values are not allowed: the calling routine is responsible for these things.

Usage

concordancefit(y, x, strata, weights, ymin = NULL, ymax = NULL, timewt = c("n", "S", "S/G", "n/G2", "I"), cluster, influence = 0, ranks = FALSE, reverse = FALSE, timefix = TRUE, keepstrata=10, std.err = TRUE)

Arguments

y the response. It can be numeric, factor, or a Surv object
x the predictor, a numeric vector
strata optional numeric vector that stratifies the data
weights options vector of case weights
ymin, ymax restrict the comparison to response values in this range
timewt the time weighting to be used
cluster, influence, ranks, reverse, timefix see the help for the concordance function
keepstrata either TRUE, FALSE, or an integer value. Computations are always done within stratum, then added. If the total number of strata greater than keepstrata, or keepstrata=FALSE, those subtotals are not kept in the output.
std.err compute the standard error; not doing so saves some compute time.

Details

This function is provided for those who want a “direct” call to the concordance calculations, without using the formula interface. A primary use has been other packages. The routine does minimal checking of its input arguments, under the assumption that this has already been taken care of by the calling routine.

Value

a list containing the results

Author(s)

Terry Therneau

See Also

concordance
Test the Proportional Hazards Assumption of a Cox Regression

Description
Test the proportional hazards assumption for a Cox regression model fit (coxph).

Usage
cox.zph(fit, transform="km", terms=TRUE, singledf=FALSE, global=TRUE)

Arguments
- **fit**: the result of fitting a Cox regression model, using the coxph or coxme functions.
- **transform**: a character string specifying how the survival times should be transformed before the test is performed. Possible values are "km", "rank", "identity" or a function of one argument.
- **terms**: if TRUE, do a test for each term in the model rather than for each separate covariate. For a factor variable with k levels, for instance, this would lead to a k-1 degree of freedom test. The plot for such variables will be a single curve evaluating the linear predictor over time.
- **singledf**: use a single degree of freedom test for terms that have multiple coefficients, i.e., the test that corresponds most closely to the plot. If terms=FALSE this argument has no effect.
- **global**: should a global chi-square test be done, in addition to the per-variable or per-term tests tests.

Details
The computations require the original x matrix of the Cox model fit. Thus it saves time if the x=TRUE option is used in coxph. This function would usually be followed by both a plot and a print of the result. The plot gives an estimate of the time-dependent coefficient $\beta(t)$. If the proportional hazards assumption holds then the true $\beta(t)$ function would be a horizontal line. The table component provides the results of a formal score test for slope=0, a linear fit to the plot would approximate the test.

Random effects terms such a frailty or random effects in a coxme model are not checked for proportional hazards, rather they are treated as a fixed offset in model.

If the model contains strata by covariate interactions, then the y matrix may contain structural zeros, i.e., deaths (rows) that had no role in estimation of a given coefficient (column). These are marked as NA. If an entire row is NA, for instance after subscripting a cox.zph object, that row is removed.

Value
an object of class "cox.zph", with components:
- **table**: a matrix with one row for each variable, and optionally a last row for the global test. Columns of the matrix contain a score test of for addition of the time-dependent term, the degrees of freedom, and the two-sided p-value.
- **x**: the transformed time axis.
time  the untransformed time values; there is one entry for each event time in the data
strata for a stratified coxph model, the stratum of each of the events
y  the matrix of scaled Schoenfeld residuals. There will be one column per term
or per variable (depending on the terms option above), and one row per event.
The row labels are a rounded form of the original times.
var  a variance matrix for the covariates, used to create an approximate standard error
band for plots
transform  the transform of time that was used
call  the calling sequence for the routine.

Note

In versions of the package before survival3.0 the function computed a fast approximation to the score test. Later versions compute the actual score test.

References


See Also

coxph, Surv.

Examples

```r
fit <- coxph(Surv(futime, fustat) ~ age + ecog.ps, data=ovarian)
temp <- cox.zph(fit)
print(temp)  # display the results
plot(temp)  # plot curves
```

---

**coxph**

**Fit Proportional Hazards Regression Model**

**Description**

Fits a Cox proportional hazards regression model. Time dependent variables, time dependent strata, multiple events per subject, and other extensions are incorporated using the counting process formulation of Andersen and Gill.

**Usage**

```r
coxph(formula, data=, weights, subset, 
na.action, init, control, 
ties=c("efron","breslow","exact"), 
singular.ok=TRUE, robust, 
model=FALSE, x=FALSE, y=TRUE, tt, method=ties, 
id, cluster, istate, statedata, ncenter=c(-1, 0, 1), ...)```
**Arguments**

**formula**
a formula object, with the response on the left of a `~` operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function. For a multi-state model the formula may be a list of formulas.

**data**
a data.frame in which to interpret the variables named in the `formula`, or in the `subset` and the `weights` argument.

**weights**
vector of case weights, see the note below. For a thorough discussion of these see the book by Therneau and Grambsch.

**subset**
expression indicating which subset of the rows of `data` should be used in the fit. All observations are included by default.

**na.action**
a missing-data filter function. This is applied to the `model.frame` after any subset argument has been used. Default is `options()$na.action`.

**init**
vector of initial values of the iteration. Default initial value is zero for all variables.

**control**
Object of class `coxph.control` specifying iteration limit and other control options. Default is `coxph.control(...)`. 

**ties**
a character string specifying the method for tie handling. If there are no tied death times all the methods are equivalent. The Efron approximation is used as the default, it is more accurate when dealing with tied death times, and is as efficient computationally. (But see below for multi-state models.) The “exact partial likelihood” is equivalent to a conditional logistic model, and is appropriate when the times are a small set of discrete values.

**singular.ok**
logical value indicating how to handle collinearity in the model matrix. If TRUE, the program will automatically skip over columns of the X matrix that are linear combinations of earlier columns. In this case the coefficients for such columns will be NA, and the variance matrix will contain zeros. For ancillary calculations, such as the linear predictor, the missing coefficients are treated as zeros.

**robust**
should a robust variance be computed. The default is TRUE if: there is a `cluster` argument, there are case weights that are not 0 or 1, or there are `id` values with more than one event.

**id**
optional variable name that identifies subjects. Only necessary when a subject can have multiple rows in the data, and there is more than one event type. This variable will normally be found in `data`.

**cluster**
optional variable which clusters the observations, for the purposes of a robust variance. If present, it implies `robust`. This variable will normally be found in `data`.

**istate**
optional variable giving the current state at the start each interval. This variable will normally be found in `data`.

**statedata**
optional data set used to describe multistate models.

**model**
logical value: if TRUE, the model frame is returned in component `model`.

**x**
logical value: if TRUE, the x matrix is returned in component `x`.

**y**
logical value: if TRUE, the response vector is returned in component `y`.

**tt**
optional list of time-transform functions.

**method**
alternate name for the `ties` argument.

**nocenter**
columns of the X matrix whose values lie strictly within this set are not recentered. Remember that a factor variable becomes a set of 0/1 columns.

... Other arguments will be passed to `coxph.control`
Details

The proportional hazards model is usually expressed in terms of a single survival time value for each person, with possible censoring. Andersen and Gill reformulated the same problem as a counting process; as time marches onward we observe the events for a subject, rather like watching a Geiger counter. The data for a subject is presented as multiple rows or "observations", each of which applies to an interval of observation [start, stop].

The routine internally scales and centers data to avoid overflow in the argument to the exponential function. These actions do not change the result, but lead to more numerical stability. Any column of the X matrix whose values lie within nocenter list are not recentered. The practical consequence of the default is to not recenter dummy variables corresponding to factors. However, arguments to offset are not scaled since there are situations where a large offset value is a purposefully used. In general, however, users should not avoid very large numeric values for an offset due to possible loss of precision in the estimates.

Value

an object of class coxph representing the fit. See coxph.object and coxphms.object for details.

Side Effects

Depending on the call, the predict, residuals, and survfit routines may need to reconstruct the x matrix created by coxph. It is possible for this to fail, as in the example below in which the predict function is unable to find tform.

```r
tfun <- function(tform) coxph(tform, data=lung)
fit <- tfun(Surv(time, status) ~ age)
predict(fit)
```

In such a case add the model=TRUE option to the coxph call to obviate the need for reconstruction, at the expense of a larger fit object.

Case weights

Case weights are treated as replication weights, i.e., a case weight of 2 is equivalent to having 2 copies of that subject's observation. When computers were much smaller grouping like subjects together was a common trick to used to conserve memory. Setting all weights to 2 for instance will give the same coefficient estimate but halve the variance. When the Efron approximation for ties (default) is employed replication of the data will not give exactly the same coefficients as the weights option, and in this case the weighted fit is arguably the correct one.

When the model includes a cluster term or the robust=TRUE option the computed variance treats any weights as sampling weights; setting all weights to 2 will in this case give the same variance as weights of 1.

Special terms

There are three special terms that may be used in the model equation. A strata term identifies a stratified Cox model; separate baseline hazard functions are fit for each strata. The cluster term is used to compute a robust variance for the model. The term + cluster(id) where each value of id is unique is equivalent to specifying the robust=TRUE argument. If the id variable is not unique, it is assumed that it identifies clusters of correlated observations. The robust estimate arises from many different arguments and thus has had many labels. It is variously known as the Huber sandwich estimator, White’s estimate (linear models/econometrics), the Horvitz-Thompson estimate (survey
sampling), the working independence variance (generalized estimating equations), the infinitesimal jackknife, and the Wei, Lin, Weissfeld (WLW) estimate.

A time-transform term allows variables to vary dynamically in time. In this case the tt argument will be a function or a list of functions (if there are more than one tt() term in the model) giving the appropriate transform. See the examples below.

One user mistake that has recently arisen is to slavishly follow the advice of some coding guides and prepend survival:: onto everything, including the special terms, e.g.,

```
survival::coxph(survival::Surv(time, status) ~ age + survival::cluster(inst),
  data=lung)
```

First, this is unnecessary: arguments within the coxph call will be evaluated within
the survival namespace, so another package’s Surv or cluster function would not be noticed. (Full qualification of the coxph call itself may be protective, however.) Second, and more importantly, the call just above will not give the correct answer. The specials are recognized by their name, and survival::cluster is not the same as cluster; the above model would treat inst as an ordinary variable. A similar issue arises from using stats::offset as a term, in either survival or glm models.

Convergence

In certain data cases the actual MLE estimate of a coefficient is infinity, e.g., a dichotomous variable where one of the groups has no events. When this happens the associated coefficient grows at a steady pace and a race condition will exist in the fitting routine: either the log likelihood converges, the information matrix becomes effectively singular, an argument to exp becomes too large for the computer hardware, or the maximum number of interactions is exceeded. (Most often number 1 is the first to occur.) The routine attempts to detect when this has happened, not always successfully. The primary consequence for the user is that the Wald statistic = coefficient/se(coefficient) is not valid in this case and should be ignored; the likelihood ratio and score tests remain valid however.

Ties

There are three possible choices for handling tied event times. The Breslow approximation is the easiest to program and hence became the first option coded for almost all computer routines. It then ended up as the default option when other options were added in order to "maintain backwards compatability". The Efron option is more accurate if there are a large number of ties, and it is the default option here. In practice the number of ties is usually small, in which case all the methods are statistically indistinguishable.

Using the "exact partial likelihood" approach the Cox partial likelihood is equivalent to that for matched logistic regression. (The clogit function uses the coxph code to do the fit.) It is technically appropriate when the time scale is discrete and has only a few unique values, and some packages refer to this as the "discrete" option. There is also an "exact marginal likelihood" due to Prentice which is not implemented here.

The calculation of the exact partial likelihood is numerically intense. Say for instance 180 subjects are at risk on day 7 of which 15 had an event; then the code needs to compute sums over all 180-choose-15 > 10^43 different possible subsets of size 15. There is an efficient recursive algorithm for this task, but even with this the computation can be insufferably long. With (start, stop) data it is much worse since the recursion needs to start anew for each unique start time.

Multi state models are a more difficult case. First of all, a proper extension of the Efron argument is much more difficult to do, and this author is not yet fully convinced that the resulting algorithm is defensible. Secondly, the current code for Efron case does not consistently compute that extended logic (and extension would require major changes in the code). Due to this complexity, the default is ties='breslow' for the multistate case. If ties='efron' is selected the current code will, in effect, only apply to to tied transitions of the same type.
A separate issue is that of artificial ties due to floating-point imprecision. See the vignette on this topic for a full explanation or the timefix option in coxph.control. Users may need to add timefix=FALSE for simulated data sets.

Penalized regression

coxph can maximise a penalised partial likelihood with arbitrary user-defined penalty. Supplied penalty functions include ridge regression (ridge), smoothing splines (pspline), and frailty models (frailty).

References


See Also

coxph.object, coxphms.object, coxph.control, cluster, strata, Surv, survfit, pspline.

Examples

```r
# Create the simplest test data set
test1 <- list(time=c(4,3,1,2,2,2,3),
               status=c(1,1,0,1,1,0,0),
               x=c(0,2,1,1,0,0),
               sex=c(0,0,0,1,1,1))
# Fit a stratified model
coxph(Surv(time, status) ~ x + strata(sex), test1)
# Create a simple data set for a time-dependent model
test2 <- list(start=c(1,2,5,2,1,7,3,4,8,8),
               stop=c(2,3,6,7,8,9,9,14,17),
               event=c(1,1,1,1,1,1,0,0,0),
               x=c(1,0,0,1,0,1,1,0,0))
summary(coxph(Surv(start, stop, event) ~ x, test2))
```

```r
# Create a simple data set for a time-dependent model
# test2 <- list(start=c(1, 2, 5, 2, 1, 7, 3, 4, 8, 8),
#                stop =c(2, 3, 6, 7, 8, 9, 9, 14,17),
#                event=c(1, 1, 1, 1, 1, 1, 0, 0, 0),
#                x =c(1, 0, 0, 1, 0, 1, 1, 0, 0) )

summary( coxph( Surv(start, stop, event) ~ x, test2))

# Fit a stratified model, clustered on patients
bladder1 <- bladder[bladder$enum < 5,]
coxph(Surv(stop, event) ~ (rx + size + number) * strata(enum),
     cluster = id, bladder1)

# Fit a time transform model using current age
coxph(Surv(time, status) ~ ph.ecog + tt(age), data=lung,
     cluster = id, bladder1)
```
**coxph.control**

Ancillary arguments for controlling coxph fits

**Description**

This is used to set various numeric parameters controlling a Cox model fit. Typically it would only be used in a call to `coxph`.

**Usage**

```r
coxph.control(eps = 1e-09, toler.chol = .Machine$double.eps^0.75,
iter.max = 20, toler.inf = sqrt(eps), outer.max = 10, timefix=TRUE)
```

**Arguments**

- **eps**
  
  Iteration continues until the relative change in the log partial likelihood is less than `eps`, or the absolute change is less than `sqrt(eps)`. Must be positive.

- **toler.chol**
  
  Tolerance for detection of singularity during a Cholesky decomposition of the variance matrix, i.e., for detecting a redundant predictor variable.

- **iter.max**
  
  Maximum number of iterations to attempt for convergence.

- **toler.inf**
  
  Tolerance criteria for the warning message about a possible infinite coefficient value.

- **outer.max**
  
  For a penalized coxph model, e.g. with pspline terms, there is an outer loop of iteration to determine the penalty parameters; maximum number of iterations for this outer loop.

- **timefix**
  
  Resolve any near ties in the time variables.

**Details**

The convergence tolerances are a balance. Users think they want THE maximum point of the likelihood surface, and for well behaved data sets where this is quadratic near the max a high accuracy is fairly inexpensive: the number of correct digits approximately doubles with each iteration. Conversely, a drop of .0001 from the maximum in any given direction will be correspond to only about $1/20$ of a standard error change in the coefficient. Statistically, more precision than this is straining at a gnat. Based on this the author originally had set the tolerance to $1e-5$, but relented in the face of multiple "why is the answer different than package X" queries.

Asking for results that are too close to machine precision (double.eps) is a fool’s errand; a reasonable criteria is often the square root of that precision. The Cholesky decomposition needs to be held to a higher standard than the overall convergence criterion, however. The `tolerance.inf` value controls a warning message; if it is too small incorrect warnings can appear, if too large some actual cases of an infinite coefficient will not be detected.

The most difficult cases are data sets where the MLE coefficient is infinite; an example is a data set where at each death time, it was the subject with the largest covariate value who perished. In that situation the coefficient increases at each iteration while the log-likelihood asymptotes to a maximum. As iteration proceeds there is a race condition condition for three endpoint: `exp(coef)` overflows, the Hessian matrix become singular, or the change in loglik is small enough to satisfy
the convergence criterion. The first two are difficult to anticipate and lead to numeric difficulties,
which is another argument for moderation in the choice of eps.

See the vignette "Roundoff error and tied times" for a more detailed explanation of the timefix
option. In short, when time intervals are created via subtraction then two time intervals that are
actually identical can appear to be different due to floating point round off error, which in turn can
make coxph and survfit results dependent on things such as the order in which operations were
done or the particular computer that they were run on. Such cases are unfortunately not rare in
practice. The timefix=TRUE option adds logic similar to all.equal to ensure reliable results. In
analysis of simulated data sets, however, where often by definition there can be no duplicates, the
option will often need to be set to FALSE to avoid spurious merging of close numeric values.

**Value**

a list containing the values of each of the above constants

**See Also**

coxph

---

**coxph.detail**

*Details of a Cox Model Fit*

**Description**

Returns the individual contributions to the first and second derivative matrix, at each unique event
time.

**Usage**

```r
coxph.detail(object, riskmat=FALSE, rorder=c("data", "time"))
```

**Arguments**

- `object` a Cox model object, i.e., the result of `coxph`.
- `riskmat` include the at-risk indicator matrix in the output?
- `rorder` should the rows of `x`, `y` and `riskmat` be returned in the original data order, or
  sorted by time within strata.

**Details**

This function may be useful for those who wish to investigate new methods or extensions to the
Cox model. The example below shows one way to calculate the Schoenfeld residuals.

**Value**

a list with components

- `time` the vector of unique event times
- `nevent` the number of events at each of these time points.
mean

A matrix with one row for each event time and one column for each variable in the Cox model, containing the weighted mean of the variable at that time, over all subjects still at risk at that time. The weights are the risk weights \( \exp(x \cdot \text{fit$coef}) \).

nrisk

Number of subjects at risk.

score

The contribution to the score vector (first derivative of the log partial likelihood) at each time point.

imat

The contribution to the information matrix (second derivative of the log partial likelihood) at each time point.

derve hazard

The hazard increment. Note that the hazard and variance of the hazard are always for some particular future subject. This routine uses object$means as the future subject.

derve varhaz

The variance of the hazard increment.

derve x, y

Copies of the input data.

derve strata

Only present for a stratified Cox model, this is a table giving the number of time points of component time that were contributed by each of the strata.

wtrisk

The weighted number at risk.

riskmat

A matrix with one row for each observation and one column for each unique event time, containing a 0/1 value to indicate whether that observation was (1) or was not (0) at risk at the given time point. Rows are in the order of the original data (after removal of any missings by coxph), or in time order.

See Also

coxph, residuals.coxph

Examples

```r
fit <- coxph(Surv(futime,fustat) ~ age + rx + ecog.ps, ovarian, x=TRUE)
fitd <- coxph.detail(fit)
# There is one Schoenfeld residual for each unique death. It is a # vector (covariates for the subject who died) - (weighted mean covariate # vector at that time). The weighted mean is defined over the subjects # still at risk, with \( \exp(x \cdot \beta) \) as the weight.

events <- fit$y[, 2] == 1
etime <- fit$y[events, 1] # the event times --- may have duplicates
indx <- match(etime, fitd$time)
schoen <- fit$x[events, ] - fitd$means[indx,]
```

---

**Description**

This class of objects is returned by the coxph class of functions to represent a fitted proportional hazards model. Objects of this class have methods for the functions print, summary, residuals, predict and survfit.
Arguments

coefficients the vector of coefficients. If the model is over-determined there will be missing values in the vector corresponding to the redundant columns in the model matrix.

var the variance matrix of the coefficients. Rows and columns corresponding to any missing coefficients are set to zero.

naive.var this component will be present only if the robust option was true. If so, the var component will contain the robust estimate of variance, and this component will contain the ordinary estimate. (A far better name would be asymp.var since it contains the model-based asymptotic variance estimate, which is not necessarily "naive"; but that ship has sailed.)

loglik a vector of length 2 containing the log-likelihood with the initial values and with the final values of the coefficients.

score value of the efficient score test, at the initial value of the coefficients.

rscore the robust log-rank statistic, if a robust variance was requested.

wald.test the Wald test of whether the final coefficients differ from the initial values.

iter number of iterations used.

linear.predictors the vector of linear predictors, one per subject. Note that this vector has been centered, see predict.coxph for more details.

residuals the martingale residuals.

means vector of values used as the reference for each covariate. For instance, a later call to predict(fit, type='risk') will give the hazard ratio between an observation and this reference. (For most covariates this will contain the mean.)

n the number of observations used in the fit.

nevent the number of events (usually deaths) used in the fit.

concordance a vector of length 6, containing the number of pairs that are concordant, discordant, tied on x, tied on y, and tied on both, followed by the standard error of the concordance statistic.

first the first derivative vector at the solution.

weights the vector of case weights, if one was used.

method the method used for handling tied survival times.

na.action the na.action attribute, if any, that was returned by the na.action routine.

timefix the value of the timefix option used in the fit

... The object will also contain the following, for documentation see the lm object: terms, assign, formula, call, and, optionally, x, y, and/or frame.

Components

The following components must be included in a legitimate coxph object.

See Also

coxph, coxph.detail, cox.zph, residuals.coxph, survfit, survreg.
**coxph.wtest**

*Compute a quadratic form*

**Description**

This function is used internally by several survival routines. It computes a simple quadratic form, while properly dealing with missings.

**Usage**

```r
coxph.wtest(var, b, toler.chol = 1e-09)
```

**Arguments**

- `var`: variance matrix
- `b`: vector
- `toler.chol`: tolerance for the internal cholesky decomposition

**Details**

Compute b' V-inverse b. Equivalent to `sum(b * solve(V, b))`, except for the case of redundant covariates in the original model, which lead to NA values in V and b.

**Value**

a real number

**Author(s)**

Terry Therneau

---

**coxphms.object**

*Multi-state Proportional Hazards Regression Object*

**Description**

This class of objects is returned by the `coxph` class of functions to represent a fitted hazards model, when the model has multiple states. The object inherits from the `coxph` class.

**Arguments**

- `states`: a character vector listing the states in the model
- `cmap`: the coefficient map. A matrix containing a column for each transition and a row for each coefficient, the value maps that transition/coefficient pair to a position in the coefficient vector. If a particular covariate is not used by a transition the matrix will contain a zero in that position, if two transitions share a coefficient the matrix will contain repeats.
smap

the stratum map. The row labeled ‘(Baseline)’ identifies transitions that do or
do not share a baseline hazard. Further rows correspond to strata() terms in the
model, each of which may apply to some transitions and not others.

rmap

mapping for the residuals and linear predictors. A two column matrix with one
row for each element of the vectors and two columns, the first contains the data
row and the second the transition.

Details

In a multi-state model a set of intermediate observations is created during the computation, with a
separate set of data rows for each transition. An observation (id and time interval) that is at risk
for more than one transition will for instance have a linear predictor and residual for each of the
potential transitions. As a result the vector of linear predictors will be longer than the number of
observations. The rmap matrix shows the mapping.

Components

The object has all the components of a coxph object, with the following additions and variations.

See Also

coxph, coxph.object

coxsurv.fit A direct interface to the ‘computational engine’ of survfit.coxph

Description

This program is mainly supplied to allow other packages to invoke the survfit.coxph function at a
‘data’ level rather than a ‘user’ level. It does no checks on the input data that is provided, which can
lead to unexpected errors if that data is wrong.

Usage

coxsurv.fit(ctype, stype, se.fit, varmat, cluster,
y, x, wt, risk, position, strata, oldid,
y2, x2, risk2, strata2, id2, unlist=TRUE)

Arguments

stype survival curve computation: 1=direct, 2=exp(-cumulative hazard)
ctype cumulative hazard computation: 1=Breslow, 2=Efron
se.fit if TRUE, compute standard errors
varmat the variance matrix of the coefficients
cluster vector to control robust variance
y the response variable used in the Cox model. (Missing values removed of
course.)
x covariate matrix used in the Cox model
wt weight vector for the Cox model. If the model was unweighted use a vector of
1s.
diabetic

risk the risk score \( \exp(X \beta + \text{offset}) \) from the fitted Cox model.

position optional argument controlling what is counted as 'censored'. Due to time
dependent covariates, for instance, a subject might have start, stop times of
(1,5)(5,30)(30,100). Times 5 and 30 are not 'real' censorings. Position is 1
for a real start, 2 for an actual end, 3 for both, 0 for neither.

strata strata variable used in the Cox model. This will be a factor.

oldid identifier for subjects with multiple rows in the original data.

y2, x2, risk2, strata2
variables for the hypothetical subjects, for which prediction is desired

id2
optional; if present and not NULL this should be a vector of identifiers of length
\( \text{nrow}(x2) \). A non-null value signifies that \( x2 \) contains time dependent covari-
ates, in which case this identifies which rows of \( x2 \) go with each subject.

unlist if FALSE the result will be a list with one element for each strata. Otherwise the
strata are “unpacked” into the form found in a \text{survfit} object.

Value

a list containing nearly all the components of a \text{survfit} object. All that is missing is to add the
confidence intervals, the type of the original model’s response (as in a coxph object), and the class.

Note

The source code for for both this function and \text{survfit.coxph} is written using noweb. For complete
documentation see the \text{inst/sourcecode.pdf} file.

Author(s)

Terry Therneau

See Also

\text{survfit.coxph}

---

diabetic \hspace{1cm} Diabetic retinopathy

description

Partial results from a trial of laser coagulation for the treatment of diabetic retinopathy.

Usage

\text{diabetic}
\text{data(diabetic, package="survival")}
Format

A data frame with 394 observations on the following 8 variables.

- **id**: subject id
- **laser**: laser type: xenon or argon
- **age**: age at diagnosis
- **eye**: a factor with levels of left right
- **trt**: treatment: 0 = no treatment, 1 = laser
- **risk**: risk group of 6-12
- **time**: time to event or last follow-up
- **status**: status of 0 = censored or 1 = visual loss

Details

The 197 patients in this dataset were a 50% random sample of the patients with "high-risk" diabetic retinopathy as defined by the Diabetic Retinopathy Study (DRS). Each patient had one eye randomized to laser treatment and the other eye received no treatment. For each eye, the event of interest was the time from initiation of treatment to the time when visual acuity dropped below 5/200 two visits in a row. Thus there is a built-in lag time of approximately 6 months (visits were every 3 months). Survival times in this dataset are therefore the actual time to blindness in months, minus the minimum possible time to event (6.5 months). Censoring was caused by death, dropout, or end of the study.

References

Huster, Brookmeyer and Self, Biometrics, 1989.

Examples

```r
# juvenile diabetes is defined as age less than 20
juvenile <- 1*(diabetic$age < 20)
coxph(Surv(time, status) ~ trt + juvenile, cluster= id, 
    data= diabetic)
```

Description

Density, cumulative distribution function, quantile function and random generation for the set of distributions supported by the `survreg` function.

Usage

```r
dsurvreg(x, mean, scale=1, distribution='weibull', params) 
psurvreg(q, mean, scale=1, distribution='weibull', params) 
qsurvreg(p, mean, scale=1, distribution='weibull', params) 
rsurvreg(n, mean, scale=1, distribution='weibull', params)
```
Arguments

- **x**: vector of quantiles. Missing values (NAs) are allowed.
- **q**: vector of quantiles. Missing values (NAs) are allowed.
- **p**: vector of probabilities. Missing values (NAs) are allowed.
- **n**: number of random deviates to produce
- **mean**: vector of location (linear predictor) parameters for the model. This is replicated to be the same length as p, q or n.
- **scale**: vector of (positive) scale factors. This is replicated to be the same length as p, q or n.
- **distribution**: character string giving the name of the distribution. This must be one of the elements of `survreg.distributions`.
- **parms**: optional parameters, if any, of the distribution. For the t-distribution this is the degrees of freedom.

Details

Elements of q or p that are missing will cause the corresponding elements of the result to be missing.

The location and scale values are as they would be for `survreg`. The label "mean" was an unfortunate choice (made in mimicry of `qnorm`); a more correct label would be "linear predictor". Since almost none of these distributions are symmetric the location parameter is not actually a mean.

The `survreg` routines use the parameterization found in chapter 2 of Kalbfleisch and Prentice. Translation to the usual parameterization found in a textbook is not always obvious. For example, the Weibull distribution has cumulative distribution function \( F(t) = 1 - e^{-(M)/t} \). The actual fit uses the fact that \( \log(t) \) has an extreme value distribution, with location and scale of \( \alpha, \sigma \), which are the location and scale parameters reported by the `survreg` function. The parameters are related by \( \sigma = 1/p \) and \( \alpha = -\log(\lambda) \). The `stats::dweibull` routine is parameterized in terms of shape and scale parameters which correspond to \( p \) and \( 1/\lambda \) in the K and P notation. Combining these we see that shape = \( 1/\sigma \) and scale = \( \exp(\alpha) \).

Value

- density (dsurvreg), probability (psurvreg), quantile (qsurvreg), or for the requested distribution with mean and scale parameters mean and sd.

References


See Also

- `survreg`, `Normal`
Examples

```r
# List of distributions available
names(survreg.distributions)
## Not run:
[1] "extreme" "logistic" "gaussian" "weibull" "exponential"
[6] "rayleigh" "loggaussian" "lognormal" "loglogistic" "t"
## End(Not run)

# Compare results
all.equal(dsurvreg(1:10, 2, 5, dist='lognormal'), dlnorm(1:10, 2, 5))

# Hazard function for a Weibull distribution
x <- seq(.1, 3, length=30)
haz <- dsurvreg(x, 2, 3)/(1-psurvreg(x, 2, 3))
## Not run:
plot(x, haz, log='xy', ylab="Hazard") #line with slope (1/scale -1)
## End(Not run)

# Estimated CDF of a simple Weibull
fit <- survreg(Surv(time, status) ~ 1, data=lung)
pp <- 1:99/100
q1 <- qsurvreg(pp, coef(fit), fit$scale)
q2 <- qweibull(pp, shape=1/fit$scale, scale=exp(coef(fit)))
all.equal(q1, q2)
## Not run:
plot(q1, pp, type='l', xlab="Months", ylab="CDF")
## End(Not run)

# per the help page for dweibull, the mean is scale * gamma(1 + 1/shape)
c(mean = exp(coef(fit))* gamma(1 + fit$scale))
```

finegray  

Create data for a Fine-Gray model

Description

The Fine-Gray model can be fit by first creating a special data set, and then fitting a weighted Cox model to the result. This routine creates the data set.

Usage

```r
finegray(formula, data, weights, subset, na.action=na.pass, etype,
prefix="fg", count, id, timefix=TRUE)
```

Arguments

- **formula**: a standard model formula, with survival on the left and covariates on the right.
- **data**: an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model.
- **weights**: optional vector of observation weights
subset: an optional vector specifying a subset of observations to be used in the fitting process.

na.action: a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options.

etype: the event type for which a data set will be generated. The default is to use whichever is listed first in the multi-state survival object.

prefix: the routine will add 4 variables to the data set: a start and end time for each interval, status, and a weight for the interval. The default names of these are "fgstart", "fgstop", "fgstatus", and "fgwt"; the prefix argument determines the initial portion of the new names.

count: a variable name in the output data set for an optional variable that will contain the replication count for each row of the input data. If a row is expanded into multiple lines it will contain 1, 2, etc.

id: optional, the variable name in the data set which identifies subjects.

timefix: process times through the aeqSurv function to eliminate potential roundoff issues.

Details:

The function expects a multi-state survival expression or variable as the left hand side of the formula, e.g. Surv(atime, astat) where astat is a factor whose first level represents censoring and remaining levels are states. The output data set will contain simple survival data (status = 0 or 1) for a single endpoint of interest. For exposition call this endpoint A and lump all others as endpoint B. In the output data set subjects who experience endpoint B become censored observations whose times are artificially extended to the right, with a decreasing case weight from interval to interval. The output data set will normally contain many more rows than the input.

The algorithm allows for delayed entry, and only a limited form of time-dependent covariates. That is, when subjects with endpoint B are extended, those future covariate values stay constant; so there is an implicit assumption that no more changes would have occurred if the event had not intervened and follow-up had been longer. For predictable time-dependent covariates the final data set could be further processed to fix this, but this is not included in the function. Geskus for example considers an example with different calendar epochs, corresponding to a change in standard medical practice for the disease, as a covariate. Dependent covariates. If there are time dependent covariates or delayed entry, e.g., the input data set had Surv(entry, exit, stat) as the left hand side, then an id statement is required. The program does data checks in this case, and needs to know which rows belong to each subject.

The output data set will often have gaps. Say that there were events at time 50 and 100 (and none between) and censoring at 60, 70, and 80. Formally, a non event subjects at risk from 50 to 100 will have different weights in each of the 3 intervals 50-60, 60-70, and 80-100, but because the middle interval does not span any event times the subsequent Cox model will never use that row. The finegray output omits such rows.

See the competing risks vignette for more details.

Value:

a data frame

Author(s):

Terry Therneau
References


See Also

coxph, aeqSurv

Examples

# Treat time to death and plasma cell malignancy as competing risks
etime <- with(mgus2, ifelse(pstat==0, futime, ptime))
event <- with(mgus2, ifelse(pstat==0, 2*death, 1))
event <- factor(event, 0:2, labels=c("censor", "pcm", "death"))

# FG model for PCM
pdata <- finegray(Surv(etime, event) ~ ., data=mgus2)
fgfit <- coxph(Surv(fgstart, fgstop, fgstatus) ~ age + sex,
weight=fgwt, data=pdata)

# Compute the weights separately by sex
adata <- finegray(Surv(etime, event) ~ . + strata(sex),
data=mgus2, na.action=na.pass)

flchain

Assay of serum free light chain for 7874 subjects.

Description

This is a stratified random sample containing 1/2 of the subjects from a study of the relationship between serum free light chain (FLC) and mortality. The original sample contains samples on approximately 2/3 of the residents of Olmsted County aged 50 or greater.

Usage

flchain
data(flchain, package="survival")

Format

A data frame with 7874 persons containing the following variables.

age age in years
sex F=female, M=male
sample.yr the calendar year in which a blood sample was obtained
kappa serum free light chain, kappa portion
lambda serum free light chain, lambda portion
flc.grp the FLC group for the subject, as used in the original analysis
In 1995 Dr. Robert Kyle embarked on a study to determine the prevalence of monoclonal gammapathy of undetermined significance (MGUS) in Olmsted County, Minnesota, a condition which is normally only found by chance from a test (serum electrophoresis) which is ordered for other causes. Later work suggested that one component of immunoglobulin production, the serum free light chain, might be a possible marker for immune disregulation. In 2010 Dr. Angela Dispenzieri and colleagues assayed FLC levels on those samples from the original study for which they had patient permission and from which sufficient material remained for further testing. They found that elevated FLC levels were indeed associated with higher death rates.

Patients were recruited when they came to the clinic for other appointments, with a final random sample of those who had not yet had a visit since the study began. An interesting side question is whether there are differences between early, mid, and late recruits.

This data set contains an age and sex stratified random sample that includes 7874 of the original 15759 subjects. The original subject identifiers and dates have been removed to protect patient identity. Subsampling was done to further protect this information.

Source
The primary investigator (A Dispenzieri) and statistician (T Therneau) for the study.

References


Examples
```r
data(flchain)
age.grp <- cut(flchain$age, c(49,54, 59,64, 69,74,79, 89, 110),
                      labels= paste(c(50,55,60,65,70,75,80,89),
                                      c(54,59,64,69,74,79,89,109), sep='- '))
table(flchain$sex, age.grp)
```
frailty

Random effects terms

Description

The frailty function allows one to add a simple random effects term to a Cox model.

Usage

frailty(x, distribution="gamma", ...)
frailty.gamma(x, sparse = (nclass > 5), theta, df, eps = 1e-05,
    method = c("em","aic", "df", "fixed"), ...)
frailty.gaussian(x, sparse = (nclass > 5), theta, df,
    method =c("reml","aic", "df", "fixed"), ...)
frailty.t(x, sparse = (nclass > 5), theta, df, eps = 1e-05, tdf = 5,
    method = c("aic", "df", "fixed"), ...)

Arguments

x the variable to be entered as a random effect. It is always treated as a factor.
distribution either the gamma, gaussian or t distribution may be specified. The routines
    frailty.gamma, frailty.gaussian and frailty.t do the actual work.
... Arguments for specific distribution, including (but not limited to)
sparse cutoff for using a sparse coding of the data matrix. If the total number of levels
    of x is larger than this value, then a sparse matrix approximation is used. The
    correct cutoff is still a matter of exploration: if the number of levels is very large
    (thousands) then the non-sparse calculation may not be feasible in terms of both
    memory and compute time. Likewise, the accuracy of the sparse approximation
    appears to be related to the maximum proportion of subjects in any one class,
    being best when no one class has a large membership.
theta if specified, this fixes the variance of the random effect. If not, the vari-
    ance is a parameter, and a best solution is sought. Specifying this implies
    method='fixed'.
df if specified, this fixes the degrees of freedom for the random effect. Specifying
    this implies method='df'. Only one of theta or df should be specified.
method the method used to select a solution for theta, the variance of the random effect.
    The fixed corresponds to a user-specified value, and no iteration is done. The
    df selects the variance such that the degrees of freedom for the random effect
    matches a user specified value. The aic method seeks to maximize Aikake’s
    information criteria 2*(partial likelihood - df). The em and reml methods are
    specific to Cox models with gamma and gaussian random effects, respectively.
    Please see further discussion below.
tdf the degrees of freedom for the t-distribution.
eps convergence criteria for the iteration on theta.
frailty

Details

The frailty plugs into the general penalized modeling framework provided by the coxph and survreg routines. This framework deals with likelihood, penalties, and degrees of freedom; these aspects work well with either parent routine.

Therneau, Grambsch, and Pankratz show how maximum likelihood estimation for the Cox model with a gamma frailty can be accomplished using a general penalized routine, and Ripatti and Palmgren work through a similar argument for the Cox model with a gaussian frailty. Both of these are specific to the Cox model. Use of gamma/ml or gaussian/reml with survreg does not lead to valid results.

The extensible structure of the penalized methods is such that the penalty function, such as frailty or pspine, is completely separate from the modeling routine. The strength of this is that a user can plug in any penalization routine they choose. A weakness is that it is very difficult for the modeling routine to know whether a sensible penalty routine has been supplied.

Note that use of a frailty term implies a mixed effects model and use of a cluster term implies a GEE approach; these cannot be mixed.

The coxme package has superseded this method. It is faster, more stable, and more flexible.

Value

this function is used in the model statement of either coxph or survreg. It’s results are used internally.

References


See Also

coxph, survreg

Examples

# Random institutional effect
coxph(Surv(time, status) ~ age + frailty(inst, df=4), lung)

# Litter effects for the rats data
rfit2a <- coxph(Surv(time, status) ~ rx +
frailty.gaussian(litter, df=13, sparse=FALSE), rats,
subset= (sex=='f'))
rfit2b <- coxph(Surv(time, status) ~ rx +
frailty.gaussian(litter, df=13, sparse=TRUE), rats,
subset= (sex=='f'))
Breast cancer data sets used in Royston and Altman (2013)

Description
The gbsg data set contains patient records from a 1984-1989 trial conducted by the German Breast Cancer Study Group (GBSG) of 720 patients with node positive breast cancer; it retains the 686 patients with complete data for the prognostic variables.

Usage

gbsg
data(cancer, package="survival")

Format
A data set with 686 observations and 11 variables.

- pid  patient identifier
- age  age, years
- meno  menopausal status (0= premenopausal, 1= postmenopausal)
- size  tumor size, mm
- grade  tumor grade
- nodes  number of positive lymph nodes
- pgr  progesterone receptors (fmol/l)
- er  estrogen receptors (fmol/l)
- hormon  hormonal therapy, 0= no, 1= yes
- rfstime recurrence free survival time; days to first of recurrence, death or last follow-up
- status  0= alive without recurrence, 1= recurrence or death

Details
These data sets are used in the paper by Royston and Altman. The Rotterdam data is used to create a fitted model, and the GBSG data for validation of the model. The paper gives references for the data source.

References

See Also
rotterdam
Stanford Heart Transplant data

Description

Survival of patients on the waiting list for the Stanford heart transplant program.

Usage

```r
heart
data(heart, package="survival")
```

Format

- **jasa**: original data
  - `birth.dt`: birth date
  - `accept.dt`: acceptance into program
  - `tx.date`: transplant date
  - `fu.date`: end of followup
  - `fustat`: dead or alive
  - `surgery`: prior bypass surgery
  - `age`: age (in years)
  - `futime`: followup time
  - `wait.time`: time before transplant
  - `transplant`: transplant indicator
  - `mismatch`: mismatch score
  - `hla.a2`: particular type of mismatch
  - `mscore`: another mismatch score
  - `reject`: rejection occurred

- **jasa1, heart**: processed data
  - `start`, `stop`, `event`: Entry and exit time and status for this interval of time
  - `age`: age-48 years
  - `year`: year of acceptance (in years after 1 Nov 1967)
  - `surgery`: prior bypass surgery 1=yes
  - `transplant`: received transplant 1=yes
  - `id`: patient id

Source


See Also

- `stanford2`
Description

Days until occurrence of cancer for male mice

Usage

data("cancer")

Format

A data frame with 181 observations on the following 4 variables.

trt treatment assignment: Control or Germ-free

days days until death

outcome outcome: codecensor, thymic lymphoma, reticulum cell sarcoma other causes

id mouse id

Details

Two groups of male mice were given 300 rads of radiation and followed for cancer incidence. One group was maintained in a germ free environment. The data set is used as an example of competing risks in Kalbfleisch and Prentice. The germ-free environment has little effect on the rate of occurrence of thymic lymphoma, but significantly delays the other causes of death.

Note

The Ontology Search website defines reticulum cell sarcoma as "An antiquated term that refers to a non-Hodgkin lymphoma composed of diffuse infiltrates of large, often anaplastic lymphocytes".

Source

The data can be found in appendix I of Kalbfleisch and Prentice.

References


Examples

hsurv <- survfit(Surv(days, outcome) ~ trt, data = hoel, id = id)
plot(hsurv, lty=1:2, col=rep(1:3, each=2), lwd=2, xscale=30.5,
    xlab="Months", ylab= "Death")
legend("topleft", c("Lymphoma control", "Lymphoma germ free",
    "Sarcoma control", "Sarcoma germ free",
    "Other control", "Other germ free"),
    col=rep(1:3, each=2), lty=1:2, lwd=2, bty='n')
hfit <- coxph(Surv(days, outcome) ~ trt, data= hoel, id = id)
is.ratetable

Verify that an object is of class ratetable.

Description

The function verifies not only the class attribute, but the structure of the object.

Usage

is.ratetable(x, verbose=FALSE)

Arguments

x

the object to be verified.

verbose

if TRUE and the object is not a ratetable, then return a character string describing the way(s) in which x fails to be a proper ratetable object.

Details

Rate tables are used by the pyears and survexp functions, and normally contain death rates for some population, categorized by age, sex, or other variables. They have a fairly rigid structure, and the verbose option can help in creating a new rate table.

Value

returns TRUE if x is a ratetable, and FALSE or a description if it is not.

See Also

pyears, survexp.

Examples

is.ratetable(survexp.us)  # True
is.ratetable(lung)        # False

kidney

Kidney catheter data

Description

Data on the recurrence times to infection, at the point of insertion of the catheter, for kidney patients using portable dialysis equipment. Catheters may be removed for reasons other than infection, in which case the observation is censored. Each patient has exactly 2 observations.

This data has often been used to illustrate the use of random effects (frailty) in a survival model. However, one of the males (id 21) is a large outlier, with much longer survival than his peers. If this observation is removed no evidence remains for a random subject effect.
Usage

kidney
data(cancer, package="survival")

Format

patient: id
time: time
status: event status
age: in years
sex: 1=male, 2=female
disease: disease type (0=GN, 1=AN, 2=PKD, 3=Other)
frail: frailty estimate from original paper

Note

The original paper ignored the issue of tied times and so is not exactly reproduced by the survival package.

Source


Examples

kfit <- coxph(Surv(time, status)~ age + sex + disease + frailty(id), kidney)
kfit0 <- coxph(Surv(time, status)~ age + sex + disease, kidney)
kfitm1 <- coxph(Surv(time,status) ~ age + sex + disease + frailty(id, dist='gauss'), kidney)

levels.Surv

Return the states of a multi-state Surv object

Description

For a multi-state Surv object, this will return the names of the states.

Usage

## S3 method for class 'Surv'
levels(x)

Arguments

x a Surv object
Value

For a multi-state Surv object, the vector of state names (excluding censoring); or NULL for an ordinary Surv object.

Examples

```r
y1 <- Surv(c(1, 5, 9, 17, 21, 30),
  factor(c(0, 1, 2, 1, 0, 2), 0:2, c("censored", "progression", "death"))
levels(y1)

y2 <- Surv(1:6, rep(0:1, 3))
levels(y2)
```

Description

Often used to add the expected survival curve(s) to a Kaplan-Meier plot generated with plot.survfit.

Usage

```r
## S3 method for class 'survfit'
lines(x, type="s", pch=3, col=1, lty=1,
  lwd=1, cex=1, mark.time=FALSE, xmax,
  fun, conf.int=FALSE, conf.times, conf.cap=.005, conf.offset=.012,
  conf.type = c("log", "log-log", "plain", "logit", "arcsin"),
  mark, noplot="(s0)", cumhaz= FALSE, ...)
## S3 method for class 'survexp'
lines(x, type="l", ...)
## S3 method for class 'survfit'
points(x, fun, censor=FALSE, col=1, pch,
  noplot="(s0)", cumhaz=FALSE, ...)
```

Arguments

- `x`: a survival object, generated from the survfit or survexp functions.
- `type`: the line type, as described in lines. The default is a step function for survfit objects, and a connected line for survexp objects. All other arguments for lines.survexp are identical to those for lines.survfit.
- `col`, `lty`, `lwd`, `cex`: vectors giving the mark symbol, color, line type, line width and character size for the added curves. Of this set only color is applicable to points.
- `pch`: plotting characters for points, in the style of matplot, i.e., either a single string of characters of which the first will be used for the first curve, etc; or a vector of characters or integers, one element per curve.
- `mark`: a historical alias for `pch`.
censor should censoring times be displayed for the points function?
mark.time controls the labeling of the curves. If FALSE, no labeling is done. If TRUE, then curves are marked at each censoring time. If mark.time is a numeric vector, then curves are marked at the specified time points.
xmax optional cutoff for the right hand of the curves.
fun an arbitrary function defining a transformation of the survival curve. For example fun=log is an alternative way to draw a log-survival curve (but with the axis labeled with log(S) values). Four often used transformations can be specified with a character argument instead: "log" is the same as using the log=T option, "event" plots cumulative events (f(y) = 1-y), "cumhaz" plots the cumulative hazard function (f(y) = -log(y)) and "cloglog" creates a complimentary log-log survival plot (f(y) = log(-log(y))) along with log scale for the x-axis.
conf.int if TRUE, confidence bands for the curves are also plotted. If set to "only", then only the CI bands are plotted, and the curve itself is left off. This can be useful for fine control over the colors or line types of a plot. A numeric value, e.g. conf.int = .90, can be used to
conf.times optional vector of times at which to place a confidence bar on the curve(s). If present, these will be used instead of confidence bands.
conf.cap width of the horizontal cap on top of the confidence bars; only used if conf.times is used. A value of 1 is the width of the plot region.
conf.offset the offset for confidence bars, when there are multiple curves on the plot. A value of 1 is the width of the plot region. If this is a single number then each curve’s bars are offset by this amount from the prior curve’s bars, if it is a vector the values are used directly.
conf.type One of "plain", "log" (the default), "log-log", "logit", or "none". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals curve ± k *se(curve), where k is determined from conf.int. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), and the logit option on log(survival/(1-survival)).
noplot for multi-state models, curves with this label will not be plotted. The default corresponds to an unspecified state.
cumhaz plot the cumulative hazard, rather than the survival or probability in state.
... other graphical parameters

Details

When the survfit function creates a multi-state survival curve the resulting object has class ‘survfitms’. The only difference in the plots is that that it defaults to a curve that goes from lower left to upper right (starting at 0), where survival curves default to starting at 1 and going down. All other options are identical.

If the user set an explicit range in an earlier plot.survfit call, e.g. via xlim or xmax, subsequent calls to this function remember the right hand cutoff. This memory can be erased by options(plot.survfit) <- NULL.

Value

a list with components x and y, containing the coordinates of the last point on each of the curves (but not of the confidence limits). This may be useful for labeling.
Side Effects

one or more curves are added to the current plot.

See Also

lines, par, plot.survfit, survfit, survexp.

Examples

fit <- survfit(Surv(time, status==2) ~ sex, pbc, subset=1:312)
plot(fit, mark.time=FALSE, xscale=365.25,
     xlab='Years', ylab='Survival')
lines(fit[1], lwd=2)  # darken the first curve and add marks

# Add expected survival curves for the two groups,
# based on the US census data
# The data set does not have entry date, use the midpoint of the study
efit <- survexp(~sex, data=pbc, times= (0:24)*182, ratetable=survexp.us,
                  rmap=list(sex=sex, age=age*365.35, year=as.Date('1979/01/01')))
temp <- lines(efit, lty=2, lwd=2:1)
text(temp, c("Male", "Female"), adj=-.1) # labels just past the ends
title(main="Primary Biliary Cirrhosis, Observed and Expected")

logan

Data from the 1972-78 GSS data used by Logan

Description

Intergenerational occupational mobility data with covariates.

Usage

logan

data(logan, package="survival")

Format

A data frame with 838 observations on the following 4 variables.

occupation subject's occupation, a factor with levels farm, operatives, craftsmen, sales, and professional
focc father's occupation
education total years of schooling, 0 to 20
race levels of non-black and black

Source

General Social Survey data, see the web site for detailed information on the variables. https://gss.norc.org/.
logLik.coxph

**logLik method for a Cox model**

**Description**

The logLik function for survival models

**Usage**

```r
## S3 method for class 'coxph'
logLik(object, ...)
## S3 method for class 'survreg'
logLik(object, ...)
```

**Arguments**

- `object` the result of a coxph or survreg fit
- `...` optional arguments for other instances of the method

**Details**

The logLik function is used by summary functions in R such as AIC. For a Cox model, this method returns the partial likelihood. The number of degrees of freedom (df) used by the fit and the effective number of observations (nobs) are added as attributes. Per Raftery and others, the effective number of observations is the taken to be the number of events in the data set.

For a survreg model the proper value for the effective number of observations is still an open question (at least to this author). For right censored data the approach of logLik.coxph is the possible the most sensible, but for interval censored observations the result is unclear. The code currently does not add a nobs attribute.

**Value**

an object of class logLik

**Author(s)**

Terry Therneau

**References**


**See Also**

logLik
**NCCTG Lung Cancer Data**

**Description**
Survival in patients with advanced lung cancer from the North Central Cancer Treatment Group. Performance scores rate how well the patient can perform usual daily activities.

**Usage**
```r
data(cancer, package="survival")
```

**Format**
- **inst**: Institution code
- **time**: Survival time in days
- **status**: censoring status 1=censored, 2=dead
- **age**: Age in years
- **sex**: Male=1 Female=2
- **ph.ecog**: ECOG performance score as rated by the physician. 0=asymptomatic, 1=symptomatic but completely ambulatory, 2= in bed <50% of the day, 3= in bed > 50% of the day but not bedbound, 4 = bedbound
- **ph.karno**: Karnofsky performance score (bad=0-good=100) rated by physician
- **pat.karno**: Karnofsky performance score as rated by patient
- **meal.cal**: Calories consumed at meals
- **wt.loss**: Weight loss in last six months (pounds)

**Note**
The use of 1/2 for alive/dead instead of the usual 0/1 is a historical footnote. For data contained on punch cards, IBM 360 Fortran treated blank as a zero, which led to a policy within the section of Biostatistics to never use "0" as a data value since one could not distinguish it from a missing value. The policy became a habit, as is often the case; and the 1/2 coding endured long beyond the demise of punch cards and Fortran.

**Source**
Terry Therneau

**References**
Description

Natural history of 241 subjects with monoclonal gammopathy of undetermined significance (MGUS).

Usage

```r
mgus
gmus1
data(cancer, package="survival")
```

Format

**mgus**: A data frame with 241 observations on the following 12 variables.

- **id**: subject id
- **age**: age in years at the detection of MGUS
- **sex**: male or female
- **dxyr**: year of diagnosis
- **pcdx**: for subjects who progress to a plasma cell malignancy
  - the subtype of malignancy: multiple myeloma (MM) is the most common, followed by amyloidosis (AM), macroglobulinemia (MA), and other lymphoproliferative disorders (LP)
- **pctime**: days from MGUS until diagnosis of a plasma cell malignancy
- **futime**: days from diagnosis to last follow-up
- **death**: 1= follow-up is until death
- **alb**: albumin level at MGUS diagnosis
- **creat**: creatinine at MGUS diagnosis
- **hgb**: hemoglobin at MGUS diagnosis
- **mspike**: size of the monoclonal protein spike at diagnosis

**mgus1**: The same data set in start,stop format. Contains the id, age, sex, and laboratory variable described above along with

- **start, stop**: sequential intervals of time for each subject
- **status**: =1 if the interval ends in an event
- **event**: a factor containing the event type: censor, death, or plasma cell malignancy
- **enum**: event number for each subject: 1 or 2

Details

Plasma cells are responsible for manufacturing immunoglobulins, an important part of the immune defense. At any given time there are estimated to be about $10^6$ different immunoglobulins in the circulation at any one time. When a patient has a plasma cell malignancy the distribution will become dominated by a single isotype, the product of the malignant clone, visible as a spike on a serum protein electrophoresis. Monoclonal gammopathy of undetermined significance (MGUS) is the presence of such a spike, but in a patient with no evidence of overt malignancy. This data
set of 241 sequential subjects at Mayo Clinic was the groundbreaking study defining the natural history of such subjects. Due to the diligence of the principle investigator 0 subjects have been lost to follow-up.

Three subjects had MGUS detected on the day of death. In data set mgus1 these subjects have the time to MGUS coded as .5 day before the death in order to avoid tied times.

These data sets were updated in Jan 2015 to correct some small errors.

Source

Mayo Clinic data courtesy of Dr. Robert Kyle.

References


Examples

# Create the competing risk curves for time to first of death or PCM
sfit <- survfit(Surv(start, stop, event) ~ sex, mgus1, id=id,
subset=(enum==1))
print(sfit) # the order of printout is the order in which they plot

plot(sfit, xscale=365.25, lty=c(2,2,1,1), col=c(1,2,1,2),
  xlab="Years after MGUS detection", ylab="Proportion")
legend(0, .8, c("Death/male", "Death/female", "PCM/male", "PCM/female"),
  lty=c(1,1,2,2), col=c(2,1,2,1), bty='n')

title("Curves for the first of plasma cell malignancy or death")
# The plot shows that males have a higher death rate than females (no
# surprise) but their rates of conversion to PCM are essentially the same.

mgus2  Monoclonal gammopathy data

Description

Natural history of 1341 sequential patients with monoclonal gammopathy of undetermined significance (MGUS). This is a superset of the mgus data, at a later point in the accrual process

Usage

mgus2
data(cancer, package="survival")

Format

A data frame with 1384 observations on the following 10 variables.

id  subject identifier
age  age at diagnosis, in years
sex  a factor with levels F M
dxyr  year of diagnosis
hgb  hemoglobin
creat  creatinine
mspike  size of the monoclonal serum spike
ptime  time until progression to a plasma cell malignancy (PCM) or last contact, in months
pstat  occurrence of PCM: 0=no, 1=yes
futime  time until death or last contact, in months
death  occurrence of death: 0=no, 1=yes

Details

This is an extension of the study found in the mgus data set, containing enrollment through 1994 and follow-up through 1999.

Source

Mayo Clinic data courtesy of Dr. Robert Kyle. All patient identifiers have been removed, age rounded to the nearest year, and follow-up times rounded to the nearest month.

References


---

model.frame.coxph  
Model.frame method for coxph objects

Description

Recreate the model frame of a coxph fit.

Usage

```r
## S3 method for class 'coxph'
model.frame(formula, ...)
```

Arguments

- `formula`  the result of a coxph fit
- `...`  other arguments to `model.frame`

Details

For details, see the manual page for the generic function. This function would rarely be called by a user, it is mostly used inside functions like `residual` that need to recreate the data set from a model in order to do further calculations.
Value

the model frame used in the original fit, or a parallel one for new data.

Author(s)

Terry Therneau

See Also

model.frame

Description

Reconstruct the model matrix for a cox model.

Usage

## S3 method for class 'coxph'
model.matrix(object, data=NULL, contrast.arg =
object$contrasts, ...)

Arguments

  object     the result of a coxph model
  data       optional, a data frame from which to obtain the data
  contrast.arg optional, a contrasts object describing how factors should be coded
  ...        other possible argument to model.frame

Details

When there is a data argument this function differs from most of the other model.matrix methods in that the response variable for the original formula is not required to be in the data.

If the data frame contains a terms attribute then it is assumed to be the result of a call to model.frame, otherwise a call to model.frame is applied with the data as an argument.

Value

The model matrix for the fit

Author(s)

Terry Therneau

See Also

model.matrix
**Examples**

```r
fit1 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung)
xfit <- model.matrix(fit1)

fit2 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung, x=TRUE)
all.equal(model.matrix(fit1), fit2$x)
```

---

**myeloid**

**Acute myeloid leukemia**

**Description**

This simulated data set is based on a trial in acute myeloid leukemia.

**Usage**

```r
myeloid
data(cancer, package="survival")
```

**Format**

A data frame with 646 observations on the following 9 variables.

- **id**: subject identifier, 1-646
- **trt**: treatment arm A or B
- **sex**: f=female, m=male
- **futime**: time to death or last follow-up
- **death**: 1 if futime is a death, 0 for censoring
- **txtime**: time to hematopoietic stem cell transplant
- **crtime**: time to complete response
- **rltime**: time to relapse of disease

**Details**

This data set is used to illustrate multi-state survival curves. The correlation between within-subject event times strongly resembles that from an actual trial, but none of the actual data values are from that source.

**References**


**Examples**

```r
coxph(Surv(futime, death) ~ trt, data=myeloid)
# See the mstate vignette for a more complete analysis
```
myeloma

Survival times of patients with multiple myeloma

Description
Survival times of 3882 subjects with multiple myeloma, seen at Mayo Clinic from 1947–1996.

Usage
myeloma
data("cancer", package="survival")

Format
A data frame with 3882 observations on the following 5 variables.

id subject identifier
year year of entry into the study
entry time from diagnosis of MM until entry (days)
futime follow up time (days)
dead status at last follow-up: 0 = alive, 1 = death

Details
Subjects who were diagnosed at Mayo will have entry =0, those who were diagnosed elsewhere and later referred will have positive values.

References

Examples
# Incorrect survival curve, which ignores left truncation
fit1 <- survfit(Surv(futime, death) ~ 1, myeloma)
# Correct curve
fit2 <- survfit(Surv(entry, futime, death) ~ 1, myeloma)

nafld
Non-alcohol fatty liver disease

Description
Data sets containing the data from a population study of non-alcoholic fatty liver disease (NAFLD). Subjects with the condition and a set of matched control subjects were followed forward for metabolic conditions, cardiac endpoints, and death.
Usage

```r
nafl1d
nafl1d2
nafl1d3
data(nafl1d, package="survival")
```

Format

nafl1d1 is a data frame with 17549 observations on the following 10 variables.

- id: subject identifier
- age: age at entry to the study
- male: 0=female, 1=male
- weight: weight in kg
- height: height in cm
- bmi: body mass index
- case.id: the id of the NAFLD case to whom this subject is matched
- futime: time to death or last follow-up
- status: 0= alive at last follow-up, 1=dead

nafl1d2 is a data frame with 400123 observations and 4 variables containing laboratory data

- id: subject identifier
- days: days since index date
- test: the type of value recorded
- value: the numeric value

nafl1d3 is a data frame with 34340 observations and 3 variables containing outcomes

- id: subject identifier
- days: days since index date
- event: the endpoint that occurred

Details

The primary reference for the NAFLD study is Allen (2018). The incidence of non-alcoholic fatty liver disease (NAFLD) has been rising rapidly in the last decade and it is now one of the main drivers of hepatology practice Tapper2018. It is essentially the presence of excess fat in the liver, and parallels the ongoing obesity epidemic. Approximately 20-25% of NAFLD patients will develop the inflammatory state of non-alcoholic steatohepatitis (NASH), leading to fibrosis and eventual end-stage liver disease. NAFLD can be accurately diagnosed by MRI methods, but NASH diagnosis currently requires a biopsy.

The current study constructed a population cohort of all adult NAFLD subjects from 1997 to 2014 along with 4 potential controls for each case. To protect patient confidentiality all time intervals are in days since the index date; none of the dates from the original data were retained. Subject age is their integer age at the index date, and the subject identifier is an arbitrary integer. As a final protection, we include only a 90% random sample of the data. As a consequence analyses results will not exactly match the original paper.

There are 3 data sets: nafl1d1 contains baseline data and has one observation per subject, nafl1d2 has one observation for each (time dependent) continuous measurement, and nafl1d3 has one observation for each yes/no outcome that occurred.
neardate

Source
Data obtained from the author.

References

neardate

Find the index of the closest value in data set 2, for each entry in data set one.

Description
A common task in medical work is to find the closest lab value to some index date, for each subject.

Usage
neardate(id1, id2, y1, y2, best = c("after", "prior"), nomatch = NA_integer_)

Arguments
id1  vector of subject identifiers for the index group
id2  vector of identifiers for the reference group
y1  normally a vector of dates for the index group, but any orderable data type is allowed
y2  reference set of dates
best  if best='prior' find the index of the first y2 value less than or equal to the target y1 value, for each subject. If best='after' find the first y2 value which is greater than or equal to the target y1 value, for each subject.
nomatch  the value to return for items without a match

Details
This routine is closely related to match and to findInterval, the first of which finds exact matches and the second closest matches. This finds the closest matching date within sets of exactly matching identifiers. Closest date matching is often needed in clinical studies. For example data set 1 might contain the subject identifier and the date of some procedure and data set set 2 has the dates and values for laboratory tests, and the query is to find the first test value after the intervention but no closer than 7 days.

The id1 and id2 arguments are similar to match in that we are searching for instances of id1 that will be found in id2, and the result is the same length as id1. However, instead of returning the first match with id2 this routine returns the one that best matches with respect to y1.

The y1 and y2 arguments need not be dates, the function works for any data type such that the expression c(y1, y2) gives a sensible, sortable result. Be careful about matching Date and DateTime values and the impact of time zones, however, see as.POSIXct. If y1 and y2 are not of the same class the user is on their own. Since there exist pairs of unmatched data types where the result could be sensible, the routine will in this case proceed under the assumption that “the user knows what they are doing”. Caveat emptor.
Value

the index of the matching observations in the second data set, or the nomatch value for no successful match

Author(s)

Terry Therneau

See Also

match, findInterval

Examples

data1 <- data.frame(id = 1:10,
                    entry.dt = as.Date(paste("2011", 1:10, "5", sep='-')))
temp1 <- c(1,4,5,1,3,6,9, 2,7,8,12,4,6,7,10,12,3)
data2 <- data.frame(id = c(1,1,1,2,2,4,4,5,5,5,6,8,8,9,10,10,12),
                    lab.dt = as.Date(paste("2011", temp1, "1", sep='-')),
                    chol = round(runif(17, 130, 280)))

#first cholesterol on or after enrollment
indx1 <- neardate(data1$id, data2$id, data1$entry.dt, data2$lab.dt)
data2[indx1, "chol"]

# Closest one, either before or after.
#
indx2 <- neardate(data1$id, data2$id, data1$entry.dt, data2$lab.dt,
                   best="prior")
ifelse(is.na(indx1), indx2, # none after, take before
       ifelse(is.na(indx2), indx1, #none before
              ifelse(abs(data2$lab.dt[indx2]- data1$entry.dt) <
                     abs(data2$lab.dt[indx1]- data1$entry.dt), indx2, indx1)))

# closest date before or after, but no more than 21 days prior to index
indx2 <- ifelse((data1$entry.dt - data2$lab.dt[indx2]) > 21, NA, indx2)
ifelse(is.na(indx1), indx2, # none after, take before
       ifelse(is.na(indx2), indx1, #none before
              ifelse(abs(data2$lab.dt[indx2]- data1$entry.dt) <
                     abs(data2$lab.dt[indx1]- data1$entry.dt), indx2, indx1)))

nsk

Natural splines with knot heights as the basis.

Description

Create the design matrix for a natural spline, such that the coefficient of the resulting fit are the values of the function at the knots.

Usage

nsk(x, df = NULL, knots = NULL, intercept = FALSE, b = 0.05,
    Boundary.knots = quantile(x, c(b, 1 - b), na.rm = TRUE))
Arguments

- **x**: the predictor variable. Missing values are allowed.
- **df**: degrees of freedom. One can supply df rather than knots; ns() then chooses df - 1 - intercept knots at suitably chosen quantiles of x (which will ignore missing values). The default, df = NULL, sets the number of inner knots as length(knots).
- **knots**: breakpoints that define the spline. The default is no knots; together with the natural boundary conditions this results in a basis for linear regression on x. Typical values are the mean or median for one knot, quantiles for more knots. See also Boundary.knots.
- **intercept**: if TRUE, an intercept is included in the basis; default is FALSE
- **b**: default placement of the boundary knots. A value of bs=0 will replicate the default behavior of ns.
- **Boundary.knots**: boundary points at which to impose the natural boundary conditions and anchor the B-spline basis. Beyond these points the function is assumed to be linear. If both knots and Boundary.knots are supplied, the basis parameters do not depend on x. Data can extend beyond Boundary.knots

Details

The nsk function behaves identically to the ns function, with two exceptions. The primary one is that the returned basis is such that coefficients correspond to the value of the fitted function at the knot points. If intercept = FALSE, there will be k-1 coefficients corresponding to the k knots, and they will be the difference in predicted value between knots 2-k and knot 1. The primary advantage to the basis is that the coefficients are directly interpretable. A second is that tests for the linear and non-linear components are simple contrasts.

The second difference with ns is one of opinion with respect to the default position for the boundary knots. The default here is closer to that found in the rms::rcs function.

This function is a trial if a new idea, its future inclusion in the package is not yet guaranteed.

Value

A matrix of dimension length(x) * df where either df was supplied or, if knots were supplied, df = length(knots) + 1 + intercept. Attributes are returned that correspond to the arguments to kns, and explicitly give the knots, Boundary.knots etc for use by predict.kns().

Note

A thin flexible metal or wooden strip is called a spline, and is the traditional method for laying out a smooth curve, e.g., for a ship's hull or an airplane wing. Pins are put into a board and the strip is passed through them, each pin is a 'knot'.

A mathematical spline is a piecewise function between each knot. A linear spline will be a set of connected line segments, a quadratic spline is a set of connected local quadratic functions, constrained to have a continuous first derivative, a cubic spline is cubic between each knot, constrained to have continuous first and second derivatives, and etc. Mathematical splines are not an exact representation of natural splines: being a physical object the wood or metal strip will have continuous derivatives of all orders. Cubic splines are commonly used because they are sufficiently smooth to look natural to the human eye.

If the mathematical spline is further constrained to be linear beyond the end knots, this is often called a 'natural spline', due to the fact that a wooden or metal spline will also be linear beyond the last knots. Another name for the same object is a 'restricted cubic spline', since it is achieved in...
code by adding further constraints. Given a vector of data points and a set of knots, it is possible to create a basis matrix $X$ with one column per knot, such that ordinary regression of $X$ on $y$ will fit the cubic spline function, hence these are also called 'regression splines'. (One of these three labels is no better or worse than another, in our opinion).

Given a basis matrix $X$ with $k$ columns, the matrix $Z = XT$ for any $k$ by $k$ nonsingular matrix $T$ is is also a basis matrix, and will result in identical predicted values, but a new set of coefficients $\gamma = (T^{-1})\beta$ in place of $\beta$. One can choose the basis functions so that $X$ is easy to construct, to make the regression numerically stable, to make tests easier, or based on other considerations. It seems as though every spline library returns a different basis set, which unfortunately makes fits difficult to compare between packages. This is yet one more basis set, chosen to make the coefficients more interpretable.

**See Also**

ns

**Examples**

```r
# make some dummy data
tdata <- data.frame(x= lung$age, y = 10*log(lung$age-35) + rnorm(228, 0, 2))
fit1 <- lm(y ~ -1 + nsk(x, df=4, intercept=TRUE) , data=tdata)
fit2 <- lm(y ~ nsk(x, df=3), data=tdata)

# the knots (same for both fits)
knots <- unlist(attributes(fit1$model[[2]])[c('Boundary.knots', 'knots')])
sort(unname(knots))

unname(coef(fit1)) # predictions at the knot points

unname(coef(fit1)[-1] - coef(fit1)[1]) # differences: yhat[2:4] - yhat[1]
unname(coef(fit2))[-1] # ditto

## Not run:
plot(y ~ x, data=tdata)
points(sort(knots), coef(fit1), col=2, pch=19)
coef(fit1)[1] + c(0, coef(fit1)[-1])

## End(Not run)
```

**nwtco**

Data from the National Wilms Tumor Study

**Description**

Measurement error example. Tumor histology predicts survival, but prediction is stronger with central lab histology than with the local institution determination.

**Usage**

```r
nwtco
data(nwtco, package="survival")
```
**Format**

A data frame with 4028 observations on the following 9 variables.

- `seqno`: id number
- `instit`: Histology from local institution
- `histol`: Histology from central lab
- `stage`: Disease stage
- `rel`: Indicator for relapse
- `edrel`: Time to relapse
- `age`: Age in months
- `in.subcohort`: Included in the subcohort for the example in the paper

**References**


**Examples**

```r
with(nwtco, table(instit,histol))
anova(coxph(Surv(edrel,rel)~histol+instit,data=nwtco))
anova(coxph(Surv(edrel,rel)~instit+histol,data=nwtco))
```

---

**ovarian**

*Ovarian Cancer Survival Data*

**Description**

Survival in a randomised trial comparing two treatments for ovarian cancer

**Usage**

```r
ovarian
data(cancer, package="survival")
```

**Format**

- `futime`: survival or censoring time
- `fustat`: censoring status
- `age`: in years
- `resid.ds`: residual disease present (1=no, 2=yes)
- `rx`: treatment group
- `ecog.ps`: ECOG performance status (1 is better, see reference)
Source

Terry Therneau

References


pbc Mayo Clinic Primary Biliary Cholangitis Data

Description

Primary sclerosing cholangitis is an autoimmune disease leading to destruction of the small bile ducts in the liver. Progression is slow but inexorably, eventually leading to cirrhosis and liver decompensation. The condition has been recognised since at least 1851 and was named "primary biliary cirrhosis" in 1949. Because cirrhosis is a feature only of advanced disease, a change of its name to "primary biliary cholangitis" was proposed by patient advocacy groups in 2014.

This data is from the Mayo Clinic trial in PBC conducted between 1974 and 1984. A total of 424 PBC patients, referred to Mayo Clinic during that ten-year interval, met eligibility criteria for the randomized placebo controlled trial of the drug D-penicillamine. The first 312 cases in the data set participated in the randomized trial and contain largely complete data. The additional 112 cases did not participate in the clinical trial, but consented to have basic measurements recorded and to be followed for survival. Six of those cases were lost to follow-up shortly after diagnosis, so the data here are on an additional 106 cases as well as the 312 randomized participants.

A nearly identical data set found in appendix D of Fleming and Harrington; this version has fewer missing values.

Usage

data(pbc, package="survival")

Format

age: in years
albumin: serum albumin (g/dl)
alk.phos: alkaline phosphatase (U/liter)
ascites: presence of ascites
ast: aspartate aminotransferase, once called SGOT (U/ml)
bili: serum bilirubin (mg/dl)
chol: serum cholesterol (mg/dl)
copper: urine copper (ug/day)
edema: 0 no edema, 0.5 untreated or successfully treated
        1 edema despite diuretic therapy
hepato: presence of hepatomegaly or enlarged liver
id: case number
platelet: platelet count
protime: standardised blood clotting time
sex: m/f
spiders: blood vessel malformations in the skin
stage: histologic stage of disease (needs biopsy)
status: status at endpoint, 0/1/2 for censored, transplant, dead
time: number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986
trt: 1/2/NA for D-penicillmain, placebo, not randomised
trig: triglycerides (mg/dl)

Source

See Also
pbcseq

Mayo Clinic Primary Biliary Cirrhosis, sequential data

**Description**
This data is a continuation of the PBC data set, and contains the follow-up laboratory data for each study patient. An analysis based on the data can be found in Murtagh, et. al.

The primary PBC data set contains only baseline measurements of the laboratory parameters. This data set contains multiple laboratory results, but only on the 312 randomized patients. Some baseline data values in this file differ from the original PBC file, for instance, the data errors in prothrombin time and age which were discovered after the original analysis (see Fleming and Harrington, figure 4.6.7).

One "feature" of the data deserves special comment. The last observation before death or liver transplant often has many more missing covariates than other data rows. The original clinical protocol for these patients specified visits at 6 months, 1 year, and annually thereafter. At these protocol visits lab values were obtained for a large pre-specified battery of tests. "Extra" visits, often undertaken because of worsening medical condition, did not necessarily have all this lab work. The missing values are thus potentially informative.

**Usage**
```r
pbcseq
data(pbc, package="survival")
```

**Format**
id: case number
age: in years
sex: m/f
trt: 1/2/NA for D-penicillmain, placebo, not randomised
time: number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986
status: status at endpoint, 0/1/2 for censored, transplant, dead
day: number of days between enrollment and this visit date
all measurements below refer to this date
albumin: serum albumin (mg/dl)
alk.phos: alkaline phosphotase (U/liter)
ascites: presence of ascites
ast: aspartate aminotransferase, once called SGOT (U/ml)
bili: serum bilirunbin (mg/dl)
chol: serum cholesterol (mg/dl)
copper: urine copper (ug/day)
edema: 0 no edema, 0.5 untreated or successfully treated
1 edema despite diuretic therapy
hepato: presence of hepatomegaly or enlarged liver
platelet: platelet count
protime: standardised blood clotting time
spiders: blood vessel malformations in the skin
stage: histologic stage of disease (needs biopsy)
trig: triglycerides (mg/dl)

Source

References

See Also
pbc

Examples

# Create the start-stop-event triplet needed for coxph
first <- with(pbcseq, c(TRUE, diff(id) !=0)) #first id for each subject
last <- c(first[-1], TRUE) #last id
time1 <- with(pbcseq, ifelse(first, 0, day))
time2 <- with(pbcseq, ifelse(last, futime, c(day[-1], 0)))
event <- with(pbcseq, ifelse(last, status, 0))
```r
fit1 <- coxph(Surv(time1, time2, event) ~ age + sex + log(bili), pbcseq)
```

---

### plot.aareg

**Plot an aareg object.**

#### Description

Plot the estimated coefficient function(s) from a fit of Aalen's additive regression model.

#### Usage

```r
## S3 method for class 'aareg'
plot(x, se=TRUE, maxtime, type='s', ...)```

#### Arguments

- `x` the result of a call to the `aareg` function
- `se` if TRUE, standard error bands are included on the plot
- `maxtime` upper limit for the x-axis.
- `type` graphical parameter for the type of line, default is "steps".
- `...` other graphical parameters such as line type, color, or axis labels.

#### Side Effects

A plot is produced on the current graphical device.

#### References


#### See Also

aareg

---

### plot.cox.zph

**Graphical Test of Proportional Hazards**

#### Description

Displays a graph of the scaled Schoenfeld residuals, along with a smooth curve.

#### Usage

```r
## S3 method for class 'cox.zph'
plot(x, resid=TRUE, se=TRUE, df=4, nsmo=40, var,
    xlab="Time", ylab, lty=1:2, col=1, lwd=1, hr=FALSE, ...)
```
Arguments

`x`  result of the `cox.zph` function.

`resid`  a logical value, if TRUE the residuals are included on the plot, as well as the smooth fit.

`se`  a logical value, if TRUE, confidence bands at two standard errors will be added.

`df`  the degrees of freedom for the fitted natural spline, df=2 leads to a linear fit.

`nsmo`  number of points to use for the lines

`var`  the set of variables for which plots are desired. By default, plots are produced in turn for each variable of a model. Selection of a single variable allows other features to be added to the plot, e.g., a horizontal line at zero or a main title. This has been superseded by a subscripting method; see the example below.

`hr`  if TRUE, label the y-axis using the estimated hazard ratio rather than the estimated coefficient. (The plot does not change, only the axis label.)

`xlab`  label for the x-axis of the plot

`ylab`  optional label for the y-axis of the plot. If missing a default label is provided. This can be a vector of labels.

`lty`, `col`, `lwd`  line type, color, and line width for the overlaid curve. Each of these can be vector of length 2, in which case the second element is used for the confidence interval.

`...`  additional graphical arguments passed to the `plot` function.

Side Effects

a plot is produced on the current graphics device.

See Also

coxph, cox.zph.

Examples

```r
vfit <- coxph(Surv(time,status) ~ trt + factor(celltype) + karno + age, data=veteran, x=TRUE)
temp <- cox.zph(vfit)
plot(temp, var=3)  # Look at Karnofsy score, old way of doing plot
plot(temp[3])  # New way with subscripting
abline(0, 0, lty=3)
# Add the linear fit as well
abline(lm(temp$y[,3] ~ temp$x)$coefficients, lty=4, col=3)
title(main="VA Lung Study")
```
Description

A plot of survival curves is produced, one curve for each strata. The log=T option does extra work to avoid log(0), and to try to create a pleasing result. If there are zeros, they are plotted by default at 0.8 times the smallest non-zero value on the curve(s).

Curves are plotted in the same order as they are listed by print (which gives a 1 line summary of each). This will be the order in which col, lty, etc are used.

Usage

```r
## S3 method for class 'survfit'
plot(x, conf.int=, mark.time=FALSE,
pch=3, col=1, lty=1, lwd=1, cex=1, log=FALSE, xscale=1, yscale=1,
xlim, ylim, xmax, fun,
xlim, ylim, xaxs="r", conf.times, conf.cap=.005,
conf.offset=.012,
conf.type = c("log", "log-log", "plain", "logit", "arcsin"),
mark, noplot="(s0)", cumhaz=FALSE,
firstx, ymin, ...)
```

Arguments

- `x`: an object of class `survfit`, usually returned by the `survfit` function.
- `conf.int`: determines whether pointwise confidence intervals will be plotted. The default is to do so if there is only 1 curve, i.e., no strata, using 95% confidence intervals. Alternatively, this can be a numeric value giving the desired confidence level.
- `mark.time`: controls the labeling of the curves. If set to FALSE, no labeling is done. If TRUE, then curves are marked at each censoring time. If mark is a numeric vector then curves are marked at the specified time points.
- `pch`: vector of characters which will be used to label the curves. The points help file contains examples of the possible marks. A single string such as "abcd" is treated as a vector c("a", "b", "c", "d"). The vector is reused cyclically if it is shorter than the number of curves. If it is present this implies mark.time = TRUE.
- `col`: a vector of integers specifying colors for each curve. The default value is 1.
- `lty`: a vector of integers specifying line types for each curve. The default value is 1.
- `lwd`: a vector of numeric values for line widths. The default value is 1.
- `cex`: a numeric value specifying the size of the marks. This is not treated as a vector; all marks have the same size.
- `log`: a logical value, if TRUE the y axis will be on a log scale. Alternately, one of the standard character strings "x", "y", or "xy" can be given to specific logarithmic horizontal and/or vertical axes.
- `xscale`: a numeric value used like yscale for labels on the x axis. A value of 365.25 will give labels in years instead of the original days.
### plot.survfit

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>yscale</td>
<td>A numeric value used to multiply the labels on the y axis. A value of 100, for instance, would be used to give a percent scale. Only the labels are changed, not the actual plot coordinates, so that adding a curve with <code>lines(surv.exp(...))</code>, say, will perform as it did without the yscale argument.</td>
</tr>
<tr>
<td>xlim, ylim</td>
<td>Optional limits for the plotting region.</td>
</tr>
<tr>
<td>xmax</td>
<td>The maximum horizontal plot coordinate. This can be used to shrink the range of a plot. It shortens the curve before plotting it, so that unlike using the xlim graphical parameter, warning messages about out of bounds points are not generated.</td>
</tr>
<tr>
<td>fun</td>
<td>An arbitrary function defining a transformation of the survival (or probability in state, or cumulative hazard) curves. For example <code>fun=log</code> is an alternative way to draw a log-survival curve (but with the axis labeled with log(S) values), and <code>fun=sqrt</code> would generate a curve on square root scale. Four often used transformations can be specified with a character argument instead: &quot;S&quot; gives the usual survival curve, &quot;log&quot; is the same as using the log=T option, &quot;event&quot; or &quot;F&quot; plots the empirical CDF $F(t) = 1 - S(t)$ ($f(y) = 1 - y$), and &quot;cloglog&quot; creates a complimentary log-log survival plot ($f(y) = \log(-\log(y))$ along with log scale for the x-axis). The terms &quot;identity&quot; and &quot;surv&quot; are allowed as synonyms for type=&quot;S&quot;. The argument &quot;cumhaz&quot; causes the cumulative hazard function to be plotted.</td>
</tr>
<tr>
<td>xlab</td>
<td>Label given to the x-axis.</td>
</tr>
<tr>
<td>ylab</td>
<td>Label given to the y-axis.</td>
</tr>
<tr>
<td>xaxs</td>
<td>Either &quot;S&quot; for a survival curve or a standard x axis style as listed in par; &quot;r&quot; (regular) is the R default. Survival curves have historically been displayed with the curve touching the y-axis, but not touching the bounding box of the plot on the other 3 sides. Type &quot;S&quot; accomplishes this by manipulating the plot range and then using the &quot;i&quot; style internally. The &quot;S&quot; style is becoming increasingly less common, however.</td>
</tr>
<tr>
<td>conf.times</td>
<td>Optional vector of times at which to place a confidence bar on the curve(s). If present, these will be used instead of confidence bands.</td>
</tr>
<tr>
<td>conf.cap</td>
<td>Width of the horizontal cap on top of the confidence bars; only used if conf.times is used. A value of 1 is the width of the plot region.</td>
</tr>
<tr>
<td>conf.offset</td>
<td>The offset for confidence bars, when there are multiple curves on the plot. A value of 1 is the width of the plot region. If this is a single number then each curve's bars are offset by this amount from the prior curve's bars, if it is a vector the values are used directly.</td>
</tr>
<tr>
<td>conf.type</td>
<td>One of &quot;plain&quot;, &quot;log&quot; (the default), &quot;log-log&quot; or &quot;logit&quot;. Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals curve $\pm k * \text{s.e.}(\text{curve})$, where k is determined from conf.int. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), and the logit option on log(survival/(1-survival)).</td>
</tr>
<tr>
<td>mark</td>
<td>A historical alias for pch</td>
</tr>
<tr>
<td>noplot</td>
<td>For multi-state models, curves with this label will not be plotted. (Also see the istate0 argument in survcheck.)</td>
</tr>
<tr>
<td>cumhaz</td>
<td>Plot the cumulative hazard rather than the probability in state or survival. Optionally, this can be a numeric vector specifying which columns of the cumhaz component to plot.</td>
</tr>
</tbody>
</table>
plot.survfit

ymin this will normally be given as part of the ylim argument.

firstx this will normally be given as part of the xlim argument.

... other arguments that will be passed forward to the underlying plot method, such as xlab or ylab.

Details

If the object contains a cumulative hazard curve, then fun='cumhaz' will plot that curve, otherwise it will plot -log(S) as an approximation. Theoretically, \( S = \exp(-\Lambda) \) where S is the survival and \( \Lambda \) is the cumulative hazard. The same relationship holds for estimates of S and \( \Lambda \) only in special cases, but the approximation is often close.

When the survfit function creates a multi-state survival curve the resulting object also has class 'survfits'. Competing risk curves are a common case. In this situation the fun argument is ignored.

When the conf.times argument is used, the confidence bars are offset by conf.offset units to avoid overlap. The bar on each curve are the confidence interval for the time point at which the bar is drawn, i.e., different time points for each curve. If curves are steep at that point, the visual impact can sometimes substantially differ for positive and negative values of conf.offset.

Value

a list with components x and y, containing the coordinates of the last point on each of the curves (but not the confidence limits). This may be useful for labeling.

Note

In prior versions the behavior of xscale and yscale differed: the first changed the scale both for the plot and for all subsequent actions such as adding a legend, whereas yscale affected only the axis label. This was normalized in version 2-36.4, and both parameters now only affect the labeling.

In versions prior to approximately 2.36 a survfit object did not contain the cumulative hazard as a separate result, and the use of fun="cumhaz" would plot the approximation -log(surv) to the cumulative hazard. When cumulative hazards were added to the object, the cumhaz=TRUE argument to the plotting function was added. In version 2.3-8 the use of fun="cumhaz" became a synonym for cumhaz=TRUE.

See Also

points.survfit, lines.survfit, par, survfit

Examples

leukemia.surv <- survfit(Surv(time, status) ~ x, data = aml)
plot(leukemia.surv, lty = 2:3)
legend(100, .9, c("Maintenance", "No Maintenance"), lty = 2:3)
title("Kaplan-Meier Curves
for AML Maintenance Study")
lsurv2 <- survfit(Surv(time, status) ~ x, aml, type='fleming')
plot(lsurv2, lty=2:3, fun="cumhaz",
xlab="Months", ylab="Cumulative Hazard")
predict.coxph  

Predictions for a Cox model

Description

Compute fitted values and regression terms for a model fitted by coxph

Usage

```r
## S3 method for class 'coxph'
predict(object, newdata,
type=c("lp", "risk", "expected", "terms", "survival"),
se.fit=FALSE, na.action=na.pass, terms=names(object$assign), collapse,
reference=c("strata", "sample", "zero"), ...)
```

Arguments

- `object`: the results of a coxph fit.
- `newdata`: Optional new data at which to do predictions. If absent predictions are for the data frame used in the original fit. When coxph has been called with a formula argument created in another context, i.e., coxph has been called within another function and the formula was passed as an argument to that function, there can be problems finding the data set. See the note below.
- `type`: the type of predicted value. Choices are the linear predictor ("lp"), the risk score exp(lp) ("risk"), the expected number of events given the covariates and follow-up time ("expected"), and the terms of the linear predictor ("terms"). The survival probability for a subject is equal to exp(-expected).
- `se.fit`: if TRUE, pointwise standard errors are produced for the predictions.
- `na.action`: applies only when the newdata argument is present, and defines the missing value action for the new data. The default is to include all observations. When there is no newdata, then the behavior of missing is dictated by the na.action option of the original fit.
- `terms`: if type="terms", this argument can be used to specify which terms should be included; the default is all.
- `collapse`: optional vector of subject identifiers. If specified, the output will contain one entry per subject rather than one entry per observation.
- `reference`: reference for centering predictions, see details below
- `...`: For future methods

Details

The Cox model is a relative risk model; predictions of type "linear predictor", "risk", and "terms" are all relative to the sample from which they came. By default, the reference value for each of these is the mean covariate within strata. The underlying reason is both statistical and practical. First, a Cox model only predicts relative risks between pairs of subjects within the same strata, and hence the addition of a constant to any covariate, either overall or only within a particular stratum, has no effect on the fitted results. Second, downstream calculations depend on the risk score exp(linear predictor), which will fall prey to numeric overflow for a linear predictor greater than .Machine$double.max.exp. The coxph routines try to approximately center the predictors out
of self protection. Using the reference="strata" option is the safest centering, since strata occasionally have different means. When the results of predict are used in further calculations it may be desirable to use a single reference level for all observations. Use of reference="sample" will use the overall means, and agrees with the linear.predictors component of the coxph object (which uses the overall mean for backwards compatibility with older code). Predictions of type="terms" are almost invariably passed forward to further calculation, so for these we default to using the sample as the reference. A reference of "zero" causes no centering to be done.

Predictions of type "expected" incorporate the baseline hazard and are thus absolute instead of relative; the reference option has no effect on these. These values depend on the follow-up time for the future subjects as well as covariates so the newdata argument needs to include both the right and left hand side variables from the formula. (The status variable will not be used, but is required since the underlying code needs to reconstruct the entire formula.)

Models that contain a frailty term are a special case: due to the technical difficulty, when there is a newdata argument the predictions will always be for a random effect of zero.

Value

A vector or matrix of predictions, or a list containing the predictions (element "fit") and their standard errors (element "se.fit") if the se.fit option is TRUE.

Note

Some predictions can be obtained directly from the coxph object, and for others it is necessary for the routine to have the entirety of the original data set, e.g., for type = terms or if standard errors are requested. This extra information is saved in the coxph object if model=TRUE, if not the original data is reconstructed. If it is known that such residuals will be required overall execution will be slightly faster if the model information is saved.

In some cases the reconstruction can fail. The most common is when coxph has been called inside another function and the formula was passed as one of the arguments to that enclosing function. Another is when the data set has changed between the original call and the time of the prediction call. In each of these the simple solution is to add model=TRUE to the original coxph call.

See Also

predict.coxph, termplot

Examples

options(na.action=na.exclude) # retain NA in predictions
fit <- coxph(Surv(time, status) ~ age + ph.ecog + strata(inst), lung)
#lung data set has status coded as 1/2
mresid <- (lung$status-1) - predict(fit, type='expected') #Martingale resid
predict(fit,type="lp")
predict(fit,type="expected")
predict(fit,type="risk",se.fit=TRUE)
predict(fit,type="terms",se.fit=TRUE)

# For someone who demands reference='zero'
pzero <- function(fit)
  predict(fit, reference="sample") + sum(coef(fit) * fit$means, na.rm=TRUE)
Predicted Values for a 'survreg' Object

Description

Predicted values for a survreg object

Usage

```r
## S3 method for class 'survreg'
predict(object, newdata, type=c("response", "link", "lp", "linear", "terms", "quantile", "uquantile"), se.fit=FALSE, terms=NULL, p=c(0.1, 0.9), na.action=na.pass, ...)
```

Arguments

- `object` result of a model fit using the `survreg` function.
- `newdata` data for prediction. If absent predictions are for the subjects used in the original fit.
- `type` the type of predicted value. This can be on the original scale of the data (response), the linear predictor ("linear", with "lp" as an allowed abbreviation), a predicted quantile on the original scale of the data ("quantile"), a quantile on the linear predictor scale ("uquantile"), or the matrix of terms for the linear predictor ("terms"). At this time "link" and linear predictor ("lp") are identical.
- `se.fit` if TRUE, include the standard errors of the prediction in the result.
- `terms` subset of terms. The default for residual type "terms" is a matrix with one column for every term (excluding the intercept) in the model.
- `p` vector of percentiles. This is used only for quantile predictions.
- `na.action` applies only when the `newdata` argument is present, and defines the missing value action for the new data. The default is to include all observations.
- `...` for future methods

Value

a vector or matrix of predicted values.

References


See Also

`survreg, residuals.survreg`
Examples

# Draw figure 1 from Escobar and Meeker, 1992.
fit <- survreg(Surv(time,status) ~ age + I(age^2), data=stanford2, dist='lognormal')
with(stanford2, plot(age, time, xlab='Age', ylab='Days',
xlim=c(0,65), ylim=c(1, 10^5), log='y', type='n'))
with(stanford2, points(age, time, pch=c(2,4)[status+1], cex=.7))
pred <- predict(fit, newdata=list(age=1:65), type='quantile',
 p=c(.1, .5, .9))
matlines(1:65, pred, lty=c(2,1,2), col=1)

# Predicted Weibull survival curve for a lung cancer subject with
# ECOG score of 2
lfit <- survreg(Surv(time, status) ~ ph.ecog, data=lung)
pct <- 1:98/100 # The 100th percentile of predicted survival is at +infinity
ptime <- predict(lfit, newdata=data.frame(ph.ecog=2), type='quantile',
 p=pct, se=TRUE)
matplot(cbind(ptime$fit, ptime$fit + 2*ptime$se.fit,
 ptme$fit - 2*ptime$se.fit)/30.5, 1-pct,
 xlab="Months", ylab="Survival", type='l', lty=c(1,2,2), col=1)

print.aareg

Print an aareg object

Description

Print out a fit of Aalen’s additive regression model

Usage

## S3 method for class 'aareg'
print(x, maxtime, test=c("aalen", "nrisk"), scale=1,...)

Arguments

x         the result of a call to the aareg function
maxtime   the upper time point to be used in the test for non-zero slope
test      the weighting to be used in the test for non-zero slope. The default weights are
           based on the variance of each coefficient, as a function of time. The alternative
           weight is proportional to the number of subjects still at risk at each time point.
scale     scales the coefficients. For some data sets, the coefficients of the Aalen model
           will be very small (10^-4); this simply multiplies the printed values by a constant,
           say 1e6, to make the printout easier to read.
...       for future methods

Details

The estimated increments in the coefficient estimates can become quite unstable near the end of
follow-up, due to the small number of observations still at risk in a data set. Thus, the test for slope
will sometimes be more powerful if this last 'tail' is excluded.
Value

the calling argument is returned.

Side Effects

the results of the fit are displayed.

References


See Also

aareg

print.summary.coxph  

Print method for summary.coxph objects

Description

Produces a printed summary of a fitted coxph model

Usage

## S3 method for class 'summary.coxph'
print(x, digits=max(getOption("digits") - 3, 3),
      signif.stars = getOption("show.signif.stars"), expand=FALSE, ...)

Arguments

x the result of a call to summary.coxph
digits significant digits to print
signif.stars Show stars to highlight small p-values
expand if the summary is for a multi-state coxph fit, print the results in an expanded format.
... For future methods
print.summary.survexp  Print Survexp Summary

Description
Prints the results of summary.survexp

Usage
## S3 method for class 'summary.survexp'
print(x, digits = max(options()$digits - 4, 3), ...)

Arguments
x
an object of class summary.survexp.
digits
the number of digits to use in printing the result.
... for future methods

Value
x, with the invisible flag set to prevent further printing.

Author(s)
Terry Therneau

See Also
link{summary.survexp}, survexp

print.summary.survfit  Print Survfit Summary

Description
Prints the result of summary.survfit.

Usage
## S3 method for class 'summary.survfit'
print(x, digits = max(options()$digits-4, 3), ...)

Arguments
x
an object of class "summary.survfit", which is the result of the summary.survfit function.
digits
the number of digits to use in printing the numbers.
... for future methods
Value

x, with the invisible flag set to prevent printing.

Side Effects

prints the summary created by summary.survfit.

See Also

options, print, summary.survfit.

print.survfit  
Print a Short Summary of a Survival Curve

Description

Print number of observations, number of events, the restricted mean survival and its standard error, and the median survival with confidence limits for the median.

Usage

## S3 method for class 'survfit'
print(x, scale=1, digits = max(options()$digits - 4,3),
print.rmean=getOption("survfit.print.rmean"),
rmean = getOption('survfit.rmean'),...)

Arguments

x  

the result of a call to the survfit function.

scale  
a numeric value to rescale the survival time, e.g., if the input data to survfit were in days, scale=365 would scale the printout to years.

digits  
Number of digits to print

print.rmean,rmean  
Options for computation and display of the restricted mean.

...  
for future results

Details

The mean and its variance are based on a truncated estimator. That is, if the last observation(s) is not a death, then the survival curve estimate does not go to zero and the mean is undefined. There are four possible approaches to resolve this, which are selected by the rmean option. The first is to set the upper limit to a constant, e.g.,rmean=365. In this case the reported mean would be the expected number of days, out of the first 365, that would be experienced by each group. This is useful if interest focuses on a fixed period. Other options are "none" (no estimate), "common" and "individual". The "common" option uses the maximum time for all curves in the object as a common upper limit for the auc calculation. For the "individual" options the mean is computed as the area under each curve, over the range from 0 to the maximum observed time for that curve. Since the end point is random, values for different curves are not comparable and the printed standard errors are an underestimate as they do not take into account this random variation. This option is provided mainly for backwards compatibility, as this estimate was the default (only) one in earlier
releases of the code. Note that SAS (as of version 9.3) uses the integral up to the last event time of each individual curve; we consider this the worst of the choices and do not provide an option for that calculation.

The median and its confidence interval are defined by drawing a horizontal line at 0.5 on the plot of the survival curve and its confidence bands. If that line does not intersect the curve, then the median is undefined. The intersection of the line with the lower CI band defines the lower limit for the median’s interval, and similarly for the upper band. If any of the intersections is not a point then we use the center of the intersection interval, e.g., if the survival curve were exactly equal to 0.5 over an interval. When data is uncensored this agrees with the usual definition of a median.

Value

x, with the invisible flag set to prevent printing. (The default for all print functions in R is to return the object passed to them; print.survfit complies with this pattern. If you want to capture these printed results for further processing, see the table component of summary.survfit.)

Side Effects

The number of observations, the number of events, the median survival with its confidence interval, and optionally the restricted mean survival (rmean) and its standard error, are printed. If there are multiple curves, there is one line of output for each.

References


See Also

summary.survfit, quantile.survfit

pseudo

Pseudo values for survival.

Description

Produce pseudo values from a survival curve.

Usage

pseudo(fit, times, type, addNA=TRUE, data.frame=FALSE, minus1=FALSE, ...)

Arguments

fit

a survfit object, or one that inherits that class.

times

a vector of time points, at which to evaluate the pseudo values.

type

the type of value, either the probability in state pstate, the cumulative hazard cumhaz or the expected sojourn time in the state sojourn.

addNA

If any observations were removed due to missing values in the fit object, add those rows (as NA) into the return. This causes the result of pseudo to match the original dataframe.
data.frame if TRUE, return the data in "long" form as a data.frame with id, time, and pseudo as variables.

minus1 use n-1 as the multiplier rather than n

... other arguments to the residuals.survfit function, which does the majority of the work, e.g., collapse and weighted.

Details

This function computes pseudo values based on a first order Taylor series, also known as the "infinitesimal jackknife" (IJ) or "dfbeta" residuals. To be completely correct these results could perhaps be called ‘IJ pseudo values’ or even pseudo pseudo-values. For moderate to large data, however, the resulting values will be almost identical, numerically, to the ordinary jackknife.

A primary advantage of this approach is computational speed. Other features, neither good nor bad, are that they will agree with robust standard errors of other survival package estimates, which are based on the IJ, and that the mean of the estimates, over subjects, is exactly the underlying survival estimate.

For the type variable, surv is an acceptable synonym for pstate, and rmt and rmst are equivalent to sojourn. All of these are case insensitive.

The result from this routine is simply n times the IJ value, where n is the number of subjects. (If the survfit call included an id option, n is the number of unique id values, otherwise the number of rows in the data set.) IJ values are well defined for all variants of the Aalen-Johansen estimate, as computed by the survfit function; indeed, they are the basis for standard errors of the result. Understanding of the properties of the pseudo-values, however, is still evolving. Validity has been shown for the simplest case (Kaplan-Meier), for competing risks, and for the corresponding sojourn times. On the other hand, one must be careful when the data includes left-truncation (P. K. Andersen, personal communication), and also with pseudo-values for the cumulative hazard. As understanding evolves, treat this routine’s results as a research tool, not production, for the more complex models.

Value

A vector, matrix, or array. The first dimension is always the number of observations in fit object, in the same order as the original data set (less any missing values that were removed when creating the survfit object); the second, if applicable, corresponds to fit$states, e.g., multi-state survival, and the last dimension to the selected time points. (If there are multiple rows for a given id, there is only one pseudovalue per unique id.)

For the data.frame option, a data frame containing values for id, time, and pseudo. If the original survfit call contained an id statement, then the values in the id column will be taken from that variable. If the id statement has a simple form, e.g., id = patno, then the name of the id column will be ‘patno’, otherwise it will be named ‘(id)’.

Note

The code will be slightly faster if the model=TRUE option is used in the survfit call. It may be essential if the survfit/pseudo pair is used inside another function.

References

pspline

Smoothing splines using a pspline basis

Description

Specifies a penalised spline basis for the predictor. This is done by fitting a comparatively small set of splines and penalising the integrated second derivative. Traditional smoothing splines use one basis per observation, but several authors have pointed out that the final results of the fit are indistinguishable for any number of basis functions greater than about 2-3 times the degrees of freedom. Eilers and Marx point out that if the basis functions are evenly spaced, this leads to significant computational simplification, they refer to the result as a p-spline.

Usage

pspline(x, df=4, theta, nterm=2.5 * df, degree=3, eps=0.1, method=
Boundary.knots=range(x), intercept=FALSE, penalty=TRUE, combine, ...)

psplineinverse(x)
Arguments

x for psline: a covariate vector. The function does not apply to factor variables. For psplineinverse x will be the result of a pspline call.

def the desired degrees of freedom. One of the arguments df or theta’ must be given, but not both. If df=0, then the AIC = (loglik -df) is used to choose an "optimal" degrees of freedom. If AIC is chosen, then an optional argument ‘caic=T’ can be used to specify the corrected AIC of Hurvich et. al.

theta roughness penalty for the fit. It is a monotone function of the degrees of freedom, with theta=1 corresponding to a linear fit and theta=0 to an unconstrained fit of nterm degrees of freedom.

nterm number of splines in the basis

degree degree of splines

eps accuracy for df

method the method for choosing the tuning parameter theta. If theta is given, then 'fixed' is assumed. If the degrees of freedom is given, then 'df' is assumed. If method='aic' then the degrees of freedom is chosen automatically using Akaike’s information criterion.

... optional arguments to the control function

Boundary.knots the spline is linear beyond the boundary knots. These default to the range of the data.

intercept if TRUE, the basis functions include the intercept.

penalty if FALSE a large number of attributes having to do with penalized fits are excluded. This is useful to create a pspline basis matrix for other uses.

combine an optional vector of increasing integers. If two adjacent values of combine are equal, then the corresponding coefficients of the fit are forced to be equal. This is useful for monotone fits, see the vignette for more details.

Value

Object of class pspline, coxph.penalty containing the spline basis, with the appropriate attributes to be recognized as a penalized term by the coxph or survreg functions.

For psplineinverse the original x vector is reconstructed.

References


See Also

coxph,survreg,ridge,frailty
Examples

```r
lfit6 <- survreg(Surv(time, status) ~ pspline(age, df=2), lung)
plot(lung$age, predict(lfit6), xlab='Age', ylab="Spline prediction")
```

```r
title("Cancer Data")
fit0 <- coxph(Surv(time, status) ~ ph.ecog + age, lung)
fit1 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,3), lung)
fit3 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,8), lung)
fit0
fit1
fit3
```

<table>
<thead>
<tr>
<th>pyears</th>
<th>Person Years</th>
</tr>
</thead>
</table>

Description

This function computes the person-years of follow-up time contributed by a cohort of subjects, stratified into subgroups. It also computes the number of subjects who contribute to each cell of the output table, and optionally the number of events and/or expected number of events in each cell.

Usage

```r
pyears(formula, data, weights, subset, na.action, rmap, ratetable, scale=365.25, expect=c('event', 'pyears'), model=FALSE, x=FALSE, y=FALSE, data.frame=FALSE)
```

Arguments

- **formula**: a formula object. The response variable will be a vector of follow-up times for each subject, or a Surv object containing the survival time and an event indicator. The predictors consist of optional grouping variables separated by + operators (exactly as in survfit), time-dependent grouping variables such as age (specified with tcut), and optionally a ratetable term. This latter matches each subject to his/her expected cohort.
- **data**: a data frame in which to interpret the variables named in the formula, or in the subset and the weights argument.
- **weights**: case weights.
- **subset**: expression saying that only a subset of the rows of the data should be used in the fit.
- **na.action**: a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is `options()$na.action`.
- **rmap**: an optional list that maps data set names to the ratetable names. See the details section below.
- **ratetable**: a table of event rates, such as `survexp.uswhite`.
- **scale**: a scaling for the results. As most rate tables are in units/day, the default value of 365.25 causes the output to be reported in years.
- **expect**: should the output table include the expected number of events, or the expected number of person-years of observation. This is only valid with a rate table.
- **data.frame**: return a data frame rather than a set of arrays.
- **model, x, y**: If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result.
**Details**

Because `pyyears` may have several time variables, it is necessary that all of them be in the same units. For instance, in the call

```r
py <- pyears(futime ~ rx, rmap=list(age=age, sex=sex, year=entry.dt),
             ratetable=survexp.us)
```

the natural unit of the ratetable is hazard per day, it is important that `futime`, `age` and `entry.dt` all be in days. Given the wide range of possible inputs, it is difficult for the routine to do sanity checks of this aspect.

The ratetable being used may have different variable names than the user's data set, this is dealt with by the `rmap` argument. The rate table for the above calculation was `survexp.us`, a call to `summary(survexp.us)` reveals that it expects to have variables `age = age in days`, `sex`, and `year = the date of study entry`, we create them in the `rmap` line. The sex variable is not mapped, therefore the code assumes that it exists in `mydata` in the correct format. (Note: for factors such as `sex`, the program will match on any unique abbreviation, ignoring case.)

A special function `tcut` is needed to specify time-dependent cutpoints. For instance, assume that `age` is in years, and that the desired final arrays have as one of their margins the age groups 0-2, 2-10, 10-25, and 25+. A subject who enters the study at age 4 and remains under observation for 10 years will contribute follow-up time to both the 2-10 and 10-25 subsets. If `cut(age,c(0,2,10,25,100))` were used in the formula, the subject would be classified according to his starting age only. The `tcut` function has the same arguments as `cut`, but produces a different output object which allows the `pyyears` function to correctly track the subject.

The results of `pyyears` are normally used as input to further calculations. The `print` routine, therefore, is designed to give only a summary of the table.

**Value**

A list with components:

- `pyyears`: an array containing the person-years of exposure. (Or other units, depending on the rate table and the scale). The dimension and dimnames of the array correspond to the variables on the right hand side of the model equation.
- `n`: an array containing the number of subjects who contribute time to each cell of the `pyyears` array.
- `event`: an array containing the observed number of events. This will be present only if the response variable is a `Surv` object.
- `expected`: an array containing the expected number of events (or person years if `expect` ="pyyears"). This will be present only if there was a `ratetable` term.
- `data`: if the `data.frame` option was set, a data frame containing the variables `n`, `event`, `pyyears` and `event` that supplants the four arrays listed above, along with variables corresponding to each dimension. There will be one row for each cell in the arrays.
- `offtable`: the number of person-years of exposure in the cohort that was not part of any cell in the `pyyears` array. This is often useful as an error check; if there is a mismatch of units between two variables, nearly all the person years may be off table.
- `tcut`: whether the call included any time-dependent cutpoints.
- `summary`: a summary of the rate-table matching. This is also useful as an error check.
quantile.survfit

Quantiles from a survfit object

Description

Retrieve quantiles and confidence intervals for them from a survfit or Surv object.
Usage

```r
## S3 method for class 'survfit'
quantile(x, probs = c(0.25, 0.5, 0.75), conf.int = TRUE,
scale, tolerance = sqrt(.Machine$double.eps), ...)
```

```r
## S3 method for class 'survfitms'
quantile(x, probs = c(0.25, 0.5, 0.75), conf.int = TRUE,
scale, tolerance = sqrt(.Machine$double.eps), ...)
```

```r
## S3 method for class 'survfit'
median(x, ...)
```

Arguments

- `x` a result of the `survfit` function
- `probs` numeric vector of probabilities with values in [0,1]
- `conf.int` should lower and upper confidence limits be returned?
- `scale` optional scale factor, e.g., `scale=365.25` would return results in years if the fit object were in days.
- `tolerance` tolerance for checking that the survival curve exactly equals one of the quantiles
- `...` optional arguments for other methods

Details

The kth quantile for a survival curve $S(t)$ is the location at which a horizontal line at height $p = 1-k$ intersects the plot of $S(t)$. Since $S(t)$ is a step function, it is possible for the curve to have a horizontal segment at exactly $1-k$, in which case the midpoint of the horizontal segment is returned. This mirrors the standard behavior of the median when data is uncensored. If the survival curve does not fall to $1-k$, then that quantile is undefined.

In order to be consistent with other quantile functions, the argument `prob` of this function applies to the cumulative distribution function $F(t) = 1-S(t)$.

Confidence limits for the values are based on the intersection of the horizontal line at 1-k with the upper and lower limits for the survival curve. Hence confidence limits use the same p-value as was in effect when the curve was created, and will differ depending on the `conf.type` option of `survfit`. If the survival curves have no confidence bands, confidence limits for the quantiles are not available.

When a horizontal segment of the survival curve exactly matches one of the requested quantiles the returned value will be the midpoint of the horizontal segment; this agrees with the usual definition of a median for uncensored data. Since the survival curve is computed as a series of products, however, there may be round off error. Assume for instance a sample of size 20 with no tied times and no censoring. The survival curve after the 10th death is $(19/20)(18/19)(17/18) \ldots (10/11) = 10/20$, but the computed result will not be exactly 0.5. Any horizontal segment whose absolute difference with a requested percentile is less than `tolerance` is considered to be an exact match.

Value

The quantiles will be a vector if the `survfit` object contains only a single curve, otherwise it will be a matrix or array. In this case the last dimension will index the quantiles.

If confidence limits are requested, then result will be a list with components `quantile`, `lower`, and `upper`, otherwise it is the vector or matrix of quantiles.
ratetable

Author(s)
Terry Therneau

See Also
survfit, print.survfit, qsurvreg

Examples

```r
fit <- survfit(Surv(time, status) ~ ph.ecog, data=lung)
quantile(fit)

cfit <- coxph(Surv(time, status) ~ age + strata(ph.ecog), data=lung)
csurv <- survfit(cfit, newdata=data.frame(age=c(40, 60, 80)),
                 conf.type ="none")
temp <- quantile(csurv, 1:5/10)
temp[2,3,] # quantiles for second level of ph.ecog, age=80
quantile(csurv[2,3,], 1:5/10) # quantiles of a single curve, same result
```

Description

This function supports ratetable() terms in a model statement, within survexp and pyears.

Usage

```r
ratetable(...)```

Arguments

```r
...  the named dimensions of a rate table```

Details

This way of mapping a rate table’s variable names to a user data frame has been superseded, instead use the `rmap` argument of the survexp, pyears, or survdiff routines. The function remains only to allow older code to be run.

Author(s)

Terry Therneau
ratetables

ratetableDate  \hspace{1cm} \textit{Convert date objects to ratetable form}

\textbf{Description}

This method converts dates from various forms into the internal form used in ratetable objects.

\textbf{Usage}

\begin{verbatim}
ratetableDate(x)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
\item \textbf{x} \hspace{1cm} a date. The function currently has methods for Date, date, POSIXt, timeDate, and chron objects.
\end{itemize}

\textbf{Details}

This function is useful for those who create new ratetables, but is normally invisible to users. It is used internally by the survexp and pyears functions to map the various date formats; if a new method is added then those routines will automatically be adapted to the new date type.

\textbf{Value}

a numeric vector, the number of days since 1/1/1960.

\textbf{Author(s)}

Terry Therneau

\textbf{See Also}

pyears, survexp

ratetables  \hspace{1cm} \textit{Census Data Sets for the Expected Survival and Person Years Functions}

\textbf{Description}

Census data sets for the expected survival and person years functions.

\textbf{Usage}

\begin{verbatim}
data(survexp, package="survival")
\end{verbatim}
rats

3623

Details
survexp.us total United States population, by age and sex, 1940 to 2012.
survexp.usr United States population, by age, sex and race, 1940 to 2014. Race is white or black.
For 1960 and 1970 the black population values were not reported separately, so the nonwhite
values were used. (Over the years, the reported tables have differed wrt reporting non-white
and/or black.)
survexp.mn total Minnesota population, by age and sex, 1970 to 2013.
Each of these tables contains the daily hazard rate for a matched subject from the population, defined
as − log(1 − q)/365.25 where q is the 1 year probability of death as reported in the original tables
from the US Census. For age 25 in 1970, for instance, p = 1 − q is is the probability that a subject
who becomes 25 years of age in 1970 will achieve his/her 26th birthday. The tables are recast in
terms of hazard per day for computational convenience.
Each table is stored as an array, with additional attributes, and can be subset and manipulated as
standard R arrays. See the help page for ratetable for details.
All numeric dimensions of a rate table must be in the same units. The survexp.us rate table
contains daily hazard rates, the age cutpoints are in days, and the calendar year cutpoints are a Date.
See Also
ratetable, survexp, pyears
Examples
survexp.uswhite <- survexp.usr[,,"white",]

rats

Rat treatment data from Mantel et al

Description
Rat treatment data from Mantel et al. Three rats were chosen from each of 100 litters, one of which
was treated with a drug, and then all followed for tumor incidence.
Usage
rats
data(cancer, package="survival")
Format
litter:
rx:
time:
status:
sex:

litter number from 1 to 100
treatment,(1=drug, 0=control)
time to tumor or last follow-up
event status, 1=tumor and 0=censored
male or female


Note
Since only 2/150 of the male rats have a tumor, most analyses use only females (odd numbered litters), e.g. Lee et al.

Source

References

rats2
Rat data from Gail et al.

Description
48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage
rats2
data(cancer, package="survival")

Format
rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
stop: exit time
status: event status, 1=tumor, 0=censored

Source
Reliability data sets

Description
A set of data for simple reliability analyses, taken from the book by Meeker and Escobar.

Usage
data(reliability, package="survival")

Details

- capacitor: Data from a factorial experiment on the life of glass capacitors as a function of voltage and operating temperature. There were 8 capacitors at each combination of temperature and voltage. Testing at each combination was terminated after the fourth failure.
  - temperature: temperature in degrees celcius
  - voltage: applied voltage
  - time: time to failure
  - status: 1=failed, 0=censored

- cracks: Data on the time until the development of cracks in a set of 167 identical turbine parts. The parts were inspected at 8 selected times.
  - day: time of inspection
  - fail: number of fans found to have cracks, at this inspection

- Data set genfan: Time to failure of 70 diesel engine fans.
  - hours: hours of service
  - status: 1=failure, 0=censored

- Data set ifluid: A data frame with two variables describing the time to electrical breakdown of an insulating fluid.
  - time: hours to breakdown
  - voltage: test voltage in kV

- Data set imotor: Breakdown of motor insulation as a function of temperature.
  - temp: temperature of the test
  - time: time to failure or censoring
  - status: 0=censored, 1=failed

- Data set turbine: Each of 432 turbine wheels was inspected once to determine whether a crack had developed in the wheel or not.
  - hours: time of inspection (100s of hours)
  - inspected: number that were inspected
  - failed: number that failed

- Data set valveSeat: Time to replacement of valve seats for 41 diesel engines. More than one seat may be replaced at a particular service, leading to duplicate times in the data set. The final inspection time for each engine will have status=0.
  - id: engine identifier
  - time: time of the inspection, in days
  - status: 1=replacement occurred, 0= not
References


Examples

```
survreg(Surv(time, status) ~ temperature + voltage, capacitor)
```

**residuals.coxph**

Calculate Residuals for a 'coxph' Fit

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

Usage

```r
## S3 method for class 'coxph'
residuals(object, 
  type=c("martingale", "deviance", "score", "schoenfeld", 
         "dfbeta", "dfbetas", "scaledsch","partial"), 
  collapse=FALSE, weighted= (type %in% c("dfbeta", "dfbetas")), ...) 
## S3 method for class 'coxphms'
residuals(object, 
  type=c("martingale", "score", "schoenfeld", 
         "dfbeta", "dfbetas", "scaledsch"), 
  collapse=FALSE, weighted= FALSE, ...) 
## S3 method for class 'coxph.null'
residuals(object, 
  type=c("martingale", "deviance","score","schoenfeld"), 
  collapse=FALSE, weighted= FALSE, ...) 
```

Arguments

- **object**
  - an object inheriting from class coxph, representing a fitted Cox regression model. Typically this is the output from the coxph function.

- **type**
  - character string indicating the type of residual desired. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", "scaledsch" and "partial". Only enough of the string to determine a unique match is required.

- **collapse**
  - vector indicating which rows to collapse (sum) over. In time-dependent models more than one row data can pertain to a single individual. If there were 4 individuals represented by 3, 1, 2 and 4 rows of data respectively, then collapse=c(1,1,1,2,3,3,4,4,4) could be used to obtain per subject rather than per observation residuals.

- **weighted**
  - if TRUE and the model was fit with case weights, then the weighted residuals are returned.

- **...**
  - other unused arguments
Value

For martingale and deviance residuals, the returned object is a vector with one element for each subject (without collapse). For score residuals it is a matrix with one row per subject and one column per variable. The row order will match the input data for the original fit. For Schoenfeld residuals, the returned object is a matrix with one row for each event and one column per variable. The rows are ordered by time within strata, and an attribute strata is attached that contains the number of observations in each strata. The scaled Schoenfeld residuals are used in the cox.zph function.

The score residuals are each individual’s contribution to the score vector. Two transformations of this are often more useful: dfbeta is the approximate change in the coefficient vector if that observation were dropped, and dfbetas is the approximate change in the coefficients, scaled by the standard error for the coefficients.

NOTE

For deviance residuals, the status variable may need to be reconstructed. For score and Schoenfeld residuals, the X matrix will need to be reconstructed.

References


See Also

coxph

Examples

```r
fit <- coxph(Surv(start, stop, event) ~ (age + surgery)* transplant, data=heart)
mresid <- resid(fit, collapse=heart$id)
```

residuals.survfit  

**II residuals from a survfit object.**

Description

Return infinitesimal jackknife residuals from a survfit object, for the survival, cumulative hazard, or restricted mean time in state (RMTS).

Usage

```r
## S3 method for class 'survfit'
residuals(object, times, 
  type="pstate", collapse, weighted=FALSE, 
  method=1, ...)
```
Arguments

- **object**: a `survfit` object
- **times**: a vector of times at which the residuals are desired
- **type**: the type of residual, see below
- **collapse**: add the residuals for all subjects in a cluster. If the `survfit` object used an `id` statement, the default is to collapse over that variable.
- **weighted**: weight the residuals by each observation’s weight
- **method**: controls a choice of algorithm. Current an internal debugging option.
- **...**: arguments for other methods

Details

This function is designed to efficiently compute the residuals at a small number of time points, also known as the infinitesimal jackknife (IJ). Primary usages are the creation of pseudo-values and IJ estimates of variance. If the residuals at all time points are needed, e.g., to compute a robust pointwise confidence interval for the survival curve, then this can be done more efficiently using the influence argument of the underlying `survfit` function. But be aware that such matrices can get very large.

The residuals are the impact of each observation or cluster on the resulting probability in state curves at the given time points, the cumulative hazard curve at those time points, or the expected sojourn time in each state up to the given time points. For a simple Kaplan-Meier the `survfit` object contains only the probability in the “initial” state, i.e., the survival fraction. For the KM case the sojourn time, the expected amount of time spent in the initial state, up to the specified endpoint, is more commonly known as the restricted mean survival time (RMST). For a multistate model this same quantity is also referred to as the restricted mean time in state (RMTS). It can be computed as the area under the respective probability in state curve. The program allows any of `pstate`, `surv`, `cumhaz`, `chaz`, `sojourn`, `rmst`, `rmts` or `auc` for the type argument, ignoring upper/lowercase, so users can choose whichever abbreviation they like best.

When `collapse=TRUE` the result has the cluster identifier (which defaults to the `id` variable) as the dimname for the first dimension. If the fit object contains more than one curve, and the same identifier is reused in two different curves this approach does not work and the routine will stop with an error. In principle this is not necessary, e.g., the result could contain two rows with the same label, showing the separate effect on each curve, but this was deemed too confusing.

Value

A matrix or array with one row per observation or cluster, and one column for each value in `times`. For a multi-state model the three dimensions are observation, time and state. For cumulative hazard, the last dimension is the set of transitions. (A competing risks model for instance has 3 states and 2 transitions.)

See Also

- `survfit`, `survfit.formula`

Examples

```r
fit <- survfit(Surv(time, status) ~ x, aml)
resid(fit, times=c(24, 48), type="RMTS")
```
Description

This is a method for the function `residuals` for objects inheriting from class `survreg`.

Usage

```r
## S3 method for class 'survreg'
residuals(object, type=c("response", "deviance", "dfbeta", "dfbetas","working","ldcase","ldresp","ldshape","matrix"), rsigma=TRUE,
collapse=FALSE, weighted=FALSE, ...)
```

Arguments

- `object`: an object inheriting from class `survreg`.
- `type`: type of residuals, with choices of "response", "deviance", "dfbeta", "dfbetas", "working", "ldcase", "ldresp", "ldshape", and "matrix".
- `rsigma`: include the scale parameters in the variance matrix, when doing computations. (I can think of no good reason not to).
- `collapse`: optional vector of subject groups. If given, this must be of the same length as the residuals, and causes the result to be per group residuals.
- `weighted`: give weighted residuals? Normally residuals are unweighted.
- `...`: other unused arguments

Value

A vector or matrix of residuals is returned. Response residuals are on the scale of the original data, working residuals are on the scale of the linear predictor, and deviance residuals are on log-likelihood scale. The dfbeta residuals are a matrix, where the ith row gives the approximate change in the coefficients due to the addition of subject i. The dfbetas matrix contains the dfbeta residuals, with each column scaled by the standard deviation of that coefficient.

The matrix type produces a matrix based on derivatives of the log-likelihood function. Let $L$ be the log-likelihood, $p$ be the linear predictor $X\beta$, and $s$ be $\log(\sigma)$. Then the 6 columns of the matrix are $L$, $dL/dp$, $\partial^2 L/\partial p^2$, $dL/ds$, $\partial^2 L/\partial s^2$ and $\partial^2 L/\partial p\partial s$. Diagnostics based on these quantities are discussed in the book and article by Escobar and Meeker. The main ones are the likelihood displacement residuals for perturbation of a case weight (ldcase), the response value (ldresp), and the shape.

For a transformed distribution such as the log-normal or Weibull, matrix residuals are based on the log-likelihood of the transformed data $\log(y)$. For a monotone function $f$ the density of $f(X)$ is the density of $X$ divided by the derivative of $f$ (the Jacobian), so subtract $\log(\text{derivative})$ from each uncensored observation’s loglik value in order to match the loglik component of the result. The other columns of the matrix residual are unchanged by the transformation.

References


See Also

predict.survreg

Examples

```r
fit <- survreg(Surv(futime, death) ~ age + sex, mgus2)
summary(fit)  # age and sex are both important

rr <- residuals(fit, type='matrix')
sum(rr[,1]) - with(mgus2, sum(log(futime[death==1])))  # loglik

plot(mgus2$age, rr[,2], col= (1+mgus2$death))  # ldresp
```

retinopathy

Diabetic Retinopathy

Description

A trial of laser coagulation as a treatment to delay diabetic retinopathy.

Usage

```r
retinopathy
data(retinopathy, package="survival")
```

Format

A data frame with 394 observations on the following 9 variables.

- **id**: numeric subject id
- **laser**: type of laser used: xenon argon
- **eye**: which eye was treated: right left
- **age**: age at diagnosis of diabetes
- **type**: type of diabetes: juvenile adult, (diagnosis before age 20)
- **trt**: 0 = control eye, 1 = treated eye
- **futime**: time to loss of vision or last follow-up
- **status**: 0 = censored, 1 = loss of vision in this eye
- **risk**: a risk score for the eye. This high risk subset is defined as a score of 6 or greater in at least one eye.

Details

The 197 patients in this dataset were a 50% random sample of the patients with "high-risk" diabetic retinopathy as defined by the Diabetic Retinopathy Study (DRS). Each patient had one eye randomized to laser treatment and the other eye received no treatment, and has two observations in the data set. For each eye, the event of interest was the time from initiation of treatment to the time when visual acuity dropped below 5/200 two visits in a row. Thus there is a built-in lag time of approximately 6 months (visits were every 3 months). Survival times in this dataset are the actual time to vision loss in months, minus the minimum possible time to event (6.5 months). Censoring was caused by death, dropout, or end of the study.
References


Examples

coxph(Surv(futime, status) ~ type + trt, cluster= id, retinopathy)

---

**rhDNase**

**rhDNASE data set**

**Description**

Results of a randomized trial of rhDNase for the treatment of cystic fibrosis.

**Usage**

rhDNase
data(rhDNase, package="survival")

**Format**

A data frame with 767 observations on the following 8 variables.

- id: subject id
- inst: enrolling institution
- trt: treatment arm: 0=placebo, 1= rhDNase
- entry.dt: date of entry into the study
- end.dt: date of last follow-up
- fev: forced expiratory volume at enrollment, a measure of lung capacity
- ivstart: days from enrollment to the start of IV antibiotics
- ivstop: days from enrollment to the cessation of IV antibiotics

**Details**

In patients with cystic fibrosis, extracellular DNA is released by leukocytes that accumulate in the airways in response to chronic bacterial infection. This excess DNA thickens the mucus, which then cannot be cleared from the lung by the cilia. The accumulation leads to exacerbations of respiratory symptoms and progressive deterioration of lung function. At the time of this study more than 90% of cystic fibrosis patients eventually died of lung disease.

Deoxyribonuclease I (DNase I) is a human enzyme normally present in the mucus of human lungs that digests extracellular DNA. Genentech, Inc. cloned a highly purified recombinant DNase I (rhDNase or Pulmozyme) which when delivered to the lungs in an aerosolized form cuts extracellular DNA, reducing the viscoelasticity of airway secretions and improving clearance. In 1992 the company conducted a randomized double-blind trial comparing rhDNase to placebo. Patients were then monitored for pulmonary exacerbations, along with measures of lung volume and flow. The primary...
endpoint was the time until first pulmonary exacerbation; however, data on all exacerbations were collected for 169 days.

The definition of an exacerbation was an infection that required the use of intravenous (IV) antibiotics. Subjects had 0–5 such episodes during the trial, those with more than one have multiple rows in the data set, those with none have NA for the IV start and end times. A few subjects were infected at the time of enrollment, subject 173 for instance has a first infection interval of -21 to 7. We do not count this first infection as an "event", and the subject first enters the risk set at day 7. Subjects who have an event are not considered to be at risk for another event during the course of antibiotics, nor for an additional 6 days after they end. (If the symptoms reappear immediately after cessation then from a medical standpoint this would not be a new infection.)

This data set reproduces the data in Therneau and Grambsch, it does not exactly reproduce those in Therneau and Hamilton due to data set updates.

References


Examples

# Build the start-stop data set for analysis, and
# replicate line 2 of table 8.13 in the book
first <- subset(rhDNase, !duplicated(id)) #first row for each subject
dnase <- tmerge(first, first, id=id, tstop=as.numeric(end.dt -entry.dt))

# Subjects whose fu ended during the 6 day window are the reason for
# this next line
temp.end <- with(rhDNase, pmin(ivstop+6, end.dt-entry.dt))
dnase <- tmerge(dnase, rhDNase, id=id,
               infect=event(ivstart),
               end= event(temp.end))

# toss out the non-at-risk intervals, and extra variables
# 3 subjects had an event on their last day of fu, infect=1 and end=1
dnase <- subset(dnase, (infect==1 | end==0), c(id:trt, fev:infect))
agfit <- coxph(Surv(tstart, tstop, infect) ~ trt + fev, cluster=id,
                data=dnase)

ridge

Ridge regression

Description

When used in a coxph or survreg model formula, specifies a ridge regression term. The likelihood is penalised by \( \theta/2 \) time the sum of squared coefficients. If scale=T the penalty is calculated for coefficients based on rescaling the predictors to have unit variance. If df is specified then \( \theta \) is chosen based on an approximate degrees of freedom.

Usage

ridge(..., theta, df=nvar/2, eps=0.1, scale=TRUE)
Arguments

... predictors to be ridged
theta penalty is theta/2 time sum of squared coefficients
df Approximate degrees of freedom
eps Accuracy required for df
scale Scale variables before applying penalty?

Value

An object of class coxph.penalty containing the data and control functions.

Note

If the expression ridge(x1, x2, x3, ...) is too many characters long then the internal terms() function will add newlines to the variable name and then the coxph routine simply gets lost. (Some labels will have the newline and some won’t.) One solution is to bundle all of the variables into a single matrix and use that matrix as the argument to ridge so as to shorten the call, e.g. mdata$many <- as.matrix(mydata[,5:53]).

References

Gray (1992) "Flexible methods of analysing survival data using splines, with applications to breast cancer prognosis" JASA 87:942–951

See Also
coxph,survreg,pspline,frailty

Examples

coxph(Surv(futime, fustat) ~ rx + ridge(age, ecog.ps, theta=1), ovarian)

lfit0 <- survreg(Surv(time, status) ~ 1, lung)
lfit1 <- survreg(Surv(time, status) ~ age + ridge(ph.ecog, theta=5), lung)
lfit2 <- survreg(Surv(time, status) ~ sex + ridge(age, ph.ecog, theta=1), lung)
lfit3 <- survreg(Surv(time, status) ~ sex + age + ph.ecog, lung)

Description

The rotterdam data set includes 2982 primary breast cancers patients whose records were included in the Rotterdam tumor bank.

Usage

rotterdam
data(cancer, package="survival")
A data frame with 2982 observations on the following 15 variables.

- **pid**: patient identifier
- **year**: year of surgery
- **age**: age at surgery
- **meno**: menopausal status (0= premenopausal, 1= postmenopausal)
- **size**: tumor size, a factor with levels <=20, 20-50, >50
- **grade**: differentiation grade
- **nodes**: number of positive lymph nodes
- **pgr**: progesterone receptors (fmol/l)
- **er**: estrogen receptors (fmol/l)
- **hormon**: hormonal treatment (0=no, 1=yes)
- **chemo**: chemotherapy
- **rtime**: days to relapse or last follow-up
- **recur**: 0= no relapse, 1= relapse
- **dt ime**: days to death or last follow-up
- **death**: 0= alive, 1= dead

These data sets are used in the paper by Royston and Altman that is referenced below. The Rotterdam data is used to create a fitted model, and the GBSG data for validation of the model. The paper gives references for the data source.

There are 43 subjects who have died without recurrence, but whose death time is greater than the censoring time for recurrence. A common way that this happens is that a death date is updated in the health record sometime after the research study ended, and said value is then picked up when a study data set is created. Vital status information can come from many sources: a patient visit for another condition, correspondence, financial transactions, or social media. But this raises serious questions about censoring. For instance subject 40 is censored for recurrence at 4.2 years and died at 6.6 years; when creating the endpoint of recurrence free survival (earlier of recurrence or death), treating them as a death at 6.6 years implicitly assumes that they were recurrence free just before death. For this to be true we would have to assume that if they had progressed in the 2.4 year interval before death (while off study), that this information would also have been noted in their general medical record, and would also be captured in the study data set. However, that may be unlikely. Death information is often in a centralized location in electronic health records, easily accessed by a programmer and merged with the study data, while recurrence may require manual review. How best to address this is an open issue.


See Also

gbsg
Examples

# liberal definition of rfs (count later deaths)
rf <- pmax(rotterdam$recur, rotterdam$death)
rfstime <- with(rotterdam, ifelse(recur==1, rtime, dtime))
fit1 <- coxph(Surv(rfstime, rf) ~ pspline(age) + meno + size +
               pspline(nodes) + er, data = rotterdam)

# conservative (no deaths after last fu for recurrence)
ignore <- with(rotterdam, recur ==0 & death==1 & rtime < dttime)
table(ignore)
rf <- with(rotterdam, ifelse(recur==1 | ignore, recur, death))
rfstime2 <- with(rotterdam, ifelse(recur==1 | ignore, rtime, dtime))
fit2 <- coxph(Surv(rfstime2, rfs2) ~ pspline(age) + meno + size +
               pspline(nodes) + er, data = rotterdam)

# Note: Both age and nodes show non-linear effects.
# Royston and Altman used fractional polynomials for the nonlinear terms

royston

Compute Royston's D for a Cox model

Description

Compute the D statistic proposed by Royston and Sauerbrei along with several pseudo-R square values.

Usage

royston(fit, newdata, ties = TRUE, adjust = FALSE)

Arguments

fit a coxph fit
newdata optional validation data set
ties make a correction for ties in the risk score
adjust adjust for possible overfitting

Details

These values are called pseudo-R-squared since they involve only the linear predictor, and not the outcome. R.D is the value that corresponds to the Royston and Sauerbrei D statistic. R.KO is the value proposed by Kent and O'Quigley. R.N is the value proposed by Nagelkerke, and C.GH corresponds to Goen and Heller's concordance measure.

An adjustment for D is based on the ratio r = (number of events)/(number of coefficients). For models which have sufficient sample size (r>20) the adjustment will be small.

The Nagelkerke value is the Cox-Snell R-squared divided by a scaling constant. The two separate values are present in the result of summary.coxph as a 2 element vector rsq, and were listed as "Rsquare" and "max possible" in older versions of the print routine. (Since superseded in the default printout by the concordance.) The Nagelkerke estimate is not returned when newdata is present.
Value

A vector containing the value of D, the estimated standard error of D, and three or four pseudo R-squared values.

References


Examples

# An example used in Royston and Sauerbrei
pbc2 <- na.omit(pbc) # no missing values
cfit <- coxph(Surv(time, status==2) ~ age + log(bili) + edema + albumin + stage + copper, data=pbc2, ties="breslow")
royston(cfit)

rttright

Compute redistribute-to-the-right weights

Description

For many survival estimands, one approach is to redistribute each censored observation’s weight to those other observations with a longer survival time (think of distributing an estate to the heirs). Then compute on the remaining, uncensored data.

Usage

rttright(formula, data, weights, subset, na.action, times, id, timefix = TRUE, renorm= TRUE)

Arguments

t formula: a formula object, which must have a Surv object as the response on the left of the ~ operator and, if desired, terms separated by + operators on the right. Each unique combination of predictors will define a separate strata.
data: a data frame in which to interpret the variables named in the formula, subset and weights arguments.
weights: The weights must be nonnegative and it is strongly recommended that they be strictly positive, since zero weights are ambiguous, compared to use of the subset argument.
subset: expression saying that only a subset of the rows of the data should be used in the fit.
na.action: a missing-data filter function, applied to the model frame, after any subset argument has been used. Default is options()$na.action.
times a vector of time points, for which to return updated weights. If missing, a time after the largest time in the data is assumed.

id optional: if the data set has multiple rows per subject, a variable containing the subject identifier of each row.

timefix correct for possible round-off error

renorm the resulting weights sum to 1 within each group

Details

The formula argument is treated exactly the same as in the survfit function.

Redistribution is recursive: redistribute the weight of the first censored observation to all those with longer time, which may include other censored observations. Then redistribute the next smallest and etc. up to the specified time value. After redistributing the weight for a censored observation to other observations that are not censored, ordinary non-censored methods can often be applied. For example, redistribution of the weights, followed by computation of the weighted cumulative distribution function, reprises the Kaplan-Meier estimator.

A primary use of this routine is illustration of methods or exploration of new methods. Methods that use RTTR directly, such as the Brier score, will often do these computations internally.

A covariate on the right hand side of the formula causes redistribution to occur within group; a censoring in group 1 redistributes weights to others in group 1, etc. This is appropriate when the censoring pattern depends upon group.

Value

a vector or matrix of weights, with one column for each requested time

See Also

survfit

Examples

afit <- survfit(Surv(time, status) ~ 1, data=aml)
rwt <- rttright(Surv(time, status) ~ 1, data=aml)

# Reproduce a Kaplan-Meier
index <- order(aml$time)
cdf <- cumsum(rwt[index]) # weighted CDF
cdf <- cdf[!duplicated(aml$time[index], fromLast=TRUE)] # remove duplicate times
cbind(time=afit$time, KM= afit$surv, RTTR= 1-cdf)

# Hormonal patients have a different censoring pattern
wt2 <- rttright(Surv(dtime, death) ~ hormon, rotterdam, times= 365*c(3, 5))
dim(wt2)
Description
In 1988 an experiment was designed and implemented at one of AT&T’s factories to investigate alternatives in the “wave soldering” procedure for mounting electronic componentes to printed circuit boards. The experiment varied a number of factors relevant to the process. The response, measured by eye, is the number of visible solder skips.

Usage
solder
data(solder, package="survival")

Format
A data frame with 900 observations on the following 6 variables.
- Opening the amount of clearance around the mounting pad (3 levels)
- Solder the amount of solder (Thick or Thin)
- Mask type and thickness of the material used for the solder mask (A1.5, A3, A6, B3, B6)
- PadType the geometry and size of the mounting pad (10 levels)
- Panel each board was divided into 3 panels
- skips the number of skips

Details
This data set is used as a detailed example in chapter 1 of Chambers and Hastie. Observations 1-360 and 541-900 form a balanced design of 3*2*10*3 = 180 observations for four of the pad types (A1.5, A3, B3, B6), while rows 361-540 match 3 of the 6 Solder*Opening combinations with pad type A6 and the other 3 with pad type A3.

References

Examples
# The balanced subset used by Chambers and Hastie
# contains the first 180 of each mask and deletes mask A6.
index <- 1 + (1:nrow(solder)) - match(solder$Mask, solder$Mask)
solder.balance <- droplevels(subset(solder, Mask != "A6" & index <= 180))
More Stanford Heart Transplant data

Description

This contains the Stanford Heart Transplant data in a different format. The main data set is in `heart`.

Usage

stanford2

Format

- **id**: ID number
- **time**: survival or censoring time
- **status**: censoring status
- **age**: in years
- **t5**: T5 mismatch score

Source


See Also

`predict.survreg`, `heart`

---

Draw a state space figure.

Description

For multi-state survival models it is useful to have a figure that shows the states and the possible transitions between them. This function creates a simple "box and arrows" figure. Its goal was simplicity.

Usage

`statefig(layout, connect, margin = 0.03, box = TRUE, cex = 1, col = 1, lwd=1, lty=1, bcol=col, acol=col, alwd=lwd, alty=lty, offset=0)`
Arguments

layout describes the layout of the boxes on the page. See the detailed description below.

connect a square matrix with one row for each state. If connect[i, j] != 0 then an arrow is drawn from state i to state j. The row names of the matrix are used as the labels for the states.

margin the fraction of white space between the label and the surrounding box, and between the box and the arrows, as a function of the plot region size.

box should boxes be drawn? TRUE or FALSE.

cex, col, lty, lwd default graphical parameters used for the text and boxes. The last 3 can be a vector of values.

bcol color for the box, if it differs from that used for the text.

acol, alwd, alty color, line type and line width for the arrows.

offset used to slight offset the arrows between two boxes x and y if there is a transition in both directions. The default of 0 leads to a double headed arrow in this case – to arrows are drawn but they coincide. A positive value causes each arrow to shift to the left, from the view of someone standing at the foot of a arrow and looking towards the arrowhead, a negative offset shifts to the right. A value of 1 corresponds to the size of the plotting region.

Details

The arguments for color, line type and line width can all be vectors, in which case they are recycled as needed. Boxes and text are drawn in the order of the rownames of connect, and arrows are drawn in the usual R matrix order.

The layout argument is normally a vector of integers, e.g., the vector (1, 3, 2) describes a layout with 3 columns. The first has a single state, the second column has 3 states and the third has 2. The coordinates of the plotting region are 0 to 1 for both x and y. Within a column the centers of the boxes are evenly spaced, with 1/2 a space between the boxes and the margin, e.g., 4 boxes would be at 1/8, 3/8, 5/8 and 7/8. If layout were a 1 column matrix with values of (1, 3, 2) then the layout will have three rows with 1, 3, and 2 boxes per row, respectively. Alternatively, the user can supply a 2 column matrix that directly gives the centers.

The values of the connect matrix should be 0 for pairs of states that do not have a transition and values between 0 and 2 for those that do. States are connected by an arc that passes through the centers of the two boxes and a third point that is between them. Specifically, consider a line segment joining the two centers and erect a second segment at right angles to the midpoint of length d times the distance from center to midpoint. The arc passes through this point. A value of d=0 gives a straight line, d=1 a right hand half circle centered on the midpoint and d= -1 a left hand half circle. The connect matrix contains values of d+1 with -1 < d < 1.

The connecting arrow are drawn from (center of box 1 + offset) to (center of box 2 + offset), where the the amount of offset (white space) is determined by the box and margin parameters. If a pair of states are too close together this can result in an arrow that points the wrong way.

Value

a matrix containing the centers of the boxes, with the invisible attribute set.
The goal of this function is to make “good enough” figures as simply as possible, and thereby to encourage users to draw them. The layout argument was inspired by the diagram package, which can draw more complex and well decorated figures, e.g., many different shapes, shading, multiple types of connecting lines, etc., but at the price of greater complexity.

Because curved lines are drawn as a set of short line segments, line types have almost no effect for that case.

**Author(s)**

Terry Therneau

**Examples**

```r
# Draw a simple competing risks figure
states <- c("Entry", "Complete response", "Relapse", "Death")
connect <- matrix(0, 4, 4, dimnames=list(states, states))
connect[1, -1] <- c(1.1, 1, 0.9)
statefig(c(1, 3), connect)
```

---

**strata**

*Identify Stratification Variables*

**Description**

This is a special function used in the context of the Cox survival model. It identifies stratification variables when they appear on the right hand side of a formula.

**Usage**

```r
strata(..., na.group=FALSE, shortlabel, sep=', ')`
```

**Arguments**

- `...`: any number of variables. All must be the same length.
- `na.group`: a logical variable, if TRUE, then missing values are treated as a distinct level of each variable.
- `shortlabel`: if TRUE omit variable names from resulting factor labels. The default action is to omit the names if all of the arguments are factors, and none of them was named.
- `sep`: the character used to separate groups, in the created label

**Details**

When used outside of a coxph formula the result of the function is essentially identical to the interaction function, though the labels from strata are often more verbose.

**Value**

a new factor, whose levels are all possible combinations of the factors supplied as arguments.
summary.aareg

See Also
coxph, interaction

Examples

```r
a <- factor(rep(1:3,4), labels=c("low", "medium", "high"))
b <- factor(rep(1:4,3))
levels(strata(b))
levels(strata(a,b,shortlabel=TRUE))

coxph(Surv(futime, fustat) ~ age + strata(rx), data=ovarian)
```

**summary.aareg**  
*Summarize an aareg fit*

**Description**

Creates the overall test statistics for an Aalen additive regression model

**Usage**

```r
## S3 method for class 'aareg'
summary(object, maxtime, test=c("aalen", "nrisk"), scale=1,...)
```

**Arguments**

- `object`  
  the result of a call to the aareg function
- `maxtime`  
  truncate the input to the model at time "maxtime"
- `test`  
  the relative time weights that will be used to compute the test
- `scale`  
  scales the coefficients. For some data sets, the coefficients of the Aalen model will be very small (10^-4); this simply multiplies the printed values by a constant, say 1e6, to make the printout easier to read.
- `...`  
  for future methods

**Details**

It is not uncommon for the very right-hand tail of the plot to have large outlying values, particularly for the standard error. The `maxtime` parameter can then be used to truncate the range so as to avoid these. This gives an updated value for the test statistics, without refitting the model.

The slope is based on a weighted linear regression to the cumulative coefficient plot, and may be a useful measure of the overall size of the effect. For instance when two models include a common variable, "age" for instance, this may help to assess how much the fit changed due to the other variables, in lieu of overlaying the two plots. (Of course the plots are often highly non-linear, so it is only a rough substitute). The slope is not directly related to the test statistic, as the latter is invariant to any monotone transformation of time.
Value

A list is returned with the following components:

- `table`: a matrix with rows for the intercept and each covariate, and columns giving a slope estimate, the test statistic, its standard error, the z-score and a p-value.
- `test`: the time weighting used for computing the test statistics.
- `test.statistic`: the vector of test statistics.
- `test.var`: the model-based variance matrix for the test statistic.
- `test.var2`: optionally, a robust variance matrix for the test statistic.
- `chisq`: the overall test (ignoring the intercept term) for significance of any variable.
- `n`: a vector containing the number of observations, the number of unique death times used in the computation, and the total number of unique death times.

See Also

`aareg`, `plot.aareg`.

Examples

```r
afit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung, dfbeta=TRUE)
summary(afit)
## Not run:
slope test se(test) robust se z p
Intercept 5.05e-03 1.9 1.54 1.55 1.23 0.219000
age 4.01e-05 108.0 109.00 106.00 1.02 0.307000
sex -3.16e-03 -19.5 5.90 5.95 -3.28 0.001030
ph.ecog 3.01e-03 33.2 9.18 9.17 3.62 0.000299
Chisq=22.84 on 3 df, p=4.4e-05; test weights=aalen
## End(Not run)

summary(afit, maxtime=600)
## Not run:
slope test se(test) robust se z p
Intercept 4.16e-03 2.13 1.48 1.47 1.450 0.146000
age 2.82e-05 85.80 106.00 100.00 0.857 0.392000
sex -2.54e-03 -20.60 5.61 5.63 -3.60 0.000256
ph.ecog 2.47e-03 31.60 8.91 8.67 3.640 0.000271
Chisq=27.08 on 3 df, p=5.7e-06; test weights=aalen
## End(Not run)
```
Summary method for Cox models

Description

Produces a summary of a fitted coxph model

Usage

```r
## S3 method for class 'coxph'
summary(object, conf.int=0.95, scale=1,...)
```

Arguments

- `object`: the result of a coxph fit
- `conf.int`: level for computation of the confidence intervals. If set to FALSE no confidence intervals are printed
- `scale`: vector of scale factors for the coefficients, defaults to 1. The printed coefficients, se, and confidence intervals will be associated with one scale unit.
- `...`: for future methods

Value

An object of class `summary.coxph`, with components:

- `n, nevent`: number of observations and number of events, respectively, in the fit
- `loglik`: the log partial likelihood at the initial and final values
- `coefficients`: a matrix with one row for each coefficient, and columns containing the coefficient, the hazard ratio `exp(coef)`, standard error, Wald statistic, and P value.
- `conf.int`: a matrix with one row for each coefficient, containing the confidence limits for `exp(coef)`
- `logtest, sctest, waldtest`: the overall likelihood ratio, score, and Wald test statistics for the model
- `concordance`: the concordance statistic and its standard error
- `used.robust`: whether an asymptotic or robust variance was used
- `rsq`: an approximate R^2 based on Nagelkerke (Biometrika 1991).
- `fail`: a message, if the underlying coxph call failed
- `call`: a copy of the call
- `na.action`: information on missing values

Note

The pseudo r-squared of Nagelkerke is attractive because it is simple, but further work has shown that it has poor properties and it is now deprecated. The value is no longer printed by default, and will eventually be removed from the object.

See Also

`coxph, print.coxph`
**Examples**

```r
fit <- coxph(Surv(time, status) ~ age + sex, lung)
summary(fit)
```

---

**summary.pyears**  
*Summary function for pyears objects*

**Description**

Create a printable table of a person-years result.

**Usage**

```r
## S3 method for class 'pyears'
summary(object, header = TRUE, call = header, n = TRUE,
event = TRUE, pyears = TRUE, expected = TRUE, rate = FALSE, rr = expected,
ci.r = FALSE, ci.rr = FALSE, totals = FALSE, legend = TRUE, vline = FALSE,
vertical = TRUE, nastring = ".", conf.level = 0.95,
scale = 1, ...)
```

**Arguments**

- `object`: a pyears object
- `header`: print out a header giving the total number of observations, events, person-years, and total time (if any) omitted from the table
- `call`: print out a copy of the call
- `n, event, pyears, expected`: logical arguments: should these elements be printed in the table?
- `rate, ci.r`: logical arguments: should the incidence rate and/or its confidence interval be given in the table?
- `rr, ci.rr`: logical arguments: should the hazard ratio and/or its confidence interval be given in the table?
- `totals`: should row and column totals be added?
- `legend`: should a legend be included in the printout?
- `vline`: should vertical lines be included in the printed tables?
- `vertical`: when there is only a single predictor, should the table be printed with the predictor on the left (vertical=TRUE) or across the top (vertical=FALSE)?
- `nastring`: what to use for missing values in the table. Some of these are structural, e.g., risk ratios for a cell with no follow-up time.
- `conf.level`: confidence level for any confidence intervals
- `scale`: a scaling factor for printed rates
- `...`: optional arguments which will be passed to the `format` function; common choices would be digits=2 or nsmall=1.
Details

The pyears function is often used to create initial descriptions of a survival or time-to-event variable; the type of material that is often found in “table 1” of a paper. The summary routine prints this information out using one of pandoc table styles. A primary reason for choosing this style is that Rstudio is then able to automatically render the results in multiple formats: html, rtf, latex, etc.

If the pyears call has only a single covariate then the table will have that covariate as one margin and the statistics of interest as the other. If the pyears call has two predictors then those two predictors are used as margins of the table, while each cell of the table contains the statistics of interest as multiple rows within the cell. If there are more than two predictors then multiple tables are produced, in the same order as the standard R printout for an array.

The "N" entry of a pyears object is the number of observations which contributed to a particular cell. When the original call includes tcut objects then a single observation may contribute to multiple cells.

Value

a copy of the object

Notes

The pandoc system has four table types: with or without vertical bars, and with single or multiple rows of data in each cell. This routine produces all 4 styles depending on options, but currently not all of them are recognized by the Rstudio-pandoc pipeline. (And we don’t yet see why.)

Author(s)

Terry Therneau and Elizabeth Atkinson

See Also

cipoisson, pyears, format

Description

Returns a list containing the values of the survival at specified times.

Usage

## S3 method for class 'survexp'
summary(object, times, scale = 1, ...)

Arguments

object the result of a call to the survexp function
times vector of times; the returned matrix will contain 1 row for each time. Missing values are not allowed.
scale numeric value to rescale the survival time, e.g., if the input data to survfit were in days, scale = 365.25 would scale the output to years.
... For future methods
Details

A primary use of this function is to retrieve survival at fixed time points, which will be properly interpolated by the function.

Value

a list with the following components:

- `surv` the estimate of survival at time t.
- `time` the timepoints on the curve.
- `n.risk` In expected survival each subject from the data set is matched to a hypothetical person from the parent population, matched on the characteristics of the parent population. The number at risk is the number of those hypothetical subject who are still part of the calculation.

Author(s)

Terry Therneau

See Also

- `survexp`

summary.survfit  

Summary of a Survival Curve

Description

Returns a list containing the survival curve, confidence limits for the curve, and other information.

Usage

```r
## S3 method for class 'survfit'
summary(object, times, censored=FALSE, scale=1,
         extend=FALSE, rmean=getOption('survfit.rmean'), ...)  
```

Arguments

- `object` the result of a call to the `survfit` function.
- `times` vector of times; the returned matrix will contain 1 row for each time. The vector will be sorted into increasing order; missing values are not allowed. If `censored=T`, the default `times` vector contains all the unique times in `fit`, otherwise the default `times` vector uses only the event (death) times.
- `censored` logical value: should the censoring times be included in the output? This is ignored if the `times` argument is present.
- `scale` numeric value to rescale the survival time, e.g., if the input data to `survfit` were in days, `scale = 365.25` would scale the output to years.
extend logical value: if TRUE, prints information for all specified times, even if there are no subjects left at the end of the specified times. This is only used if the times argument is present.
rmean Show restricted mean: see \texttt{print.survfit} for details
... for future methods

\textbf{Value}

a list with the following components:

\begin{description}
\item[surv] the estimate of survival at time $t+0$.
\item[time] the timepoints on the curve.
\item[n.risk] the number of subjects at risk at time $t-0$ (but see the comments on weights in the \texttt{survfit} help file).
\item[n.event] if the \texttt{times} argument is missing, then this column is the number of events that occurred at time $t$. Otherwise, it is the cumulative number of events that have occurred since the last time listed until time $t+0$.
\item[n.entered] This is present only for counting process survival data. If the \texttt{times} argument is missing, this column is the number of subjects that entered at time $t$. Otherwise, it is the cumulative number of subjects that have entered since the last time listed until time $t$.
\item[n.exit.censored] if the \texttt{times} argument is missing, this column is the number of subjects that left without an event at time $t$. Otherwise, it is the cumulative number of subjects that have left without an event since the last time listed until time $t+0$. This is only present for counting process survival data.
\item[std.err] the standard error of the survival value.
\item[conf.int] level of confidence for the confidence intervals of survival.
\item[lower] lower confidence limits for the curve.
\item[upper] upper confidence limits for the curve.
\item[strata] indicates stratification of curve estimation. If \texttt{strata} is not NULL, there are multiple curves in the result and the surv, time, n.risk, etc. vectors will contain multiple curves, pasted end to end. The levels of \texttt{strata} (a factor) are the labels for the curves.
\item[call] the statement used to create the \texttt{fit} object.
\item[na.action] same as for \texttt{fit}, if present.
\item[table] table of information that is returned from \texttt{print.survfit} function.
\item[type] type of data censoring. Passed through from the \texttt{fit} object.
\end{description}

\textbf{Details}

This routine has two uses: printing out a survival curve at specified time points (often yearly), or extracting the values at specified time points for further processing. In the first case we normally want \texttt{extend=FALSE}, i.e., don’t print out data past the end of the curve. If the \texttt{times} option only contains values beyond the last point in the curve then there is nothing to print and an error message will result. For the second usage we almost always want \texttt{extend=TRUE}, so that the results will have a predictable length.

The \texttt{survfit} object itself will have a row of information at each censoring or event time, it does not save information on each unique entry time. For printout at two time points $t_1, t_2$, this function
will give the number at risk at the smallest event times that are >= t1 and >= t2, respectively, the survival curve at the largest recorded times <= t1 and <= t2, and the number of events and censorings in the interval t1 < t <= t2.

When the routine is called with counting process data many users are confused by counts that are too large. For example, Surv(c(0, 0, 5, 5), c(2, 3, 8, 10), c(1, 0, 1, 0)) followed by a request for the values at time 4. The survfit object has entries only at times 2, 3, 8, and 10; there are 2 subjects at risk at time 8, so that is what will be printed.

See Also

survfit, print.summary.survfit

Examples

summary( survfit( Surv(futime, fustat)~1, data=ovarian))
summary( survfit( Surv(futime, fustat)~rx, data=ovarian))

Surv

Create a Survival Object

Description

Create a survival object, usually used as a response variable in a model formula. Argument matching is special for this function, see Details below.

Usage

Surv(time, time2, event,
    type=c('right', 'left', 'interval', 'counting', 'interval2', 'mstate'),
    origin=0)

is.Surv(x)

Arguments

time for right censored data, this is the follow up time. For interval data, the first argument is the starting time for the interval.

event The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For interval censored data, the status indicator is 0=right censored, 1=event at time, 2=left censored, 3=interval censored. For multiple endpoint data the event variable will be a factor, whose first level is treated as censoring. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.

time2 ending time of the interval for interval censored or counting process data only. Intervals are assumed to be open on the left and closed on the right, (start, end]. For counting process data, event indicates whether an event occurred at the end of the interval.

type character string specifying the type of censoring. Possible values are "right", "left", "counting", "interval", "interval2" or "mstate".
origin for counting process data, the hazard function origin. This option was intended to be used in conjunction with a model containing time dependent strata in order to align the subjects properly when they cross over from one strata to another, but it has rarely proven useful.

x any R object.

Details

When the type argument is missing the code assumes a type based on the following rules:

- If there are two unnamed arguments, they will match time and event in that order. If there are three unnamed arguments they match time, time2 and event.
- If the event variable is a factor then type mstate is assumed. Otherwise type right if there is no time2 argument, and type counting if there is.

As a consequence the type argument will normally be omitted.

When the survival type is "mstate" then the status variable will be treated as a factor. The first level of the factor is taken to represent censoring and remaining ones a transition to the given state. (If the status variable is a factor then mstate is assumed.)

Interval censored data can be represented in two ways. For the first use type = "interval" and the codes shown above. In that usage the value of the time2 argument is ignored unless event=3. The second approach is to think of each observation as a time interval with (-infinity, t2) for left censored, (t1, infinity) for right censored, (t1, t2) for exact and (t1, t2) for an interval. This is the approach used for type = interval2. Infinite values can be represented either by actual infinity (Inf) or NA. The second form has proven to be the more useful one.

Presently, the only methods allowing interval censored data are the parametric models computed by survreg and survival curves computed by survfit; for both of these, the distinction between open and closed intervals is unimportant. The distinction is important for counting process data and the Cox model.

The function tries to distinguish between the use of 0/1 and 1/2 coding for censored data via the condition if (max(status)==2). If 1/2 coding is used and all the subjects are censored, it will guess wrong. In any questionable case it is safer to use logical coding, e.g., Surv(time, status==3) would indicate that ‘3’ is the code for an event. For multi-state survival the status variable will be a factor, whose first level is assumed to correspond to censoring.

Surv objects can be subscripted either as a vector, e.g. x[1:3] using a single subscript, in which case the drop argument is ignored and the result will be a survival object; or as a matrix by using two subscripts. If the second subscript is missing and drop=F (the default), the result of the subscripting will be a Surv object, e.g., x[1:3,,drop=F], otherwise the result will be a matrix (or vector), in accordance with the default behavior for subscripting matrices.

Value

An object of class Surv. There are methods for print, is.na, and subscripting survival objects. Surv objects are implemented as a matrix of 2 or 3 columns that has further attributes. These include the type (left censored, right censored, counting process, etc.) and labels for the states for multi-state objects. Any attributes of the input arguments are also preserved in inputAttributes. This may be useful for other packages that have attached further information to data items such as labels; none of the routines in the survival package make use of these values, however.

In the case of is.Surv, a logical value TRUE if x inherits from class "Surv", otherwise an FALSE.
**Note**

The use of 1/2 coding for status is an interesting historical artifact. For data contained on punch cards, IBM 360 Fortran treated blank as a zero, which led to a policy within the Mayo Clinic section of Biostatistics to never use "0" as a data value since one could not distinguish it from a missing value. Policy became habit, as is often the case, and the use of 1/2 coding for alive/dead endured long after the demise of the punch cards that had sired the practice. At the time Surv was written many Mayo data sets still used this obsolete convention, e.g., the lung data set found in the package.

**See Also**

coxph, survfit, survreg, lung.

**Examples**

```r
with(aml, Surv(time, status))
survfit(Surv(time, status) ~ ph.ecog, data=lung)
Surv(heart$start, heart$stop, heart$event)
```

---

**Description**

The list of methods that apply to Surv objects

**Usage**

```r
## S3 method for class 'Surv'
anyDuplicated(x, ...)
## S3 method for class 'Surv'
as.character(x, ...)
## S3 method for class 'Surv'
as.data.frame(x, ...)
## S3 method for class 'Surv'
as.integer(x, ...)
## S3 method for class 'Surv'
as.matrix(x, ...)
## S3 method for class 'Surv'
as.numeric(x, ...)
## S3 method for class 'Surv'
c(...)
## S3 method for class 'Surv'
duplicated(x, ...)
## S3 method for class 'Surv'
format(x, ...)
## S3 method for class 'Surv'
head(x, ...)
## S3 method for class 'Surv'
is.na(x)
## S3 method for class 'Surv'
length(x)
```
## S3 method for class 'Surv'
mean(x, ...)
## S3 method for class 'Surv'
median(x, na.rm=FALSE, ...)
## S3 method for class 'Surv'
names(x)
## S3 replacement method for class 'Surv'
names(x) <- value
## S3 method for class 'Surv'
quantile(x, probs, na.rm=FALSE, ...)
## S3 method for class 'Surv'
plot(x, ...)
## S3 method for class 'Surv'
rep(x, ...)
## S3 method for class 'Surv'
rep.int(x, ...)
## S3 method for class 'Surv'
rep_len(x, ...)
## S3 method for class 'Surv'
rev(x)
## S3 method for class 'Surv'
t(x)
## S3 method for class 'Surv'
tail(x, ...)
## S3 method for class 'Surv'
unique(x, ...)

### Arguments

- **x**: a Surv object
- **probs**: a vector of probabilities
- **na.rm**: remove missing values from the calculation
- **value**: a character vector of up to the same length as x, or NULL
- **...**: other arguments to the method

### Details

These functions extend the standard methods to Surv objects. The arguments and results from these are mostly as expected, with the following further details:

- The `as.character` function uses "5+" for right censored at time 5, "5-" for left censored at time 5, "[2,7]" for an observation that was interval censored between 2 and 7, "(1,6]" for a counting process data denoting an observation which was at risk from time 1 to 6, with an event at time 6, and "(1,6+]" for an observation over the same interval but not ending with an event. For a multi-state survival object the type of event is appended to the event time using ":type".
- The `print` and `format` methods make use of `as.character`.
- The `as.numeric` and `as.integer` methods perform these actions on the survival times, but do not affect the censoring indicator.
- The `as.matrix` and `t` methods return a matrix.
The length of a Surv object is the number of survival times it contains, not the number of items required to encode it, e.g., x <- Surv(1:4, 5:9, c(1,0,1,0)); length(x) has a value of 4. Likewise names(x) will be NULL or a vector of length 4. (For technical reasons, any names are actually stored in the rownames attribute of the object.)

For a multi-state survival object levels returns the names of the endpoints, otherwise it is NULL.

The median, quantile and plot methods first construct a survival curve using survfit, then apply the appropriate method to that curve.

The concatenation method c() is asymmetric, its first argument determines the execution path. For instance c(Surv(1:4), Surv(5:6)) will concatenate the two objects, c(Surv(1:4), 5:6) will give an error, and c(5:6, Surv(1:4)) is equivalent to c(5:6, as.vector(Surv(1:4))).

See Also
Surv

Surv2

Create a survival object

Description
Create a survival object from a timeline style data set. This will almost always be the response variable in a formula.

Usage
Surv2(time, event, repeated=FALSE)

Arguments
time
  a timeline variable, such as age, time from enrollment, date, etc.

event
  the outcome at that time. This can be a 0/1 variable, TRUE/FALSE, or a factor. If the latter, the first level of the factor corresponds to 'no event was observed at this time'.

repeated
  if the same level of the outcome repeats, without an intervening event of another type, should this be treated as a new event?

Details
This function is still experimental.

When used in a coxph or survfit model, Surv2 acts as a trigger to internally convert a timeline style data set into counting process style data, which is then acted on by the routine.

The repeated argument controls how repeated instances of the same event code are treated. If TRUE, they are treated as new events, an example where this might be desired is repeated infections in a subject. If FALSE, then repeats are not a new event. An example would be a data set where we wanted to use diabetes, say, as an endpoint, but this is repeated at each medical visit.
Surv2data

Value

An object of class Surv2. There are methods for print, is.na and subscripting.

See Also

Surv2data, coxph, survfit

Surv2data

Convert data from timecourse to (time1,time2) style

Description

The multi-state survival functions coxph and survfit allow for two forms of input data. This routine converts between them. The function is normally called behind the scenes when Surv2 is as the response.

Usage

Surv2data(formula, data, subset, id)

Arguments

formula a model formula
data a data frame
subset optional, selects rows of the data to be retained
id a variable that identified multiple rows for the same subject, normally found in the referenced data set

Details

For timeline style data, each row is uniquely identified by an (identifier, time) pair. The time could be a date, time from entry to a study, age, etc, (there may often be more than one time variable). The identifier and time cannot be missing. The remaining covariates represent values that were observed at that time point. Often, a given covariate is observed at only a subset of times and is missing at others. At the time of death, in particular, often only the identifier, time, and status indicator are known.

In the resulting data set missing covariates are replaced by their last known value, and the response y will be a Surv(time1, time2, endpoint) object.

Value

a list with elements

mf an updated model frame (fewer rows, unchanged columns)
S2.y the constructed response variable
S2.state the current state for each of the rows
survcheck

 Checks of a survival data set

Description

Perform a set of consistency checks on survival data

Usage

survcheck(formula, data, subset, na.action, id, istate, istate0="(s0)",
  timefix=TRUE,...)

Arguments

formula a model formula with a Surv object as the response
data data frame in which to find the id, istate and formula variables
subset expression indicating which subset of the rows of data should be used in the fit.
  All observations are included by default.
na.action a missing-data filter function. This is applied to the model.frame after any subset
  argument has been used. Default is options()$na.action.
id an identifier that labels unique subjects
istate an optional vector giving the current state at the start of each interval
istate0 default label for the initial state of each subject (at their first interval) when
  istate is missing
timefix process times through the aeqSurv function to eliminate potential roundoff is-
  sues.
... other arguments, which are ignored (but won’t give an error if someone added
  weights for instance)

Details

This routine will examine a multi-state data set for consistency of the data. The basic rules are
that if a subject is at risk they have to be somewhere, can not be two states at once, and should
make sensible transitions from state to state. It reports the number of instances of the following
conditions:

overlap two observations for the same subject that overlap in time, e.g. intervals of (0, 100) and
  (90, 120). If y is simple (time, status) survival observation intervals implicitly start at 0, so in
  that case any duplicate identifiers will generate an overlap.
jump a hole in a subject’s timeline, where they are in one state at the end of the prior interval, but
  a new state in the at the start subsequent interval.
gap one or more gaps in a subject’s timeline; they are presumably in the same state at their return
  as when they left.
teleport two adjacent intervals for a subject, with the first interval ending in one state and the subse-
  quent interval starting in another. They have instantaneously changed states with experiencing
  a transition.

The total number of occurrences of each is present in the flags vector. Optional components give
the location and identifiers of the flagged observations.
Value

- **states**: the vector of possible states
- **.transitions**: a matrix giving the count of transitions from one state to another
- **statecount**: table of the number of visits per state, e.g., 18 subjects had 2 visits to the "infection" state
- **flags**: a vector giving the counts of each check
- **istate**: a copy of the istate vector, if it was supplied; otherwise a constructed istate that satisfies all the checks
- **overlap**: a list with the row number and id of overlaps (not present if there are no overlaps)
- **gaps**: a list with the row number and id of gaps (not present if there are no gaps)
- **teleport**: a list with the row number and id of inconsistent rows (not present if there are none)
- **jumps**: a list with the row number and id of jumps (not present if there are no jumps)

Note

For data sets with time-dependent covariates, a given subject will often have intermediate rows with a status of 'no event at this time'. (numeric value of 0). For instance a subject who started in state 1 at time 0, transitioned to state 2 at time 10, had a covariate x change from 135 to 156 at time 20, and a final transition to state 3 at time 30. The response would be `Surv(c(0, 10, 20), c(10, 20, 30), c(2, 0, 3))`: the status variable records changes in state, and there was no change at time 20. The istate variable would be (1, 2, 2); it contains the current state, and so the value is unchanged when status = censored.

Thus, when there are intermediate observations istate is not simply a lagged version of the status, and may be more challenging to create. One approach is to let survcheck do the work: call it with an istate argument that is correct for the first row of each subject, or no istate argument at all, and then insert the returned value into ones data frame.

---

survcondense  **Shorten a (time1, time2) survival dataset**

Description

Counting process data sets can sometimes grow to be unwieldy, this can be used to compact one.

Usage

```r
survcondense(formula, data, subset, weights, na.action= na.pass, id, start = "tstart", end = "tstop", event = "event")
```
Arguments

- **formula**: a formula object, with the response on the left of a \(~\) operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function.
- **data**: a data.frame in which to interpret the variables named in the `formula` and the `id` argument argument.
- **subset**: optional subset expression to apply to the data set
- **weights**: optional variable name for case weights
- **na.action**: optional removal of missing values
- **id**: variable name that identifies subjects
- **start**: optional character string, giving the name of the start time variable in the result
- **end**: optional character string, giving the name of the stop time variable in the result
- **event**: optional character string, giving the name of the event variable in the result

Details

Through the use of the `survSplit` and `tmerge` functions, a counting process data set will gain more and more rows of data. Occasionally it is useful to collapse this surplus back down, e.g., when interest is to be focused on only a few covariates, or for debugging. The right hand side of `formula` will often have only a few variables, in this use.

If a row of data is censored, and represents the same covariates and identifier as the row below it, then the two rows can be merged together using a single (time1, time2) interval. The compression can sometimes be large.

The `start`, `stop` and `end` options are used when the left hand side of the formula has expressions that are not a simple name, e.g., `Surv(time1, time2, death | progression)` would be a case where `event` is used to set the outcome variable’s name.

Value

- a data frame

Author(s)

Terry Therneau

See Also

- `survSplit`, `tmerge`

Examples

```r
dim(aml)
test1 <- survSplit(Surv(time, status) \~ ., data=aml, 
                    cut=c(10, 20, 30), id="newid")
dim(test1)

# remove the added rows
test2 <- survcondense(Surv(tstart, time, status) \~ x, test1, id=newid)
dim(test2)
```
survdiff

Test Survival Curve Differences

Description

Tests if there is a difference between two or more survival curves using the \( G^\rho \) family of tests, or for a single curve against a known alternative.

Usage

survdiff(formula, data, subset, na.action, rho=0, timefix=TRUE)

Arguments

formula

a formula expression as for other survival models, of the form \( \text{Surv}(\text{time, status}) \sim \text{predictors} \). For a one-sample test, the predictors must consist of a single \text{offset}(sp) term, where sp is a vector giving the survival probability of each subject. For a k-sample test, each unique combination of predictors defines a subgroup. A \text{strata} term may be used to produce a stratified test. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the \text{strata} function with its \text{na.group}=T argument.

data

an optional data frame in which to interpret the variables occurring in the formula.

subset

expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.

na.action

a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is options()$na.action.

rho

a scalar parameter that controls the type of test.

timefix

process times through the \text{aeqSurv} function to eliminate potential roundoff issues.

Value

a list with components:

n

the number of subjects in each group.

obs

the weighted observed number of events in each group. If there are strata, this will be a matrix with one column per stratum.

exp

the weighted expected number of events in each group. If there are strata, this will be a matrix with one column per stratum.

chisq

the chisquare statistic for a test of equality.

var

the variance matrix of the test.

strata

optionally, the number of subjects contained in each stratum.

pvalue

the p-value corresponding to the Chisquare statistic.
Description

This function implements the G-rho family of Harrington and Fleming (1982), with weights on each death of \( S(t)^\rho \), where \( S(t) \) is the Kaplan-Meier estimate of survival. With \( \rho = 0 \) this is the log-rank or Mantel-Haenszel test, and with \( \rho = 1 \) it is equivalent to the Peto & Peto modification of the Gehan-Wilcoxon test.

Peto and Peto show that the Gehan-Wilcoxon test can be badly biased if the two groups have different censoring patterns, and proposed an alternative. Prentice and Marek later showed an actual example where this issue occurs. For most data sets the Gehan-Wilcoxon and Peto-Peto-Prentice variant will hardly differ, however.

If the right hand side of the formula consists only of an offset term, then a one sample test is done. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the \texttt{factor} function with its \texttt{exclude} argument to recode the right-hand-side covariate.

References


Examples

```r
## Two-sample test
survdiff(Surv(futime, fustat) ~ rx, data=ovarian)
## Stratified 7-sample test
survdiff(Surv(time, status) ~ pat.karno + strata(inst), data=lung)
## Expected survival for heart transplant patients based on
## US mortality tables
expect <- survexp(futime ~ 1, data=jasa, cohort=FALSE,
  rmap= list(age=(accept.dt - birth.dt), sex=1, year=accept.dt),
  ratetable=survexp.us)
## actual survival is much worse (no surprise)
survdiff(Surv(jasa$futime, jasa$fustat) ~ offset(expect))
# The free light chain data set is close to the population.
e2 <- survexp(futime ~ 1, data=flchain, cohort=FALSE,
  rmap= list(age= age*365.25, sex=sex,
  year=as.Date(paste0(sample.yr, "-07-01"))),
  ratetable= survexp.mn)
survdiff(Surv(futime, death) ~ offset(e2), flchain)
```

\textit{survexp} \hspace{1cm} \textit{Compute Expected Survival}
Description

Returns either the expected survival of a cohort of subjects, or the individual expected survival for each subject.

Usage

```
surexp(formula, data, weights, subset, na.action, rmap, times,  
    method=c("ederer", "hakulinen", "conditional", "individual.h",  
        "individual.s"),  
    cohort=TRUE, conditional=FALSE,  
    ratetable=survival::survexp.us, scale=1,  
    se.fit, model=FALSE, x=FALSE, y=FALSE)
```

Arguments

- **formula**: formula object. The response variable is a vector of follow-up times and is optional. The predictors consist of optional grouping variables separated by the `+` operator (as in `survfit`), and is often ~1, i.e., expected survival for the entire group.
- **data**: data frame in which to interpret the variables named in the formula, subset and weights arguments.
- **weights**: case weights. This is most useful when conditional survival for a known population is desired, e.g., the data set would contain all unique age/sex combinations and the weights would be the proportion of each.
- **subset**: expression indicating a subset of the rows of data to be used in the fit.
- **na.action**: function to filter missing data. This is applied to the model frame after subset has been applied. Default is `options()$na.action`.
- **rmap**: an optional list that maps data set names to the ratetable names. See the details section below.
- **times**: vector of follow-up times at which the resulting survival curve is evaluated. If absent, the result will be reported for each unique value of the vector of times supplied in the response value of the formula.
- **method**: computational method for the creating the survival curves. The individual option does not create a curve, rather it retrieves the predicted survival individual.s or cumulative hazard individual.h for each subject. The default is to use method='ederer' if the formula has no response, and method='hakulinen' otherwise.
- **cohort**: logical value. This argument has been superseded by the method argument. To maintain backwards compatibility, if is present and FALSE, it implies method='individual.s'.
- **conditional**: logical value. This argument has been superseded by the method argument. To maintain backwards compatibility, if it is present and TRUE it implies method='conditional'.
- **ratetable**: a table of event rates, such as `survexp.mn`, or a fitted Cox model. Note the `survival::` prefix in the default argument is present to avoid the (rare) case of a user who expects the default table but just happens to have an object named "survexp.us" in their own directory.
- **scale**: numeric value to scale the results. If `ratetable` is in units/day, `scale = 365.25` causes the output to be reported in years.
se.fit compute the standard error of the predicted survival. This argument is currently ignored. Standard errors are not a defined concept for population rate tables (they are treated as coming from a complete census), and for Cox models the calculation is hard. Despite good intentions standard errors for this latter case have not been coded and validated.

model,x,y flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.

Details

Individual expected survival is usually used in models or testing, to 'correct' for the age and sex composition of a group of subjects. For instance, assume that birth date, entry date into the study, sex and actual survival time are all known for a group of subjects. The survexp.us population tables contain expected death rates based on calendar year, sex and age. Then

```r
haz <- survexp(fu.time ~ 1, data=mydata,
               rmap = list(year=entry.dt, age=(birth.dt-entry.dt)),
               method='individual.h'))
```

gives for each subject the total hazard experienced up to their observed death time or last follow-up time (variable fu.time) This probability can be used as a rescaled time value in models:

```r
glm(status ~ 1 + offset(log(haz)), family=poisson)
glm(status ~ x + offset(log(haz)), family=poisson)
```

In the first model, a test for intercept=0 is the one sample log-rank test of whether the observed group of subjects has equivalent survival to the baseline population. The second model tests for an effect of variable x after adjustment for age and sex.

The ratetable being used may have different variable names than the user’s data set, this is dealt with by the rmap argument. The rate table for the above calculation was survexp.us, a call to summary(survexp.us) reveals that it expects to have variables age = age in days, sex, and year = the date of study entry, we create them in the rmap line. The sex variable was not mapped, therefore the function assumes that it exists in mydata in the correct format. (Note: for factors such as sex, the program will match on any unique abbreviation, ignoring case.)

Cohort survival is used to produce an overall survival curve. This is then added to the Kaplan-Meier plot of the study group for visual comparison between these subjects and the population at large. There are three common methods of computing cohort survival. In the “exact method” of Ederer the cohort is not censored, for this case no response variable is required in the formula. Hakulinen recommends censoring the cohort at the anticipated censoring time of each patient, and Verheul recommends censoring the cohort at the actual observation time of each patient. The last of these is the conditional method. These are obtained by using the respective time values as the follow-up time or response in the formula.

Value

if cohort=TRUE an object of class survexp, otherwise a vector of per-subject expected survival values. The former contains the number of subjects at risk and the expected survival for the cohort at each requested time. The cohort survival is the hypothetical survival for a cohort of subjects enrolled from the population at large, but matching the data set on the factors found in the rate table.
References


See Also

`survfit`, `pyears`, `survexp.us`, `ratetable`, `survexp.fit`.

Examples

```r
# Stanford heart transplant data
# We don't have sex in the data set, but know it to be nearly all males.
# Estimate of conditional survival
fit1 <- survexp(futime ~ 1, rmap=list(sex="male", year=accept.dt,
   age=(accept.dt-birth.dt)), method="conditional", data=jasa)
summary(fit1, times=1:10*182.5, scale=365) #expected survival by 1/2 years

# Estimate of expected survival stratified by prior surgery
survexp(~ surgery, rmap=list(sex="male", year=accept.dt,
   age=(accept.dt-birth.dt)), method="ederer", data=jasa,
   times=1:10 * 182.5)

## Compare the survival curves for the Mayo PBC data to Cox model fit
##
pfit <- coxph(Surv(time,status>0) ~ trt + log(bili) + log(protime) + age +
   platelet, data=pbc)
plot(survfit(Surv(time, status>0) ~ trt, data=pbc), mark.time=FALSE)
lines(survexp(~ trt, ratetable=pfit, data=pbc), col='purple')
```

survexp.fit  Compute Expected Survival

Description

Compute expected survival times.

Usage

```
survexp.fit(group, x, y, times, death, ratetable)
```
Arguments

- **group**: if there are multiple survival curves this identifies the group, otherwise it is a constant. Must be an integer.
- **x**: A matrix whose columns match the dimensions of the ratetable, in the correct order.
- **y**: the follow up time for each subject.
- **times**: the vector of times at which a result will be computed.
- **death**: a logical value, if TRUE the conditional survival is computed, if FALSE the cohort survival is computed. See survexp for more details.
- **ratetable**: a rate table, such as survexp.uswhite.

Details

For conditional survival y must be the time of last follow-up or death for each subject. For cohort survival it must be the potential censoring time for each subject, ignoring death.

For an exact estimate times should be a superset of y, so that each subject at risk is at risk for the entire sub-interval of time. For a large data set, however, this can use an inordinate amount of storage and/or compute time. If the times spacing is more coarse than this, an actuarial approximation is used which should, however, be extremely accurate as long as all of the returned values are > .99.

For a subgroup of size 1 and times > y, the conditional method reduces to exp(-h) where h is the expected cumulative hazard for the subject over his/her observation time. This is used to compute individual expected survival.

Value

A list containing the number of subjects and the expected survival(s) at each time point. If there are multiple groups, these will be matrices with one column per group.

Warning

Most users will call the higher level routine survexp. Consequently, this function has very few error checks on its input arguments.

See Also

- survexp, survexp.us.

---

**survexp.object**

**Expected Survival Curve Object**

Description

This class of objects is returned by the survexp class of functions to represent a fitted survival curve.

Objects of this class have methods for summary, and inherit the print, plot, points and lines methods from survfit.
Arguments

- **surv**: the estimate of survival at time \( t+0 \). This may be a vector or a matrix.
- **n.risk**: the number of subjects who contribute at this time.
- **time**: the time points at which the curve has a step.
- **std.err**: the standard error of the cumulative hazard or \(-\log(\text{survival})\).
- **strata**: if there are multiple curves, this component gives the number of elements of the \( \text{time} \) etc. vectors corresponding to the first curve, the second curve, and so on. The names of the elements are labels for the curves.
- **method**: the estimation method used. One of "Ederer", "Hakulinen", or "conditional".
- **na.action**: the returned value from the na.action function, if any. It will be used in the printout of the curve, e.g., the number of observations deleted due to missing values.
- **call**: an image of the call that produced the object.

Structure

The following components must be included in a legitimate `survfit` object.

Subscripts

Survexp objects that contain multiple survival curves can be subscripted. This is most often used to plot a subset of the curves.

Details

In expected survival each subject from the data set is matched to a hypothetical person from the parent population, matched on the characteristics of the parent population. The number at risk printed here is the number of those hypothetical subject who are still part of the calculation. In particular, for the Ederer method all hypotheticals are retained for all time, so **n.risk** will be a constant.

See Also

- `plot.survfit`
- `summary.survexp`
- `print.survfit`
- `survexp`.

```
 survfit Create survival curves

Description

This function creates survival curves from either a formula (e.g. the Kaplan-Meier), a previously fitted Cox model, or a previously fitted accelerated failure time model.

Usage

``survfit(formula, ...)```
survfit.coxph

Arguments

- `formula`: either a formula or a previously fitted model
- `...`: other arguments to the specific method

Details

A survival curve is based on a tabulation of the number at risk and number of events at each unique death time. When time is a floating point number the definition of "unique" is subject to interpretation. The code uses `factor()` to define the set. For further details see the documentation for the appropriate method, i.e., `?survfit.formula` or `?survfit.coxph`.

A survfit object may contain a single curve, a set of curves (vector), a matrix of curves, or even a 3 way array: `dim(fit)` will reveal the dimensions. Predicted curves from a coxph model have one row for each stratum in the Cox model fit and one column for each specified covariate set. Curves from a multi-state model have one row for each stratum and a column for each state, the strata correspond to predictors on the right hand side of the equation. The default printing and plotting order for curves is by column, as with other matrices.

Value

An object of class `survfit` containing one or more survival curves.

Note

Older releases of the code also allowed the specification for a single curve to omit the right hand of the formula, i.e., `survfit(Surv(time, status))`, in which case the formula argument is not actually a formula. Handling this case required some non-standard and fairly fragile manipulations, and this case is no longer supported.

Author(s)

Terry Therneau

See Also

- `survfit.formula`, `survfit.coxph`, `survfit.object`, `print.survfit`, `plot.survfit`, `quantile.survfit`, `residuals.survfit`, `summary.survfit`
## Usage

```r
default_usage <- function() {
  survfit(formula, newdata,
          se.fit=TRUE, conf.int=.95, individual=FALSE, stype=2, ctype,
          conf.type=c("log","log-log","plain","none","logit","arcsin"),
          censor=TRUE, start.time, id, influence=FALSE,
          na.action=na.pass, type, ...)}
default_usage()
}
default_usage()
```

## Arguments

- `formula`: A `coxph` object.
- `newdata`: A data frame with the same variable names as those that appear in the `coxph` formula. One curve is produced per row. The curve(s) produced will be representative of a cohort whose covariates correspond to the values in `newdata`.
- `se.fit`: A logical value indicating whether standard errors should be computed. Default is `TRUE` for standard models, `FALSE` for multi-state (code not yet present for that case).
- `conf.int`: The level for a two-sided confidence interval on the survival curve(s). Default is 0.95.
- `individual`: Deprecated argument, replaced by the general `id`.
- `stype`: Computation of the survival curve, 1=direct, 2=exponential of the cumulative hazard.
- `ctype`: Whether the cumulative hazard computation should have a correction for ties, 1=no, 2=yes.
- `conf.type`: One of "none", "plain", "log" (the default), "log-log" or "logit". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals `curve +/- k * se(curve)`, where k is determined from `conf.int`. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option uses the log hazard or log(-log(survival)), and the logit log(survival/(1-survival)).
- `censor`: If FALSE time points at which there are no events (only censoring) are not included in the result.
- `id`: Optional variable name of subject identifiers. If this is present, it will be search for in the `newdata` data frame. Each group of rows in `newdata` with the same subject `id` represents the covariate path through time of a single subject, and the result will contain one curve per subject. If the `coxph` fit had strata then that must also be specified in `newdata`. If `newid` is not present, then each individual row of `newdata` is presumed to represent a distinct subject.
- `start.time`: Optional starting time, a single numeric value. If present the returned curve contains survival after `start.time` conditional on surviving to `start.time`.
- `influence`: Option to return the influence values.
- `na.action`: The `na.action` to be used on the `newdata` argument.
type older argument that encompassed stype and ctype, now deprecated
p0 optional, a vector of probabilities. The returned curve will be for a cohort with
this mixture of starting states. Most often a single state is chosen
... for future methods

Details

This routine produces Pr(state) curves based on a coxph model fit. For single state models it produces the single curve for S(t) = Pr(remain in initial state at time t), known as the survival curve; for multi-state models a matrix giving probabilities for all states. The stype argument states the type of estimate, and defaults to the exponential of the cumulative hazard, better known as the Breslow estimate. For a multi-state Cox model this involves the exponential of a matrix. The argument stype=1 uses a non-exponential or ‘direct’ estimate. For a single endpoint coxph model the code evaluates the Kalbfleisch-Prentice estimate, and for a multi-state model it uses an analog of the Aalen-Johansen estimator. The latter approach is the default in the mstate package.

The ctype option affects the estimated cumulative hazard, and if stype=2 the estimated P(state) curves as well. If not present it is chosen so as to be concordant with the ties option in the coxph call. (For multistate coxphms objects only ctype=1 is currently implemented.) Likewise the choice between a model based and robust variance estimate for the curve will mirror the choice made in the coxph call, any clustering is also inherited from the parent model.

If the newdata argument is missing, then a curve is produced for a single “pseudo” subject with covariate values equal to the means component of the fit. The resulting curve(s) almost never make sense, but the default remains due to an unwarranted attachment to the option shown by some users and by other packages. Two particularly egregious examples are factor variables and interactions. Suppose one were studying interspecies transmission of a virus, and the data set has a factor variable with levels (“pig”, “chicken”) and about equal numbers of observations for each. The “mean” covariate level will be 0.5 – is this a flying pig? As to interactions assume data with sex coded as 0/1, ages ranging from 50 to 80, and a model with age*sex. The “mean” value for the age:sex interaction term will be about 30, a value that does not occur in the data. Users are strongly advised to use the newdata argument. For these reasons predictions from a multistate coxph model require the newdata argument.

If the coxph model contained an offset term, then the data set in the newdata argument should also contain that variable.

When the original model contains time-dependent covariates, then the path of that covariate through time needs to be specified in order to obtain a predicted curve. This requires newdata to contain multiple lines for each hypothetical subject which gives the covariate values, time interval, and strata for each line (a subject can change strata), along with an id variable which demarks which rows belong to each subject. The time interval must have the same (start, stop, status) variables as the original model: although the status variable is not used and thus can be set to a dummy value of 0 or 1, it is necessary for the response to be recognized as a Surv object. Last, although predictions with a time-dependent covariate path can be useful, it is very easy to create a prediction that is senseless. Users are encouraged to seek out a text that discusses the issue in detail.

When a model contains strata but no time-dependent covariates the user of this routine has a choice. If newdata argument does not contain strata variables then the returned object will be a matrix of survival curves with one row for each strata in the model and one column for each row in newdata. (This is the historical behavior of the routine.) If newdata does contain strata variables, then the result will contain one curve per row of newdata, based on the indicated stratum of the original model. In the rare case of a model with strata by covariate interactions the strata variable must be included in newdata, the routine does not allow it to be omitted (predictions become too confusing). (Note that the model Surv(time, status) ~ age*strata(sex) expands internally to strata(sex) + age:sex; the sex variable is needed for the second term of the model.)
See **survfit** for more details about the counts (number of events, number at risk, etc.)

**Value**

an object of class "survfit". See **survfit.object** for details. Methods defined for survfit objects are print, plot, lines, and points.

**Notes**

If the following pair of lines is used inside of another function then the `model=TRUE` argument must be added to the coxph call: `fit <- coxph(...); survfit(fit)`. This is a consequence of the non-standard evaluation process used by the `model.frame` function when a formula is involved.

Let $\log[S(t; z)]$ be the log of the survival curve for a fixed covariate vector $z$, then $\log[S(t; x)] = e^{(x-z)\beta} \log[S(t; z)]$ is the log of the curve for any new covariate vector $x$. There is an unfortunate tendency to refer to the reference curve with $z = 0$ as 'THE' baseline hazard. However, any $z$ can be used as the reference point, and more importantly, if $x - z$ is large the computation can suffer severe roundoff error. It is always safest to provide the desired $x$ values directly via newdata.

**References**


**See Also**

`print.survfit`, `plot.survfit`, `lines.survfit`, `coxph`, `Surv`, `strata`.

---

### survfit.formula

**Compute a Survival Curve for Censored Data**

**Description**

Computes an estimate of a survival curve for censored data using the Aalen-Johansen estimator. For ordinary (single event) survival this reduces to the Kaplan-Meier estimate.

**Usage**

```r
## S3 method for class 'formula'
survfit(formula, data, weights, subset, na.action, 
stype=1, ctype=1, id, cluster, robust, istance, timefix=TRUE, 
etype, model=FALSE, error, ...)
```
Arguments

formula a formula object, which must have a Surv object as the response on the left of the ~ operator and, if desired, terms separated by + operators on the right. One of the terms may be a strata object. For a single survival curve the right hand side should be ~ 1.

data a data frame in which to interpret the variables named in the formula, subset and weights arguments.

weights The weights must be nonnegative and it is strongly recommended that they be strictly positive, since zero weights are ambiguous, compared to use of the subset argument.

subset expression saying that only a subset of the rows of the data should be used in the fit.

na.action a missing-data filter function, applied to the model frame, after any subset argument has been used. Default is options()$na.action.

stype the method to be used estimation of the survival curve: 1 = direct, 2 = exp(cumulative hazard).

ctype the method to be used for estimation of the cumulative hazard: 1 = Nelson-Aalen formula, 2 = Fleming-Harrington correction for tied events.

id identifies individual subjects, when a given person can have multiple lines of data.

cluster used to group observations for the infinitesimal jackknife variance estimate, defaults to the value of id.

robust logical, should the function compute a robust variance. For multi-state survival curves this is true by default. For single state data see details, below.

istate for multi-state models, identifies the initial state of each subject or observation.

timefix process times through the aeqSurv function to eliminate potential roundoff issues.

etype a variable giving the type of event. This has been superseded by multi-state Surv objects and is deprecated; see example below.

model include a copy of the model frame in the output

error this argument is no longer used

... The following additional arguments are passed to internal functions called by survfit.

se.fit logical value, default is TRUE. If FALSE then standard error computations are omitted.

conf.type One of "none", "plain", "log" (the default), "log-log", "logit" or "arcsin". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals curve +- k *se(curve), where k is determined from conf.int. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), the logit option on log(survival/(1-survival)) and arcsin on arcsin(survival).

conf.lower a character string to specify modified lower limits to the curve, the upper limit remains unchanged. Possible values are "usual" (unmodified), "peto", and "modified". The modified lower limit is based on an "effective n" argument. The confidence bands will agree with the usual calculation at each death time, but unlike the usual bands the confidence interval
becomes wider at each censored observation. The extra width is obtained by multiplying the usual variance by a factor m/n, where n is the number currently at risk and m is the number at risk at the last death time. (The bands thus agree with the un-modified bands at each death time.) This is especially useful for survival curves with a long flat tail. The Peto lower limit is based on the same "effective n" argument as the modified limit, but also replaces the usual Greenwood variance term with a simple approximation. It is known to be conservative.

start.time numeric value specifying a time to start calculating survival information. The resulting curve is the survival conditional on surviving to start.time.

cnf.int the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.

se.fit a logical value indicating whether standard errors should be computed. Default is TRUE.

influence a logical value indicating whether to return the infinitesimal jackknife (influence) values for each subject. These contain the values of the derivative of each value with respect to the case weights of each subject i: ∂p/∂w_i, evaluated at the vector of weights. The resulting object will contain influence.surv and influence.chaz components. Alternatively, options of influence=1 or influence=2 will return values for only the survival or hazard curves, respectively.

p0 this applies only to multi-state curves. An optional vector giving the initial probability across the states. If this is missing, then p0 is estimated using the frequency of the starting states of all observations at risk at start.time, or if that is not specified, at the time of the first event.

type an older argument that combined stype and ctype, now deprecated. Legal values were "kaplan-meier" which is equivalent to stype=1, ctype=1, "fleming-harrington" which is equivalent to stype=2, ctype=1, and "fh2" which is equivalent to stype=2, ctype=2.

Details

If there is a data argument, then variables in the formula, weights, subset, id, cluster and istate arguments will be searched for in that data set.

The routine returns both an estimated probability in state and an estimated cumulative hazard estimate. The cumulative hazard estimate is the Nelson-Aalen (NA) estimate or the Fleming-Harrington (FH) estimate, the latter includes a correction for tied event times. The estimated probability in state can estimated either using the exponential of the cumulative hazard, or as a direct estimate using the Aalen-Johansen approach. For single state data the AJ estimate reduces to the Kaplan-Meier and the probability in state to the survival curve; for competing risks data the AJ reduces to the cumulative incidence (CI) estimator. For backward compatibility the type argument can be used instead.

When the data set includes left censored or interval censored data (or both), then the EM approach of Turnbull is used to compute the overall curve. Currently this algorithm is very slow, only a survival curve is produced, and it does not support a robust variance.

Robust variance: If a robust is TRUE, or for multi-state curves, then the standard errors of the results will be based on an infinitesimal jackknife (IJ) estimate, otherwise the standard model based estimate will be used. For single state curves, the default for robust will be TRUE if one of: there is a cluster argument, there are non-integer weights, or there is a id statement and at least one of the id values has multiple events, and FALSE otherwise. The default represents our best guess about
when one would most often desire a robust variance. When there are non-integer case weights and (time1, time2) survival data the routine is at an impasse: a robust variance likely is called for, but requires either id or cluster information to be done correctly; it will default to robust=FALSE.

One unanticipated side effect of defaulting to a robust variance when there are non integer case weights is that a fit using interval censored data, which iterates an underlying KM using an updated weight vector, now returns a robust variance by default. Based on Sun (2001) this may be preferred, as the naive estimate ignores the estimation of the weights. The prior behavior can be obtained with robust=FALSE.

With the IJ estimate, the leverage values themselves can be returned as arrays with dimensions: number of subjects, number of unique times, and for a multi-state model, the number of unique states. Be forewarned that these arrays can be huge. If there is a cluster argument this first dimension will be the number of clusters and the variance will be a grouped IJ estimate; this can be an important tool for reducing the size. A numeric value for the influence argument allows finer control: 0= return neither (same as FALSE), 1= return the influence array for probability in state, 2= return the influence array for the cumulative hazard, 3= return both (same as TRUE).

Value
an object of class "survfit". See survfit.object for details. Methods defined for survfit objects are print, plot, lines, and points.

References

See Also
survfit.coxph for survival curves from Cox models, survfit.object for a description of the components of a survfit object, print.survfit, plot.survfit, lines.survfit, coxph, Surv.

Examples
# fit a Kaplan-Meier and plot it
fit <- survfit(Surv(time, status) ~ x, data = aml)
plot(fit, lty = 2:3)
legend(100, .8, c("Maintained", "Nonmaintained"), lty = 2:3)
#fit a Cox proportional hazards model and plot the
#predicted survival for a 60 year old
fit <- coxph(Surv(futime, fustat) ~ age, data = ovarian)
plot(survfit(fit, newdata=data.frame(age=60)),
    xscale=365.25, xlab = "Years", ylab="Survival")

# Here is the data set from Turnbull
# There are no interval censored subjects, only left-censored (status=3),
# right-censored (status 0) and observed events (status 1)
#
# Time
# 1 2 3 4
# Type of observation
# death 12 6 2 3
# losses 3 2 0 3
# late entry 2 4 2 5
#
tdata <- data.frame(time =c(1,1,1,2,2,2,3,3,3,4,4,4),
    status=rep(c(1,0,2),4),
    n =c(12,3,2,6,2,4,2,0,2,3,3,5))
fit <- survfit(Surv(time, time, status, type='interval') ~1,
    data=tdata, weight=n)

# Three curves for patients with monoclonal gammopathy.
# 1. KM of time to PCM, ignoring death (statistically incorrect)
# 2. Competing risk curves (also known as "cumulative incidence")
# 3. Multi-state, showing Pr(in each state, at time t)
#
fitKM <- survfit(Surv(stop, event=="pcm") ~1, data=mgus1,
    subset=(start==0))
fitCR <- survfit(Surv(stop, event) ~1,
    data=mgus1, subset=(start==0))
fitMS <- survfit(Surv(start, stop, event) ~ 1, id=id, data=mgus1)

## Not run:
# CR curves show the competing risks
plot(fitCR, xscale=365.25, xmax=7300, mark.time=FALSE,
    col=2:3, xlab="Years post diagnosis of MGUS",
    ylab="P(state)")
lines(fitKM, fun="event", xmax=7300, mark.time=FALSE,
    conf.int=FALSE)
text(3652, .4, "Competing risk: death", col=3)
text(5840, .15,"Competing risk: progression", col=2)
text(5480, .30,"KM:prog")
## End(Not run)

### survfit.matrix

Create Aalen-Johansen estimates of multi-state survival from a matrix
of hazards.

Description

This allows one to create the Aalen-Johansen estimate of P, a matrix with one column per state and
one row per time, starting with the individual hazard estimates. Each row of P will sum to 1. Note
that this routine has been superseded by the use of multi-state Cox models, and will eventually be removed.

Usage

```r
## S3 method for class 'matrix'
survfit(formula, p0, method = c("discrete", "matexp"),
    start.time, ...)
```

Arguments

- `formula`: a matrix of lists, each element of which is either NULL or a survival curve object.
- `p0`: the initial state vector. The names of this vector are used as the names of the states in the output object. If there are multiple curves then `p0` can be a matrix with one row per curve.
- `method`: use a product of discrete hazards, or a product of matrix exponentials. See details below.
- `start.time`: optional; start the calculations at a given starting point
- `...`: further arguments used by other `survfit` methods

Details

On input the matrix should contain a set of predicted curves for each possible transition, and NULL in other positions. Each of the predictions will have been obtained from the relevant Cox model. This approach for multistate curves is easy to use but has some caveats. First, the input curves must be consistent. The routine checks as best it can, but can easy be fooled. For instance, if one were to fit two Cox models, obtain predictions for males and females from one, and for treatment A and B from the other, this routine will create two curves but they are not meaningful. A second issue is that standard errors are not produced.

The names of the resulting states are taken from the names of the vector of initial state probabilities. If they are missing, then the dimnames of the input matrix are used, and lacking that the labels '1', '2', etc. are used.

For the usual Aalen-Johansen estimator the multiplier at each event time is the matrix of hazards $H$ (also written as $I + dA$). When using predicted survival curves from a Cox model, however, it is possible to get predicted hazards that are greater than 1, which leads to probabilities less than 0. If the `method` argument is not supplied and the input curves are derived from a Cox model this routine instead uses the approximation $\expm(H-I)$ as the multiplier, which always gives valid probabilities. (This is also the standard approach for ordinary survival curves from a Cox model.)

Value

- a `survfitms` object

Note

The R syntax for creating a matrix of lists is very fussy.

Author(s)

- Terry Therneau
survfit.object

Survival Curve Object

Description

This class of objects is returned by the `survfit` class of functions to represent a fitted survival curve. For a multi-state model the object has class c('survfitms', 'survfit').

Objects of this class have methods for the functions print, summary, plot, points and lines. The `print.survfit` method does more computation than is typical for a print method and is documented on a separate page.

Arguments

- `n` total number of subjects in each curve.
- `time` the time points at which the curve has a step.
- `n.risk` the number of subjects at risk at t.
- `n.event` the number of events that occur at time t.
- `n.enter` for counting process data only, and only if there was an id argument, the number of subjects that enter the risk set during the current interval. If there are event/censoring times at 1, 3, 5 for instance, someone who enters at time 1 is counted in the (1, 3] interval, i.e., appears in the row for time 3.
- `n.censor` for counting process data only, the number of subjects who exit the risk set without an event, at time t. (For right censored data, this number can be computed from the successive values of the number at risk).
- `surv` the estimate of survival at time t+0. This may be a vector or a matrix. The latter occurs when a set of survival curves is created from a single Cox model, in which case there is one column for each covariate set.
**pstate**
a multi-state survival will have the pstate component instead of surv. It will be a matrix containing the estimated probability of each state at each time, one column per state.

**std.err**
for a survival curve this contains standard error of the cumulative hazard or -log(survival), for a multi-state curve it contains the standard error of prev. This difference is a reflection of the fact that each is the natural calculation for that case.

**cumhaz**
optional. Contains the cumulative hazard for each possible transition.

**strata**
if there are multiple curves, this component gives the number of elements of the time vector corresponding to the first curve, the second curve, and so on. The names of the elements are labels for the curves.

**upper**
optional upper confidence limit for the survival curve or pstate

**lower**
options lower confidence limit for the survival curve or pstate

**start.time**
optional, the starting time for the curve if other than 0

**p0, sp0**
for a multistate object, the distribution of starting states. If the curve has a strata dimension, this will be a matrix one row per stratum. The sp0 element has the standard error of p0, if p0 was estimated.

**newdata**
for survival curves from a fitted model, this contains the covariate values for the curves

**n.all**
the total number of observations that were available For counting process data, and any time that the start.time argument was used, not all may have been used in creating the curve, in which case this value will be larger than n above. The print and plot routines in the package do not use this value, it is for information only.

**conf.type**
the approximation used to compute the confidence limits.

**conf.int**
the level of the confidence limits, e.g. 90 or 95%.

**transitions**
for multi-state data, the total number of transitions of each type.

**na.action**
the returned value from the na.action function, if any. It will be used in the printout of the curve, e.g., the number of observations deleted due to missing values.

**call**
an image of the call that produced the object.

**type**
type of survival censoring.

**influence.p, influence.c**
optional influence matrices for the pstate (or surv) and for the cumhaz estimates. A list with one element per stratum, each element of the list is an array indexed by subject, time, state.

**version**
the version of the object. Will be missing, 2, or 3

**Structure**
The following components must be included in a legitimate survfit or survfits object.

**Subscripts**
Survfit objects can be subscripted. This is often used to plot a subset of the curves, for instance. From the user’s point of view the survfit object appears to be a vector, matrix, or array of curves. The first dimension is always the underlying number of curves or “strata”; for multi-state models the state is always the last dimension. Predicted curves from a Cox model can have a second dimension which is the number of different covariate prediction vectors.
Details

The `survfit` object has evolved over time: when first created there was no thought of multi-state models for instance. This evolution has almost entirely been accomplished by the addition of new elements. One change in survival version 3 is the addition of a `survfitconf` routine which will compute confidence intervals for a `survfit` object. This allows the computation of CI intervals to be deferred until later, if desired, rather than making them a permanent part of the object. Later iterations of the base routines may omit the confidence intervals.

The `survfit` object starts at the first observation time, but survival curves are normally plotted from time 0. A helper routine `survfit0` can be used to add this first time point and align the data.

See Also

`plot.survfit`, `summary.survfit`, `print.survfit`, `survfit`, `survfit0`

---

**survfit0**

Convert the format of a `survfit` object.

Description

Add the point for a starting time (time 0) to a survfit object’s elements. This is useful for plotting.

Usage

```r
survfit0(x, start.time=0)
```

Arguments

- `x`: a `survfit` object
- `start.time`: the desired starting time; see details below.

Details

Survival curves are traditionally plotted forward from time 0, but since the true starting time is not known as a part of the data, the `survfit` routine does not include a time 0 value in the resulting object. Someone might look at cumulative mortgage defaults versus calendar year, for instance, with the ‘time’ value a Date object. The plotted curve probably should not start at $0 = 1970/01/01$. Due to this uncertainty, it was decided not to include a "time 0" as part of a `survfit` object. If the original `survfit` call included a `start.time` argument, that value is of course retained.

Whether that (1989) decision was wise or foolish, it is now far too late to change it. (We tried it once as a trial, resulting in over 20 errors in the survival test suite. We extrapolate that it might break $1/2 - 2/3$ of the other CRAN packages that depend on survival, if made a default.) If the original `survfit` call included a `start.time` argument, that value is of course retained.

One problem with this choice is that some functions must choose a starting point, plots for example. This utility function is used by `plot.survfit` and `summary.survfit` to do so, adding a new time point at the front of each curve in a consistent way: the optional argument to the `survfit0` function as the first choice (if supplied), then the user's `start.time` if present, otherwise $\min(0, x$ timeframe). The resulting object is *not* guaranteed to work with functions that further manipulate a `survfit` object such as subscripting, aggregation, pseudovalues, etc. (remember the 20 errors). Rather it is intended as a penultimate step, most often when creating a plot.
Value

A reformulated version of the object with an initial data point at start.time added. The time, surv, pstate, cумhaz, std.err, std.cумhaz and other components will all be aligned, so as to make plots and summaries easier to produce.

Description

This program is mainly supplied to allow other packages to invoke the survfit.coxph function at a 'data' level rather than a 'user' level. It does no checks on the input data that is provided, which can lead to unexpected errors if that data is wrong.

Usage

survfitcoxph.fit(y, x, wt, x2, risk, newrisk, strata, se.fit, survtype, vartype, varmat, id, y2, strata2, unlist=TRUE)

Arguments

y the response variable used in the Cox model. (Missing values removed of course.)
x covariate matrix used in the Cox model
wt weight vector for the Cox model. If the model was unweighted use a vector of 1s.
x2 matrix describing the hypothetical subjects for which a curve is desired. Must have the same number of columns as x.
risk the risk score exp(X beta) from the fitted Cox model. If the model had an offset, include it in the argument to exp.
newrisk risk scores for the hypothetical subjects
strata strata variable used in the Cox model. This will be a factor.
se.fit if TRUE the standard errors of the curve(s) are returned
survtype 1=Kalbfleisch-Prentice, 2=Nelson-Aalen, 3=Efron. It is usual to match this to the approximation for ties used in the coxph model: KP for 'exact', N-A for 'breslow' and Efron for 'efron'.
vartype 1=Greenwood, 2=Aalen, 3=Efron
varmat the variance matrix of the coefficients
id optional; if present and not NULL this should be a vector of identifiers of length nrow(x2). A mon-null value signifies that x2 contains time dependent covariates, in which case this identifies which rows of x2 go with each subject.
y2 survival times, for time dependent prediction. It gives the time range [time1,time2] for each row of x2. Note: this must be a Surv object and thus contains a status indicator, which is never used in the routine, however.
strata2 vector of strata indicators for x2. This must be a factor.
unlist if FALSE the result will be a list with one element for each strata. Otherwise the strata are “unpacked” into the form found in a survfit object.
Value

A list containing nearly all the components of a `survfit` object. All that is missing is to add the confidence intervals, the type of the original model’s response (as in a coxph object), and the class.

Note

The source code for both this function and `survfit.coxph` is written using noweb. For complete documentation see the `inst/sourcecode.pdf` file.

Author(s)

Terry Therneau

See Also

`survfit.coxph`

---

### Deprecated functions in package `survival`

**Description**

These functions are temporarily retained for compatibility with older programs, and may transition to defunct status.

**Usage**

```r
survConcordance(formula, data, weights, subset, na.action)  # use concordance
survConcordance.fit(y, x, strata, weight)  # use concordancefit
```

**Arguments**

- `formula`: a formula object, with the response on the left of a `~` operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function.
- `data`: a data frame
- `weights, subset, na.action`: as for coxph
- `x, y, strata, weight`: predictor, response, strata, and weight vectors for the direct call

**See Also**

`Deprecated`
O’Brien’s Test for Association of a Single Variable with Survival

Description

Peter O’Brien’s test for association of a single variable with survival. This test is proposed in Biometrics, June 1978.

Usage

survobrien(formula, data, subset, na.action, transform)

Arguments

formula
a valid formula for a cox model.
data
a data frame which to interpret the variables named in the formula, or in the subset and the weights argument.
subset
expression indicating which subset of the rows of data should be used in the fit. All observations are included by default.
na.action
a missing-data filter function. This is applied to the model frame after any subset argument has been used. Default is options()$na.action.
transform
the transformation function to be applied at each time point. The default is O’Brien’s suggestion logit(tr) where tr = (rank(x) - 1/2)/length(x) is the rank shifted to the range 0-1 and logit(x) = log(x/(1-x)) is the logit transform.

Value

a new data frame. The response variables will be column names returned by the Surv function, i.e., "time" and "status" for simple survival data, or "start", "stop", "status" for counting process data. Each individual event time is identified by the value of the variable .strata.. Other variables retain their original names. If a predictor variable is a factor or is protected with I(), it is retained as is. Other predictor variables have been replaced with time-dependent logit scores.

The new data frame will have many more rows that the original data, approximately the original number of rows * number of deaths/2.

Method

A time-dependent cox model can now be fit to the new data. The univariate statistic, as originally proposed, is equivalent to single variable score tests from the time-dependent model. This equivalence is the rationale for using the time dependent model as a multivariate extension of the original paper.

In O’Brien’s method, the x variables are re-ranked at each death time. A simpler method, proposed by Prentice, ranks the data only once at the start. The results are usually similar.

Note

A prior version of the routine returned new time variables rather than a strata. Unfortunately, that strategy does not work if the original formula has a strata statement. This new data set will be the same size, but the coxph routine will process it slightly faster.
References


See Also

survdiff

Examples

```r
xx <- survobrien(Surv(futime, fustat) ~ age + factor(rx) + I(ecog.ps),
                 data=ovarian)
coxph(Surv(time, status) ~ age + strata(.strata.), data=xx)
```
init  optional vector of initial values for the parameters.
scale  optional fixed value for the scale. If set to <=0 then the scale is estimated.
control  a list of control values, in the format produced by survreg.control. The default value is survreg.control()
model,x,y  flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.
score  return the score vector. (This is expected to be zero upon successful convergence.)
robust  Use robust sandwich error instead of the asymptotic formula. Defaults to TRUE if there is a cluster argument.
cluster  Optional variable that identifies groups of subjects, used in computing the robust variance. Like model variables, this is searched for in the dataset pointed to by the data argument.
...  other arguments which will be passed to survreg.control.

Details

All the distributions are cast into a location-scale framework, based on chapter 2.2 of Kalbfleisch and Prentice. The resulting parameterization of the distributions is sometimes (e.g. gaussian) identical to the usual form found in statistics textbooks, but other times (e.g. Weibull) it is not. See the book for detailed formulas.

When using weights be aware of the difference between replication weights and sampling weights. In the former, a weight of ’2’ means that there are two identical observations, which have been combined into a single row of data. With sampling weights there is a single observed value, with a weight used to achieve balance with respect to some population. To get proper variance with replication weights use the default variance, for sampling weights use the robust variance. Replication weights were once common (when computer memory was much smaller) but are now rare.

Value

an object of class survreg is returned.

References


See Also

survreg.object, survreg.distributions, pspline, frailty, ridge

Examples

# Fit an exponential model: the two fits are the same
survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='weibull',
       scale=1)
survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian,
       dist="exponential")

# # A model with different baseline survival shapes for two groups, i.e.,
# two different scale parameters
survreg(Surv(time, status) ~ ph.ecog + age + strata(sex), lung)

# There are multiple ways to parameterize a Weibull distribution. The survreg
# function embeds it in a general location-scale family, which is a
# different parameterization than the rweibull function, and often leads
# to confusion.
# survreg's scale = 1/(rweibull shape)
# survreg's intercept = log(rweibull scale)
# For the log-likelihood all parameterizations lead to the same value.
y <- rweibull(1000, shape=2, scale=5)
survreg(Surv(y)~1, dist="weibull")

# Economists fit a model called 'tobit regression', which is a standard
# linear regression with Gaussian errors, and left censored data.
tobinfit <- survreg(Surv(durable, durable>0, type='left') ~ age + quant,
data=tobin, dist='gaussian')

survreg.control

Package options for survreg and coxph

Description

This function checks and packages the fitting options for survreg

Usage

survreg.control(maxiter=30, rel.tolerance=1e-09,
toler.chol=1e-10, iter.max, debug=0, outer.max=10)

Arguments

maxiter maximum number of iterations
rel.tolerance relative tolerance to declare convergence
toler.chol Tolerance to declare Cholesky decomposition singular
iter.max same as maxiter
d debug print debugging information
outer.max maximum number of outer iterations for choosing penalty parameters

Value

A list with the same elements as the input

See Also

survreg
survreg.distributions  Parametric Survival Distributions

Description

List of distributions for accelerated failure models. These are location-scale families for some transformation of time. The entry describes the cdf $F$ and density $f$ of a canonical member of the family.

Usage

survreg.distributions

Format

There are two basic formats, the first defines a distribution de novo, the second defines a new distribution in terms of an old one.

name: name of distribution
variance: function(parms) returning the variance (currently unused)
init(x,weights,...): Function returning an initial estimate of the mean and variance (used for initial values in the iteration)
density(x,parms): Function returning a matrix with columns $F$, $1-F$, $f'$/$f$, and $f''/f$
quantile(p,parms): Quantile function
scale: Optional fixed value for the scale parameter
parms: Vector of default values and names for any additional parameters
deviance(y,scale,parms): Function returning the deviance for a saturated model; used only for deviance residuals.

and to define one distribution in terms of another

name: name of distribution
dist: name of parent distribution
trans: transformation (eg log)
dtrans: derivative of transformation
itrans: inverse of transformation
scale: Optional fixed value for scale parameter

Details

There are four basic distributions: extreme, gaussian, logistic and t. The last three are parametrised in the same way as the distributions already present in R. The extreme value cdf is

$$F = 1 - e^{-e^t}.$$  

When the logarithm of survival time has one of the first three distributions we obtain respectively weibull, lognormal, and loglogistic. The location-scale parameterization of a Weibull distribution found in survreg is not the same as the parameterization of rweibull.
The other predefined distributions are defined in terms of these. The exponential and rayleigh
distributions are Weibull distributions with fixed scale of 1 and 0.5 respectively, and loggaussian
is a synonym for lognormal.

For speed parts of the three most commonly used distributions are hardcoded in C: for this reason the
elements of survreg.distributions with names of "Extreme value", "Logistic" and "Gaussian"
should not be modified. (The order of these in the list is not important, recognition is by name.)
As an alternative to modifying survreg.distributions a new distribution can be specified as a
separate list. This is the preferred method of addition and is illustrated below.

See Also

survreg, pweibull, pnorm, plogis, pt, survregDtest

Examples

# time transformation
survreg(Surv(time, status) ~ ph.ecog + sex, dist='weibull', data=lung)
# change the transformation to work in years
# intercept changes by log(365), everything else stays the same
my.weibull <- survreg.distributions$weibull
my.weibull$trans <- function(y) log(y/365)
my.weibull$itrans <- function(y) 365*exp(y)
survreg(Surv(time, status) ~ ph.ecog + sex, lung, dist=my.weibull)

# Weibull parametrisation
y<-rweibull(1000, shape=2, scale=5)
survreg(Surv(y)~1, dist="weibull")
# survreg scale parameter maps to 1/shape, linear predictor to log(scale)
# Cauchy fit
mycauchy <- list(name='Cauchy',
  init= function(x, weights, ...)
    c(median(x), mad(x)),
  density= function(x, parms) {
    temp <- 1/(1 + x^2)
    cbind(.5 + atan(x)/pi, .5+ atan(-x)/pi,
    temp/pi, -2 *x*temp, 2*temp*(4*x^2*temp -1))
  },
  quantile= function(p, parms) tan((p-.5)*pi),
  deviance= function(...) stop('deviance residuals not defined')
)
survreg(Surv(log(time), status) ~ ph.ecog + sex, lung, dist=mycauchy)
COMPONENTS

The following components must be included in a legitimate `survreg` object.

- **coefficients**: the coefficients of the `linear.predictors`, which multiply the columns of the model matrix. It does not include the estimate of error (sigma). The names of the coefficients are the names of the single-degree-of-freedom effects (the columns of the model matrix). If the model is over-determined there will be missing values in the coefficients corresponding to non-estimable coefficients.

- **icoef**: coefficients of the baseline model, which will contain the intercept and log(scale), or multiple scale factors for a stratified model.

- **var**: the variance-covariance matrix for the parameters, including the log(scale) parameter(s).

- **loglik**: a vector of length 2, containing the log-likelihood for the baseline and full models.

- **iter**: the number of iterations required

- **linear.predictors**: the linear predictor for each subject.

- **df**: the degrees of freedom for the final model. For a penalized model this will be a vector with one element per term.

- **scale**: the scale factor(s), with length equal to the number of strata.

- **idf**: degrees of freedom for the initial model.

- **means**: a vector of the column means of the coefficient matrix.

- **dist**: the distribution used in the fit.

- **weights**: included for a weighted fit.

The object will also have the following components found in other model results (some are optional): `linear.predictors, weights, x, y, model, call, terms` and `formula`. See `lm`.

See Also

- `survreg`, `lm`
Details

If the `survreg` function rejects your user-supplied distribution as invalid, this routine will tell you why it did so.

Value

TRUE if the distribution object passes the tests, and either FALSE or a vector of character strings if not.

Author(s)

Terry Therneau

See Also

`survreg.distributions`, `survreg`

Examples

```r
# An invalid distribution (it should have "init =" on line 2)
# survreg would give an error message
mycauchy <- list(name='Cauchy',
                 init=function(x, weights, ...)
                   c(median(x), mad(x)),
                 density=function(x, parms) {
                   temp <- 1/(1 + x^2)
                   cbind(.5 + atan(temp)/pi, .5+ atan(-temp)/pi,
                         temp/pi, -2 *x*temp, 2*temp^2*(4*x^2*temp -1))
                   },
                 quantile=function(p, parms) tan((p-.5)*pi),
                 deviance=function(...) stop('deviance residuals not defined'))

survregDtest(mycauchy, TRUE)
```

**survSplit**

*Split a survival data set at specified times*

Description

Given a survival data set and a set of specified cut times, split each record into multiple subrecords at each cut time. The new data set will be in ‘counting process’ format, with a start time, stop time, and event status for each record.

Usage

```r
survSplit(formula, data, subset, na.action=na.pass,
          cut, start="tstart", id, zero=0, episode,
          end="tstop", event="event")
```
Arguments

- **formula**: a model formula
- **data**: a data frame
- **subset, na.action**: rows of the data to be retained
- **cut**: the vector of timepoints to cut at
- **start**: character string with the name of a start time variable (will be created if needed)
- **id**: character string with the name of new id variable to create (optional). This can be useful if the data set does not already contain an identifier.
- **zero**: If `start` doesn’t already exist, this is the time that the original records start.
- **episode**: character string with the name of new episode variable (optional)
- **end**: character string with the name of event time variable
- **event**: character string with the name of censoring indicator

Details

Each interval in the original data is cut at the given points; if an original row were (15, 60] with a cut vector of (10,30, 40) the resulting data set would have intervals of (15,30], (30,40] and (40, 60]. Each row in the final data set will lie completely within one of the cut intervals. Which interval for each row of the output is shown by the `episode` variable, where 1= less than the first cutpoint, 2= between the first and the second, etc. For the example above the values would be 2, 3, and 4.

The routine is called with a formula as the first argument. The right hand side of the formula can be used to delimit variables that should be retained; normally one will use ~ . as a shorthand to retain them all. The routine will try to retain variable names, e.g. `Surv(adam, joe, fred)~.` will result in a data set with those same variable names for `tstart`, `end`, and `event` options rather than the defaults. Any user specified values for these options will be used if they are present, of course. However, the routine is not sophisticated; it only does this substitution for simple names. A call of `Surv(time, stat==2)` for instance will not retain "stat" as the name of the event variable.

Rows of data with a missing time or status are copied across unchanged, unless the `na.action` argument is changed from its default value of `na.pass`. But in the latter case any row that is missing for any variable will be removed, which is rarely what is desired.

Value

New, longer, data frame.

See Also

- `Surv`, `cut`, `reshape`

Examples

```r
fit1 <- coxph(Surv(time, status) ~ karno + age + trt, veteran)
plot(cox.zph(fit1)[1])
# a cox.zph plot of the data suggests that the effect of Karnofsky score
# begins to diminish by 60 days and has faded away by 120 days.
# Fit a model with separate coefficients for the three intervals.
# vet2 <- survSplit(Surv(time, status) ~., veteran,
# cut=c(60, 120), episode ="timegroup")
```
fit2 <- coxph(Surv(tstart, time, status) ~ karno* strata(timegroup) +
   age + trt, data= vet2)
c(overall= coef(fit1)[1],
   t0_60 = coef(fit2)[1],
   t60_120= sum(coef(fit2)[c(1,4)]),
   t120 = sum(coef(fit2)[c(1,5)]))

---

tcut

Factors for person-year calculations

Description

Attaches categories for person-year calculations to a variable without losing the underlying continuous representation.

Usage

tcut(x, breaks, labels, scale=1)
## S3 method for class 'tcut'
levels(x)

Arguments

- **x**: numeric/date variable
- **breaks**: breaks between categories, which are right-continuous
- **labels**: labels for categories
- **scale**: Multiply x and breaks by this.

Value

An object of class tcut

See Also

cut, pyears

Examples

# For pyears, all time variable need to be on the same scale; but
# futime is in months and age is in years
test <- mgus2
test$years <- test$futime/30.5  # follow-up in years

# first grouping based on years from starting age (= current age)
# second based on years since enrollment (all start at 0)
test$agegrp <- tcut(test$age, c(0,60, 70, 80, 100),
   c("<=60", "60-70", "70-80", ">80")
test$fgrp <- tcut(rep(0, nrow(test)), c(0, 1, 5, 10, 100),
   c("0-1yr", "1-5yr", "5-10yr", ">10yr")

# death rates per 1000, by age group
pfit1 <- pyears(Surv(years, death) ~ agegrp, scale =1000, data=test)
round(pfit1$event/ pfit1$pyears)
#death rates per 100, by follow-up year and age
# there are excess deaths in the first year, within each age stratum
pfit2 <- pyears(Surv(years, death) ~ fgrp + agegrp, scale =1000, data=test)
round(pfit2$event/ pfit2$pyears)

---

**tmerge**

*Time based merge for survival data*

**Description**

A common task in survival analysis is the creation of start,stop data sets which have multiple intervals for each subject, along with the covariate values that apply over that interval. This function aids in the creation of such data sets.

**Usage**

```
tmerge(data1, data2, id,..., tstart, tstop, options)
```

**Arguments**

- `data1`: the primary data set, to which new variables and/or observation will be added
- `data2`: second data set in which all the other arguments will be found
- `id`: subject identifier
- `...`: operations that add new variables or intervals, see below
- `tstart`: optional variable to define the valid time range for each subject, only used on an initial call
- `tstop`: optional variable to define the valid time range for each subject, only used on an initial call
- `options`: a list of options. Valid ones are idname, tstartname, tstopname, delay, na.rm, and tdcstart. See the explanation below.

**Details**

The program is often run in multiple passes, the first of which defines the basic structure, and subsequent ones that add new variables to that structure. For a more complete explanation of how this routine works refer to the vignette on time-dependent variables.

There are 4 types of operational arguments: a time dependent covariate (tdc), cumulative count (cumtdc), event (event) or cumulative event (cumevent). Time dependent covariates change their values before an event, events are outcomes.

- A new time dependent covariate variable will created. The argument `y` is assumed to be on the scale of the start and end time, and each instance describes the occurrence of a “condition” at that time. The second argument `x` is optional. In the case where `x` is missing the count variable starts at 0 for each subject and becomes 1 at the time of the event. If `x` is present the value of the time dependent covariate is initialized to value of `init`, if present, or the `tdcstart` option otherwise, and is updated to the value of `x` at each observation.
  - If the option `na.rm=TRUE` missing values of `x` are first removed, i.e., the update will not create missing values.
newname = cmumtdc(y, x, init) Similar to tdc, except that the event count is accumulated over time for each subject. The variable x must be numeric.
newname = event(y, x) Mark an event at time y. In the usual case that x is missing the new 0/1 variable will be similar to the 0/1 status variable of a survival time.
newname = cumevent(y, x) Cumulative events.

The function adds three new variables to the output data set: tstart, tstop, and id. The options argument can be used to change these names. If, in the first call, the id argument is a simple name, that variable name will be used as the default for the idname option. If data1 contains the tstart variable then that is used as the starting point for the created time intervals, otherwise the initial interval for each id will begin at 0 by default. This will lead to an invalid interval and subsequent error if say a death time were \( <= 0 \).

The na.rm option affects creation of time-dependent covariates. Should a data row in data2 that has a missing value for the variable be ignored or should it generate an observation with a value of NA? The default of TRUE causes the last non-missing value to be carried forward. The delay option causes a time-dependent covariate’s new value to be delayed, see the vignette for an example.

Value

a data frame with two extra attributes tm.retain and tcount. The first contains the names of the key variables, and which names correspond to tdc or event variables. The tcount variable contains counts of the match types. New time values that occur before the first interval for a subject are "early", those after the last interval for a subject are "late", and those that fall into a gap are of type "gap". All these are are considered to be outside the specified time frame for the given subject. An event of this type will be discarded. An observation in data2 whose identifier matches no rows in data1 is of type "missid" and is also discarded. A time-dependent covariate value will be applied to later intervals but will not generate a new time point in the output.

The most common type will usually be "within", corresponding to those new times that fall inside an existing interval and cause it to be split into two. Observations that fall exactly on the edge of an interval but within the (min, max] time for a subject are counted as being on a "leading" edge, "trailing" edge or "boundary". The first corresponds for instance to an occurrence at 17 for someone with an intervals of (0,15] and (17, 35]. A tdc at time 17 will affect this interval but an event at 17 would be ignored. An event occurrence at 15 would count in the (0,15] interval. The last case is where the main data set has touching intervals for a subject, e.g. (17, 28] and (28,35] and a new occurrence lands at the join. Events will go to the earlier interval and counts to the latter one. A last column shows the number of additions where the id and time point were identical. When this occurs, the tdc and event operators will use the final value in the data (last edit wins), but ignoring missing, while cmumtdc and cmumevent operators add up the values.

These extra attributes are ephemeral and will be discarded if the dataframe is modified. This is intentional, since they will become invalid if for instance a subset were selected.

Author(s)

Terry Therneau

See Also

neardate

Examples

# The pbc data set contains baseline data and follow-up status
# for a set of subjects with primary biliary cirrhosis, while the
# pbcseq data set contains repeated laboratory values for those
# subjects.
# The first data set contains data on 312 subjects in a clinical trial plus
# 106 that agreed to be followed off protocol, the second data set has data
# only on the trial subjects.

temp <- subset(pbc, id <= 312, select=c(id:sex, stage)) # baseline data
pbc2 <- tmerge(temp, temp, id=id, endpt = event(time, status))
pbc2 <- tmerge(pbc2, pbcseq, id=id, ascites = tdc(day, ascites),
               bili = tdc(day, bili), albumin = tdc(day, albumin),
               protime = tdc(day, protime), alk.phos = tdc(day, alk.phos))

fit <- coxph(Surv(tstart, tstop, endpt==2) ~ protime + log(bili), data=pbc2)

---

tobin | Tobin’s Tobit data

**Description**

Economists fit a parametric censored data model called the ‘tobit’. These data are from Tobin’s original paper.

**Usage**

tobin
data(tobin, package="survival")

**Format**

A data frame with 20 observations on the following 3 variables.

- **durable**: Durable goods purchase
- **age**: Age in years
- **quant**: Liquidity ratio (x 1000)

**Source**


**Examples**

tfit <- survreg(Surv(durable, durable>0, type='left') ~ age + quant,
data=tobin, dist='gaussian')
predict(tfit,type="response")
Liver transplant waiting list

Description

Subjects on a liver transplant waiting list from 1990-1999, and their disposition: received a transplant, died while waiting, withdrew from the list, or censored.

Usage

transplant
data(transplant, package="survival")

Format

A data frame with 815 (transplant) observations on the following 6 variables.

- age: age at addition to the waiting list
- sex: m or f
- abo: blood type: A, B, AB or O
- year: year in which they entered the waiting list
- futime: time from entry to final disposition
- event: final disposition: censored, death, ltx or withdraw

Details

This represents the transplant experience in a particular region, over a time period in which liver transplant became much more widely recognized as a viable treatment modality. The number of liver transplants rises over the period, but the number of subjects added to the liver transplant waiting list grew much faster. Important questions addressed by the data are the change in waiting time, who waits, and whether there was a consequent increase in deaths while on the list.

Blood type is an important consideration. Donor livers from subjects with blood type O can be used by patients with A, B, AB or 0 blood types, whereas an AB liver can only be used by an AB recipient. Thus type O subjects on the waiting list are at a disadvantage, since the pool of competitors is larger for type O donor livers.

This data is of historical interest and provides a useful example of competing risks, but it has little relevance to current practice. Liver allocation policies have evolved and now depend directly on each individual patient’s risk and need, assessments of which are regularly updated while a patient is on the waiting list. The overall organ shortage remains acute, however.

The transplant data set was a version used early in the analysis, transplant2 has several additions and corrections, and was the final data set and matches the paper.

References

Examples

#since event is a factor, survfit creates competing risk curves
pfit <- survfit(Surv(futime, event) ~ abo, transplant)
pfit[,2] #time to liver transplant, by blood type
plot(pfit[,2], mark.time=FALSE, col=1:4, lwd=2, xmax=735,
    xscale=30.5, xlab="Months", ylab="Fraction transplanted",
    xaxt = 'n')
temp <- c(0, 6, 12, 18, 24)
axis(1, temp*30.5, temp)
legend(450, .35, levels(transplant$abo), lty=1, col=1:4, lwd=2)

# competing risks for type O
plot(pfit[4,], xscale=30.5, xmax=735, col=1:3, lwd=2)
legend(450, .4, c("Death", "Transplant", "Withdrawal"), col=1:3, lwd=2)

udca

Data from a trial of ursoodeoxycholic acid

Description

Data from a trial of ursodeoxycholic acid (UDCA) in patients with primary biliary cirrhosis (PBC).

Usage

udca
udca2
data(udca, package="survival")

Format

A data frame with 170 observations on the following 15 variables.

id  subject identifier
trt  treatment of 0=placebo, 1=UDCA
entry.dt  date of entry into the study
last.dt  date of last on-study visit
stage  stage of disease
bili  bilirubin value at entry
riskscore  the Mayo PBC risk score at entry
death.dt  date of death
tax.dt  date of liver transplant
hprogress.dt  date of histologic progression
varices.dt  appearance of esophageal varices
ascites.dt  appearance of ascites
enceph.dt  appearance of encephalopathy
double.dt  doubling of initial bilirubin
worsen.dt  worsening of symptoms by two stages
Details

This data set is used in the Therneau and Grambsch. The udca1 data set contains the baseline variables along with the time until the first endpoint (any of death, transplant, . . . , worsening). The udca2 data set treats all of the endpoints as parallel events and has a stratum for each.

References


Examples

# values found in table 8.3 of the book
fit1 <- coxph(Surv(futime, status) ~ trt + log(bili) + stage, 
               cluster = id, data=udca1)
fit2 <- coxph(Surv(futime, status) ~ trt + log(bili) + stage + 
               strata(endpoint), cluster=id, data=udca2)

untangle.specials

Help Process the ‘specials’ Argument of the ‘terms’ Function.

Description

Given a terms structure and a desired special name, this returns an index appropriate for subscripting the terms structure and another appropriate for the data frame.

Usage

untangle.specials(tt, special, order=1)

Arguments

- **tt**
  - a terms object.

- **special**
  - the name of a special function, presumably used in the terms object.

- **order**
  - the order of the desired terms. If set to 2, interactions with the special function will be included.

Value

- a list with two components:
  - **vars**
    - a vector of variable names, as would be found in the data frame, of the specials.
  - **terms**
    - a numeric vector, suitable for subscripting the terms structure, that indexes the terms in the expanded model formula which involve the special.
Examples

```r
formula <- Surv(tt, ss) ~ x + z*strata(id)
tms <- terms(formula, specials="strata")
## the specials attribute
attr(tms, "specials")
## main effects
untangle.specials(tms, "strata")
## and interactions
untangle.specials(tms, "strata", order=1:2)
```

uspop2

Projected US Population

Description

US population by age and sex, for 2000 through 2020

Format

The data is a matrix with dimensions age, sex, and calendar year. Age goes from 0 through 100, where the value for age 100 is the total for all ages of 100 or greater.

Details

This data is often used as a "standardized" population for epidemiology studies.

Source


See Also

uspop

Examples

```r
us50 <- uspop2[51:101,, "2000"] # US 2000 population, 50 and over
age <- as.integer(dimnames(us50)[[1]])
smat <- model.matrix(~ factor(floor(age/5)) -1)
ustot <- t(smat) %*% us50 # totals by 5 year age groups
temp <- c(50, 55, 60, 65, 70, 75, 80, 85, 90, 95)
dimnames(ustot) <- list(c(paste(temp, temp+4, sep="-")), c("male", "female"))
```
vcov.coxph     Variance-covariance matrix

Description

Extract and return the variance-covariance matrix.

Usage

## S3 method for class 'coxph'
vcov(object, complete=TRUE, ...)
## S3 method for class 'survreg'
vcov(object, complete=TRUE, ...)

Arguments

object         a fitted model object
complete       logical indicating if the full variance-covariance matrix should be returned.
               This has an effect only for an over-determined fit where some of the coeffi-
               cients are undefined, and coef(object) contains corresponding NA values. If
               complete=TRUE the returned matrix will have row/column for each coefficient,
               if FALSE it will contain rows/columns corresponding to the non-missing coeffi-
               cients. The coef() function has a similar complete argument.
...
      additional arguments for method functions

Details

For the coxph and survreg functions the returned matrix is a particular generalized inverse: the
row and column corresponding to any NA coefficients will be zero. This is a side effect of the
generalized cholesky decomposition used in the underlying computation.

Value

a matrix

veteran     Veterans' Administration Lung Cancer study

Description

Randomised trial of two treatment regimens for lung cancer. This is a standard survival analysis
data set.

Usage

data(cancer, package="survival")
### Format

- **trt:** 1=standard, 2=test
- **celltype:** 1=squamous, 2=smallcell, 3=adenocarcinoma, 4=large
- **time:** survival time
- **status:** censoring status
- **karno:** Karnofsky performance score (100=good)
- **diagtime:** months from diagnosis to randomisation
- **age:** in years
- **prior:** prior therapy 0=no, 10=yes

### Source


### Description

Sort survival objects into a partial order, which is the same one used internally for many of the calculations.

### Usage

```r
## S3 method for class 'Surv'
xtfrm(x)
```

### Arguments

- **x**  
  a `Surv` object

### Details

This creates a partial ordering of survival objects. The result is sorted in time order, for tied pairs of times right censored events come after observed events (censor after death), and left censored events are sorted before observed events. For counting process data `(tstart, tstop, status)` the ordering is by stop time, status, and start time, again with censoring last. Interval censored data is sorted using the midpoint of each interval.

The `xtfrm` routine is used internally by `order` and `sort`, so these results carry over to those routines.

### Value

A vector of integers which will have the same sort order as `x`.

### Author(s)

Terry Therneau
yates

Population prediction

Description

Compute population marginal means (PMM) from a model fit, for a chosen population and statistic.

Usage

yates(fit, term, population = c("data", "factorial", "sas"),
levels, test = c("global", "trend", "pairwise"), predict = "linear",
options, nsim = 200, method = c("direct", "sgtt"))

Arguments

fit        a model fit. Examples using lm, glm, and coxph objects are given in the vignette.
term      the term from the model which is to be evaluated. This can be written as a character string or as a formula.
population the population to be used for the adjusting variables. User can supply their own data frame or select one of the built in choices. The argument also allows "empirical" and "yates" as aliases for data and factorial, respectively, and ignores case.
levels optional, what values for term should be used.
test the test for comparing the population predictions.
predict what to predict. For a glm model this might be the 'link' or 'response'. For a coxph model it can be linear, risk, or survival. User written functions are allowed.
options optional arguments for the prediction method.
nsim number of simulations used to compute a variance for the predictions. This is not needed for the linear predictor.
method the computational approach for testing equality of the population predictions. Either the direct approach or the algorithm used by the SAS glm procedure for "type 3" tests.

Details

The many options and details of this function are best described in a vignette on population prediction.

See Also

sort, order

Examples

test <- c(Surv(c(10, 9, 9, 8, 8, 7, 5, 5, 4), rep(1:0, 5)), Surv(6.2, NA))
test
sort(test)
Value

an object of class yates with components of
- `estimate` a data frame with one row for each level of the term, and columns containing the level, the mean population predicted value (mppv) and its standard deviation.
- `tests` a matrix giving the test statistics
- `mvar` the full variance-covariance matrix of the mppv values
- `summary` optional: any further summary if the values provided by the prediction method.

Author(s)

Terry Therneau

Examples

```r
fit1 <- lm(skips ~ Solder*Opening + Mask, data = solder)
yates(fit1, ~Opening, population = "factorial")
```

```r
fit2 <- coxph(Surv(time, status) ~ factor(ph.ecog)*sex + age, lung)
yates(fit2, ~ ph.ecog, predict="risk") # hazard ratio
```

---

Method for adding new models to the yates function.

Description

This is a method which is called by the yates function, in order to setup the code to handle a particular model type. Methods for glm, coxph, and default are part of the survival package.

Usage

```r
yates_setup(fit, ...)
```

Arguments

- `fit` a fitted model object
- `...` optional arguments for some methods

Details

If the predicted value should be the linear predictor, the function should return NULL. The yates routine has particularly efficient code for this case. Otherwise it should return a prediction function or a list of two elements containing the prediction function and a summary function. The prediction function will be passed the linear predictor as a single argument and should return a vector of predicted values.

Note

See the vignette on population prediction for more details.
Author(s)
Terry Therneau

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